Retinoid X recepto Novel human polynu

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Kaposi's sarcoma-a KSHV LUR DNA (nucl KSHV long unique c

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Human adenosine Al Nucleotide sequenc

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DNA clone pCEK

Human secreted pro FLGA insert stabil Human colon cancer

Nephila clavipes

N.clavipes draglin

Nephila clavipes

AAV23250 AAZ38196

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N. clavipes spider Epstein Barr Virus Partial mouse WRN

N.clavipes draglin

AAQ14183 AAZ38195

Nephila clavipes s N. clavipes spider

ALIGNMENTS

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Human gene signatu

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Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antivaral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidsm; SCID; AIDS;
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AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatoriopic; vulnerary; antiparkinsonian; nootropic; neuroprotective; costeopathic; antiparkinsonian; nootropic; neuroprotective; costeopathic; antiparkinsonian; nootropic; neuroprotective; costeopathic; antiparkinsonian; immunosuppressant; immunosimulant; cardiant; thrombolytic; coapulant; vasotropic; antidiabetic; hypotensive; dermatchological; immunosuppressive; antidiabetic; hypotensive; dermatchological; immunosuppressive; antidiabetic; hypotensive; dermatchological; immunosuppressive; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis; graft vs host disease, cardiovascular disease, diabetes mellitus, hypothyroidism, cholesterol ester storage, systemic lupus crythematosus, severe combined immunodeficiency (SCID), AIDS, viral, allergies, aplastic anneania, burns, wounds, bone and cartilage damage, competurial not fungal infection, malarial autonic mocturial or fungal infection, malarial autonic mocture and and cartilage damage, competure and and cartilage damage, competure and cartilage and cartilage and cartilage and cartilage and cartilag
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proteins, called parcreatic cancer antigens, given in AAB54008 to
AAB5466. The human pancreatic cancer antigens have cytostatic.
CAAB5466. The human pancreatic cancer antigens, and can be used in gene therapy. The polynucleotide and proteins can be used for preventing, treating, or ameliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the proteins can be identified. The pancreatic anscer antigens can be used to detect, treat or prevent pancreatic disorders, especially cancer.
CAAD015ts and antagonists to the antigens can be used to design nucleic acid hybridisation probes that can be used in chromosome mapping, linkage and hybridisation probes that can be used to generate antibodies and diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including both in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to generate antibodies both in vivo and in vitro diagnostic and therapeutic methods. The proteins cancer neutral, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal or proliferative disorders. AAC99222 to AAC99240 and AA
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                                                                 to AAC99231 encode the human pancreatic cancer
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ophthalmological, nephrotropic, cytostatic, hepatotropic, antiarteriosclerotic, antiarthritic, antirheumatic activity and can be used for gene therapy. The nucleic acid sequences may find use as tools to identify agents against anglogenic diseases. The polypeptides may be used in medicaments for gene therapy to treat anglogenic diseases. (I) in sense or antisense form may be used. The genomic genes may also be used with suitable promoters and/or enhancers. The sequences (nucleic acid and proteins) may be used to treat psoriasis, arthritis, especially theumatoid arthritis, haemangloma, majofibroma, eye diseases, especially diabetic retinopathy, neovascular glaucoma, kidney disease, such as glomerulonephritis, diabetic nephropathy, malign nephrosclerosis, thrombotic microangipathic syndrome, transplantation rejection and plomerulopathy, fibrotic disease, such as liver cirrhosis, mesangial cell proliferative disease, arteriosclerosis and injury to nerve tissue.
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                                                                                                                                                                                                                                      Score 898.4; DB 21; Length 956; Pred. No. 2e-144;
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                                                                                                                                                                                                 Sequence 956 BP; 192 A; 288 C; 287 G; 189 T; 0 other;
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G; 189 T; 0 other;

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Sequence 956

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Proliferation-associated protein; differentiation-associated protein; BST; expressed sequence tag; endothelial cell; anti-antiogenic; antiposenic; anti-arthritic; antiflatoric; hepatotropic; antiflatteriosclerotic; nephrotropic; antidiabetic; ophthalmological; antimunosuppressive; neuroprotective; gene therapy; psorlasis; arthritis; hemangloma; diabetic retinopathy; glomerulon ephritis; liver cirrhosis; transplant rejection; arteriosclerosis; nervous tissue injury; human; sa;
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          8465 atgogtattctgtgggcgccatttgcgcagggtggtggtgttctgtcatttacacacgtc
 tgctcg-tcacgcccgctgtgtcctccct-ccctcccttccttgggcagaatgaattcg
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This invention describes novel nucleic acid sequence (I) obtained from an endothelial cell comprising any of 59 sequences (defined and given in the specification), its allelic variant, or complement. The products of the invention have anti-angiogenic, angiogenic, antipsoriatic, anti-arthritic, antifibrotic, antiarteriosclerotic, nephrotropic, antidiabetic, ophthalmological, hepatotropic, immunosuppressive and neuroprotective activity. (I) are implicated in differentiation and proliferation of endothelial cells. (I) are used for expression of polypeptides (IV) that are useful for identifying agents (A) for treatment of angiogenic disease, to express (IV) from gene therapy vectors for treatment of such diseases and as antisense reagents. (IV) are also used to raise specific antibodies. Angiogenic diseases that may be treated include psoriasis, arthritis, hemangioma, diabetic retinopathy, glomerulonephitis, transplant rejection, liver cirrhosis, arteriosclerosis and injuries to nervous tissue. AAA98102-A98161 represent proliferation-associated and differentiation-associated EST (expressed sequence tag) derived sequences which are described in the method of the invention.
Nucleic acid sequences from human endothelial cells, useful for getherapy of anglogenesis and for identifying antianglogenic agents
                                                                                                                                                                                  Claim la; Page 95; 115pp; German.
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Pilarsky

B,

Hinzmann

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WPI; 2000-572267/53

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Score 898.4; DB 21;
Pred. No. 2e-144;
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Pred. No. 1.7e-98;
0; Mismatches 524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7780 BP; 2314 A; 1974 C; 1896 G; 1593 T;
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                                                                                                                                                     Human; HNRCR; nuclear receptor coreceptor;
                     BP.
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                   CDNA; 7780
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Matches 1029; Conservative
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                                                                                                                     HNRCR nucleotide sequence
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P-PSDB; AAB12454.
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            ENG CO LTD SHANGHA
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                                                                                                                   nuclear receptor coreceptor;
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                                                             BP.
                                                                                                    Human HNRCR encoding cDNA SEQ
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                                                            AAA60629 standard; cDNA; 7900
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Matches 1013; Conservative
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                                                                              aaggtgtaccatgagaacatcaagacaaccaggtgatgaggaaaaactcattttattt
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The present sequence is one of 3351 sequences in a library of human polynucleotides. The library is used to detect differentially expressed dense correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotide and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polynucleotides and their gene products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and preventive interventions. The polynucleotides, polypeptides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Innis MA, Garcia PD, Klinger J, Kassam A;
Kennedy GC, Pot D, Lamson G, Drmanac R;
Dickson M, Labat I, Leshkowitiz D;
LW, Strache-Crain B;
 tggtcggccatcgcccggatggtgggctccaagactgtgtcgcagtgtaagaacttctac 1960
                               1686 tgggcagcaattgctaaaatggtgggaacgaaaagtgaagctcaatgtaaaaacttctat 1745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibodies against them can be used in pharmaceutical compositions to treat the cancers and proliferative disorders such as neoplasia,
                                                               a
Or
                                                                                                                                                                                                                                                                                                                       cytostatic; gene therapy; colon cancer; prostate cancer; cancer; lung cancer; cancer detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Library of polynucleotides for diagnosing a cancerous state of mammalian cell and detecting cancer, particularly of the colon prostate, comprises 3351 human polynucleotide sequences -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 427 BP; 94 A; 143 C; 159 G; 31 T; 0 other;
                                                                                                                                                                                                                                                                                       Novel human polynucleotide, SEQ ID NO: 2976.
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                                                                                                                                                                                       BP.
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dysplasia and hyperplasia.
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, Drmanac S,
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Kita D, Garcia V,
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                                                                                                                 Polynucleotide library used to determine cancerous states of mammalian
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                                                                                                                                                                                                                                 cancer cell line polynucleotide sequence SEQ ID NO:2661
                                                                            accgcagcagcgcccccagtggaggaggaggagaagcagaagcccccgcggctgaggag
                                                                                                                                                                                                                                                                                                                                                                                  Human; colon cancer; tumour; diagnosis; gene expression product; probe; detection; cancerous state; metastasis; identification; breast cancer; oestrogen receptor-positive breast cancer; therapy; oestrogen receptor-negative breast cancer; lung cancer; ss.
                    ccggcccccactgagcccactccggcctctgaagccaccggagcccctacgccccacca
                                      geacccccatcgccctctgcacctcctctgtggtccccaaggaggaggaggaggaggaggag
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, Drmanac S, I
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Crkvenjakov R, Dickson M, Drmanac
Garcia V, Jones LW, Stache-Crain
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                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                      AAA02670 standard; cDNA; 872
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98US-0085537.
98US-0085696.
98US-0105234.
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Reinhard C, Giese K, F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHIR ) CHIRON
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo saptens
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15-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                Human colon
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Gaps

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Length 427;

4.8%; Score 409.4; DB 22; Length 98.6%; Pred. No. 3.3e-61; Live 0; Mismatches 6; Indels

Best\_Local Similarity 98.6 Matches 413; Conservative

Query Match

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Introduction to represent polynuticollines, the present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting and expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
AAA00010 to AAA02716 represent polynucleotides isolated from cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             negative breast cancer, lung cancer, and colon cancer.
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Sequence 872 BP; 345 A; 133 C; 203 G; 185 T; 6 other;

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                                                                                                                                            cagctcatggaggccttggaaaaaaggtggagcgcatcgaaaacaacccgcgccgg 970
                                                                                                                                                                                                                                                                                                                                                                                                  319 aagagaacagcaagaaagatttcag---cgagttgggcagaggggagctggtctttcagc 375
                                                               731 attetggaaggeetggggeeceaggtggagetgeegetgtacaaceageeetecgaeaee 790
                                                                                                                                                                                     ttcaagaagaagaatcacgctcggaaacaatggaagcagaagttctgccagcgctatgac 910
                                                                                                                                                                                                                                                                             cagoticatggaggcatgggagaaaaaagtggacagaatagaaaataatcotoggaggaaa 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gaataatgagaaacaaatgcggcagct-ctcgtgattccacctatgatgtttgatgcaga 494
                                                                                                                         791 cggcagtatcatgagaacatcaaaataaaccaggcgatgcggaagaagctaatcttgtac 850
                                     Gaps
                                                                                           atttttgaaggtcttggcccaaaagttgaactgccactgtataaccagccatcagatacc 78
                                                                                                                                                                                                                                                                                                                         gttcatgcagcatcccaagaactttggcctgatcgcatcattcctggagaggaagacagt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gtttatccagcatccaaaaaactttggactaattgcatcatacttggagaggaagagtgt
                                  9
tch 4.4%; Score 376; DB 21; Length 872; al Similarity 67.7%; Pred. No. 1.8e-55; 578; Conservative 5; Mismatches 265; Indels
   Query Match
                    Best Local
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                               Matches
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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                          5' EST; expressed sequence tag; secreted protein; cDNA isolation; nerapy; chromosome mapping; ss.
735 cagaaggaattatgggaaacgcagaggcagaaaccagcaaattgctcgaccctcgcaaga 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnostic, forensic, gene therapy and chromosome mapping procedures
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.6%; Score 311.2; DB 21;
99.4%; Pred. No. 1.6e-44;
                                                                                                                                                                                                                                                                                                                                                      Human secreted protein 5' EST, SEQ ID NO: 33415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID 33415; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy; chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression and secretion vectors.
                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                       AAC29340 standard; cDNA; 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-FEB-2000; 2000EP-0200610.
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                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                   1569 aggagaaggaaaag 1582
                                                                                                                                                                   855 aaagaaagatgaag 868
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A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 787 "GS" sequences given in AAT1901-T25837 and which is able to hybridse to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of CDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                       181 geograteaccegeteaatggetaatgaggeeaacagegaggaggeeateacceeceage
                                                                              1680 agaaggaggetgtggeetecaaaggeegeaaaactgeeaacageeagggaagaegeaaag
                                                                                                                                                                                                                                                                                                                                                             AAT25693 standard; cDNA to mRNA; 226 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gene signature HUMGS07893.
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The present invention describes a library of human polynucleotides comprising the sequences given in AAZ12532 to AAZ1779. Also described is
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                                                                                                                          caggaccaagggggggggggctgctcg-tcacgcccgctgtgtcctccctccctccctt
                                                                                                                                                                                                                                  ccttgggcagaatgaattcgatgcgtattctgtggccgccatttgcgcagggtggtggta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, gene; gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer;
                                                                                                   ï
                                                                           Length 226;
sequences) as a means of diagnosing abnormal cell function or recognising different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human gene expression product cDNA sequence SEQ ID NO:4382.
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cell types
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Kita D, Labat I;
Randazzo F, Reinhard
                                                                                                                                                                                                                                                                                 8505 ttctgtcatttacacacgtcgttctaattaaaaagcgaattata 8548
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                                       56 T; 1 other;
                                                                          Score 206.2; DB 1
Pred. No. 1.2e-26;
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Escobedo J, Garcia PD, Garcia V, Giese K,
Jones W. Kassam A, Kennedy GC, Kita D, Li
Lamson G, Leshkowitz D, Pot D, Randazzo F,
                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 2075; 2479pp; English.
                                       Sequence 226 BP; 43 A; 65 C; 61 G;
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98US-0072910.
98US-0075954.
98US-0080114.
98US-0080515.
                                                                           2.4%;
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                                                                          Query Match 2.45
Best Local Similarity 97.85
Matches 219; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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24-FEB-1998;
31-MAR-1998;
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W09958675-A2

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cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in AAZ12532 to AAZ17779. The polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polynucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, and in a concern for contains and analyses of the invention are specially exect to contain and analyses of the diagnosis, broancer, breast cancer, and lung cancer. The polynucleotides can also be used to screen for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide analogues and antagonists.
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3, DB 20; Length 789; Indels / Match 2.2%; Score 187.8; DB 20; Local Similarity 72.9%; Pred. No. 2e-23; les 282; Conservative 0; Mismatches 102; Query Match Best Loca Matches

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Gaps

cagatctctaagctgaagaagaagcagcaacagctggaggaggaggctgccaagccgccc 625 685 805 506 aaggaggagctgatccagaacatggaccgcgtggaccgagagatcaccatggtagagcag 565 cagatecttaaactgaaaaagaaacaacaacagettgaagaagaggeagetaaaceteet 296 atcatctacgacgagaaccggaagaaggctgaagctgcacatcggattctggaaggcctg 745 attatttatgatgagaatcggaaaaagcagaagaagctcataaaatttttgaaggtct- 415 474 aacatcaaaataaaccaggcgatgcggaagaagctaatcttgtacttcaagaggagg-aa 864 746 gggccccaggtggagctgccgctgtacaaccagccctccgacacccggcagtatcatgag gagoottgagaagoocgtgtcaccgccgcccatcgagtcgaagcaccgcagcctggtgcag 989 908 237 999 297 357 626 ò g ò g ò qq ò a ò

tcacgctcggaaacaatggaagcagaa 891 535 tcatgccagaaaacaaagggaaccaaa 865 ð g

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AAA01573 standard; cDNA; 300 12 RESULT

AAA01573;

(first entry)

19-MAY-2000

cancer cell line polynucleotide sequence SEQ ID NO:1564 Human colon

Human; colon cancer; tumour; diagnosis; gene expression product; probe; detection; cancerous state; metastasis; identification; breast cancer; oestrogen receptor-positive breast cancer; therapy; oestrogen receptor-negative breast cancer; lung cancer; ss. 

Homo

AAA00010 to AAA02716 represent polynucleotides isolated from CDNA libraries constructed from human colon cancer cell lines. The present libraries describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of J, Innis MA, Garcia PD, Sudduth-Klinger J; Randazzo F, Kennedy GC, Pot D, Kassam A; Crkvenjakov R, Dickson M, Drmanac S, Labat I; Garcia V, Jones LW, Stache-Crain B; Polynucleotide library used to determine cancerous states of mammalian progress of the progress of th iveness of cancer to therapy). This is particularly for breast oestrogen receptor-positive breast cancer, oestrogen receptor negative breast cancer, lung cancer, and colon cancer. Sequence 300 BP; 124 A; 50 C; 64 G; 62 T; 0 other; Claim 1; Page 557; 1097pp; English. 98US-0085426. 98US-0085537. 98US-0085696. 99WO-US10602 98US-0105234 98US-0105877 Williams LT, Escort Reinhard C, Glese K, Rar Famson G, Drmanac R, Cr WPI; 2000-126369/11. (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC. responsiveness of 13-MAY-1999; 21-0CT-1998; 27-0CT-1998; 14-MAY-1998; 15-MAY-1998; 18-NOV-1999 15-MAY-1998 cells NAMES OF COLOR OF STREET O

ö 75; Indels Score 155; DB 21; Pred. No. 6.4e-18; ); Mismatches 75; ö 1.8%; Best Local Similarity 72.7 Matches 200; Conservative Query Match

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                                                                                                                                                                                                                                                                                                                                                                                     A cDNA clone (AAT31931) codes for retinoid X receptor interacting protein RTP13 (AAR99798), which is a candidate transcriptional co-activator. It was isolated from a mouse liver cDNA library. The cDNA can be used for the recombinant prodn. of RIP13 in
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                                                                                              Retinoid X receptor interacting protein; RXR; RIP; RIP13;
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Pred. No. 1.4e-15;
                                                                           Retinoid X receptor interacting protein RIP13
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2..1861
/*tag= a
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                   BP.
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52.58;
                 AAT31931 standard; DNA; 1922
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Best Local Similarity 52.5
Matches 435; Conservative
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P-PSDB; AAR99738.
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nson G, Drmanac R;
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or
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Leshkowitiz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human polynucleotide, SEQ ID NO: 3293.
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99US-0142311.
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WO9913886-A1

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The present sequence is one of 3351 sequences in a library of human polynucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used correlated probes for detection of mRNA and to produce probes for detection of mRNA and to produce additional copies of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotide and for detection of transcription levels. Ribozymes the polynucleotide and for detection of transcription levels Ribozymes their gene products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and antibodies against them can be used in pharmaceutical compositions to treat the cancers and be used in pharmaceutical compositions to the acceptance of the proposition of the proposi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          720 ctgcacatcggattctggaaggcctggggcccaggtggagctgccgctgtacaaccagc 779
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Pred. No. 8.6e-14;
0; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 342 BP; 135 A; 57 C; 81 G; 68 T; 1 other;
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                         Claim 9; Page 1037; 1046pp; English.
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ID AAX53491 standard; DNA; 114955 BP.
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Initiation against at read and the juxta-section between codding and non-codding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between codding and non-codding regions and all segments of RNAs encoding proteins associated with one corresponding for ageneres AAX55272-74. These multiple target of general from sequences AAX5527-74. These multiple target oligonucleotides (specifically AAX5180-271) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded conditation, respiration pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (GoPD), and cancers such as leukemias, tymphomas, carcinomas e.g. colon cancer, breast cancer, melanoma, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastasized to the lungs, including breast and prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The specification describes antisense oligonucleotides (AAX52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and
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                                                                                                                                                                                                                                                                                                                                                                                                        New antisense oligonucleotides used in treatment of, e.g. pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T; 21427 other;
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Db 110365 CNNHNNNSGGGCGGGGGGGCCCCCNNHNNNSCGGGCGCGCGCGCGCCCCNNHNNNSGCG 110306 Db 110305 GCCGCCGCGCGCCCCNNHNNNSGCGGGCGCGCGCGCGCGCCCCNNHNNNSGCCACGA 110246 110185 NNNSGCCACGACGAGCVCNNHNNNSGCCACGAGGAGCVCVNNHNNNSGCCACGACGAGGV 110126 Db 109945 CVCVVCGCCGACNNHNNNSCVVCGCCGACCNNHNNNSVCVVCGCCGACCNNHNNNSCVCV 109886 Db 110776 GCGAGCCCGACVGGGCCGACGCCGACGCCCCNNHNNNSGGGCCCGGGCCCVGCCGCVCCC 110717 DD 110716 CGCCNNHNNNSCCCGGCGCCCCGCGCCCCNNHNNNSGGCGGCGGCNNHNNNSGGCG 110657 DD 110656 GGCGCGNNHNNNSGCCGGCGCGCCCNNHNNNSGGCGGGCGCCCCGNNHNNNSGGCGGGC 110597 GGCGCGGNHHNNNSGGCGGCGCGCGCGGNHHNNNSGGCGGCGCGCGCGCGGGNHNNNSG 110537 110245 NNHNNNSGCCACGACGAGGNHNNNNSGCCACGAGGAGCNNHNNNSGCCACGACGAGGAGCVNNH 110186 110065 CCACGACGAGGACCVCVCGCNNHNNNSGCCACGAGGCCVCVVCGCCNNHNNNSGCCACGAC 110006 Db 110956 GCAGCCCNNHNNNSCCCCGCGCCCGGCCCCGGGAGNNHNNNSTCGCCGGAGCCGC 110897 GCGCAGCAGCACCONNHNNNSGCCGCACCGCCACCCCCCCCCNNHNNNSGCCCCC 110837 GCGGGCGCGCGGGGCNHNNNSGGCGGGCGCGCGCGCGCCNNHNNSGGCGGGCGCGCGC 110477 110476 GGGCCCUNHNNNSGCGCGGGCCCCNNHNNNSGGCGCGGGGCCCCNNHNNNSCGGCGCG 110417 agtecatgagecececegggaggacgeageteceaceagecagetececeage 3000 3241 tggtcacccactgcccctgggcctccatgacactgcccggcccgtcctgccgcgccacc 3300 2703 gcagggccaccactgccaagagctcgggcgcccccaggacagcgactccagtgctacct 2762 gccaccycaaaaacctycayccyyayaygcyacyccctcaycaycctyycaycaycccccy 3060 gaagetgeetgggggacccccttgetggacttccggcctgcccttccccgtgccccccg 3180 caccatctccaacccgcctccctctctctgccaagcaccccagcgtcctcgagag 3360 3421 tgccaaggccccggtggccctgtcaccatggggctgccctgcccatggaccccaaaaa 3480 3541 accggagagcctgggggtgcccacagcccaggaggcgtccgtgctgagagggacagctct 3600 3601 gggctcagttccgggcggaagcatcaccaaaggcattcccagcacacgggtgccctcgga 3660 ---agggcaccatcaccaggatcatcggcgaggacagcccgagtcgcttggaccgcggcc 3776 actggacctgaagcagctgaagcagcgagcggctgccatccccccatccaggtcaccaa 2821 aaggeccagectecteacecegaetggegaececegggeeaatgeeteaceceagaagee DD 110836 GCAGGVGCGCCGVGCGCNNHNNNSCGCGCCCGGGCVGVVVGCCCGCGCGNNHNNNSGC gggcaagagcaggcacccccgccgacaaggaggccttcgcagccgaggccca Db 110416 GGGCCCCNNHNNNSGCGGCGCGGGGGC------CCCNNHNNNSGGCGGGGGGGGGCCCC gcaaataggtgccatctcccaaggaatgtcggtccagctccacgtcccgtactcagagca gctggcacccttcagcggagtgaagcaggagcagctgtccccacggggccaggctgggcc 110005 GAGCYCVYCGCCGNNHNNNSGCCACGACGAGCYCVYCGCCGANNHNNNSGCCACGACGAG gcagtgcagacgaggtggatgaggccg--aggggcgacaagaaccggctgctgtcccc tyangtyatcaaggcctcccgcatgccccggacccctcagccttctcctacgctccacc cagogocatcacatacogogotcoatcacocoaoggoaogocagotgacgtoctgtaca-2763 3181 3301 3121 3481 3661 Db 110596 3361 3720 g ò ŏ ò ö õ ò qq õ à ŏ ò ò qq õ g ò g a õ g δ õ

DD 109765 GACCNNHNNNSGACGAGCVCVVCGCCGACCNNHNNNSCGACGACCVVVCGCCGACCNNH 109706 109585 NSGGCCGCCGCCCCNNHNNNSGGGCCCCVAGNNHNNNSGGGGCCCCVAGCNNHNN 109526 109405 GCCNNHNNNSGGGGCCCVAGGCGAGCANNHNNNSGGGCCCVAGGCGAGCCAGNNHNNN 109346 109105 HNNNSGGGGCCCCVAGGCGAGGCCAGGCCGCCGNNHNNNSGGGGCCCCVAGGCGAGCCAGG 109046 109705 NNNSACGACGAGGACCVAVCGCCGACCNHINNNSCACGAGGVCVVVCGCCGACCNHINN 109646 SGGGCCCCVAGCCNNHNNNSGGGCCCVAGGCGNNHNNNSGGGCCCCVAGGCGANNHNNN 109466 109345 SGGGCCCVAGGCGAGCCAGGNHNNNSGGGCCCVAGCCGAGCCAGGCNHNNNSGGGG 109286 SGGGCCCCVAGGCGAGNNHNNNSGGGCCCCVAGGCGAGCNNHNNNSGGGGCCCVAGGCGA 109406 109285 CCCVAGGCGAGCCAGCCGNHNNNSGGGGCCCVAGGCGAGCCAGCCCNHNNNSGGGC 109226 109165 GGCCCVAGGCGAGCCAGGCGCCCCNNHNNNSGGGGCCCVAGGCGAGCCAGGCGCCCCCNN 109106 109045 CGCCGCCGCNNHNNNSGGGCCCCVAGGCGAGCCAGGCGCCCCCCNNHNNNSGGGGCCC 108986 CCCNNHNNNSGGGGCCCVAGGCGAGCCAGGCGCCGCCGCCCCNHNNNSGGGGCCCVAG 108866 gacacagcccccaccacctcaaagagcagcaccacatccgcgggtccatcacacaaggga 4076 4484 -----aggaggeggecgetecatecatgagatecegegaggaggetgegge 4304 acacycccyayctycccctygyccccycyccyctcaaygaygyctccatcacycaygyca 4364 ccaycayctcggggggctccattgcgcgcggcgccccggtcattgtgcctgagctgggta 4604 agccgcggcagagccccttgacctatgaggaccacgggggcaccctttgccggccacctcc 4664 cgtccagcaaggcatcccaggaccgaaagctgacgtcgacgcctcgtgagatcgccaagt 4784 cacgaggttcgcccgtgaccatgcgggagcccacgccgcgcctgcaggagggcagccttt 4724 4845 ttcgggggggtgagtggggcgtggacctgtatcgcacatccccctggccttcgacccca 4904 Db 109645 sccacGacGacGaCCCGacCNNHNNNSGCCACGACGACCVCVCGCGGACCNNHNN CCVAGGCGAGCCAGGCCCNNHNNNSGGGGCCCVAGGCGAGCCAGGCGCCGNNHNNNSGG 4485 acgcccgggcactggaacgtgcctgctacgaggagactgaagagccggccagggaccg cctatgagggtggcatgtctgtgacccagtgctccaaggaggacggcagagcagctcag 109825 AGCVCVVCGCCGACCNNHNNNSCGAGCVCVVCGCCGACCNNHNNNSACGAGCVCVVCGCC gacccccccatgagacggccgccccaagcgcacctatgacatgatgagggccgcgtgg teceteggtectacgtggaggcacaggaggactacetgcgtcgggaggccaagetectaa agcgggagggcacgcctccgccccaccgccctcacgggacctgaccgaggcctacaaga cgcaggccctgggccccctgaagctgaagccggcccatgagggcctggtggccacggtga gcagagccatctcctcagccagcatcgaaggtctcatgggccgtgccatcccgccggagc ccccgctcaagtacgacaccggcgcgtccaccactggctccaaaaagcacgacgtacgct ccctcatcggcagcccggacgttcccacccgtgcacccgctggatgtgatggccg coccycacagcaccgtgcccgagcaccacaccccatctcgccctatgagcacctgc 4137 4425 4785 109465 4305 4017 109525 4197 108925 ŏ ò ŏ ga δλ q g g ŏ g ò a δ QQ δ g g Q οý ŏ ò

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Db 108629 CCNNHNNNSAGGCGCCGCCCCCCCCCNNHNNNSCAGGCGCCGCCCCCCCCCCCCNHNN 108570
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Sequence 1, Ap Sequence 1, Ap Sequence 1, Ap Sequence 17, A Sequence 5, Ap Sequence 5, Ap

Sequence 5, Appli Sequence 5, Appli Sequence 4, Appli Sequence 4, Appli Patent No. 5482709

Sequence 6, Appli Sequence 6, Appli Sequence 23, Appl Sequence 78, Appl

ALIGNMENTS

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LENGTH: 1922 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CITY: Boston
STATE: MA
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US-08-372-652-9
  ; Search time 177.51 Seconds (without alignments) 9140.813 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd
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Perfect score:
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Maximum DB
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                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                             Run on:
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Sequence 9, Application US/08372652
Patent No. 593269
GENERAL INFORMATION:
APPLICANT: Moore, David
APPLICANT: Seol, Wongi
APPLICANT: Chol, Hueng-Sik
TITLE OF INVENTION: RETINOID X RECEPTOR-INTERACTING
TITLE OF INVENTION: POLYPEPTIDES AND RELATED MOLECULES AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street, Suite 3100
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Pred. No. 2.7e-17;
0; Mismatches 375; Indels 1
                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA

ZIP: 02110-2804
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OSFTANKS SYSTEM: PC-DOS/MS-DOS
SOFTWARP: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/372,652
FILING DATE: 13-047810:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 30,162
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TELECOMMUNICATION INFORMATION:
TELEFHONE: 617/542-5070
TELEFAX: 617/542-8966
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 9:
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Sequence 9, Application PC/TUS9516311
Sequence 9, David
APPLICANT: Moore, David
APPLICANT: Seol, Wongi
APPLICANT: Choi, Hungy Sik
TITLE OF INVENTION: RETINOID X RECEPTOR-INTERACTING
TITLE OF INVENTION: POLYPEPTIDES AND RELATED MOLECULES AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street, Suite 3100
                                                                                                                                                                                                                                                                           1156 TAAATCAAAGAAACAGGAAATTTTTCGTAAGTTGAACTCTTCTGGTGGAGGTGACTCTGA
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STATE: MA
COUNTRY:
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                                                          Version #1.30
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Pred. No. 2.7e-17;
0; Mismatches 375;
                                                                                                                                                                                                                                                                                                                               00786/246001
COMPUTER: IBM PC_COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16311
FILING DATE:
                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/372,652
FILING DATE: 13-JAN-1995
ATTORNEY/AGNT INFORMATION:
NAME: CLARK, PAUL T.
                                                                                                                                                                                                                                                                    NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00
                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.7%;
Best Local Similarity 52.5%;
Matches 435; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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1687 CCCTTACAACCCTCTGACCATACGGATGCTCAGCAGTACACCACCTACACAGATCGCATG 1746
                                                                                                     7447 gggcctccccgcggggagc---gggcccctcgctggcccccaccacgcctgggacgagga 7503
                                                                                                                                  1747 CGCCCCATCTGCCATCACCCAAGCAGCTCCACAACAACAGAACCGCATCTGGGAGAGGGA 1806
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                                             cocctacaacccctgatcatgcggctgcaggcgggtgtcatggcttccccaccccacc
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                                                                                                                                                                                  APPLICANT: Bohenky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Immediate Early Protein From Kaposi''
TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
TITLE OF INVENTION: Encoding Same And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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PatentIn Release #1.0, Version #1.30
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Pred. No. 4.8e-11;
0; Mismatches 792
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STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/728,323A
                                                                                                                                                                                                                                                                  Sequence 1, Application US/08728323A Patent No. 5948676 GENERAL INFORMATION:
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
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MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 3489 base pairs
TYPE: nucleic acid
STRANDEDNESS: sindle
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                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 435
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STATE: New York
COUNTRY: U.S.A.
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US-08-728-323A-1
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2420 AGGAGCAGGAGTTAGAGGAGCAGGAGCAGGAGTTAGAGGAGCAGGAGCAGGAGTTAGAGG 2479 1886 AGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATG 1945 1946 AGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATG 2005 2006 AGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGGAGGATGAGCAGCAGCAGGATG 2065 2066 AGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGGAGCAGGATGAGCAGGAGCAGC 2125 acgaaaagcagttccctgagatccgcaagcagcgcgagctgcaggagcgcatgcagagca 1058 gggtgggccagcgggggcagtgggctgtccatgtcggccgccgcagcgagcacgaggtgt 1118 2180 ATGAGCAGCAGCAGCAGGATGAGCAGCAGCAGCAGGATGAGCAGCAGCAGCAGGATGAGC 2239 cagagatcatcgatggcctctcagagcaggagaacctggagaagcagatgcgccagctgg 1178 cogigatecegeceatgetgaegetgaeeageageagegeateaagtteateaaeatga 1238 2300 AGGAGTTAGAGGAGCAGGAGCAGGAGTTAGAGGATCAGGAGCAGGAGTTAGAGGAGCAGG 2359 acgggcttatggccgaccccatgaaggtgtacaaagaccgccaggtcatgaacatgtgga 1298 1299 gigagoaggagaaggagacoticogggagaagitoaigoagoaicocaagaacitig--- 1355 1412 CACAGCAGCAGAGCCACAGCAGCAGGAGCCCTGCAGGAGCCACAACAGCAGGAGCCAC 1471 AGCAGCAGGAGCCCTGCAGGAGCCACAACAGCAGGAGCCACAACAGCAGGAGCCACAGC 1531 AGCAGGAGCCACAGCA----GCAGGAGCCACAGCAGCAGCAGCACCACAGCAGCAGGAGC 1585 1826 AGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGCAGGATG 1885 579 tgaagaagaagcagcaacagctggaggaggaggctgccaagccgcccgagcctgagaagc 638 agaaccggaagaaggctgaagctgcacatcggattctggaaggcctgggggccccaggtgg 758 aagacctcaccaaggaccgtagcctgacgggcaagctggaaccggtgtctccccccagcc 458 tccagaacatggaccgcgtggaccgagagatcaccatggtagagcagcagatctctaagc 578 agetgeegetgtacaaccageetteegacacceggeagtateatgagaacateaaaataa 818 tgcctgaccccctgctgcgaccgtcaccctgctggccacgggccagcctgcgggatctg 398 ccgtgtcaccgcccatcgagtcgaagcaccgcagcctggtgcagatcatctacgacg accaggcgatgcggaagaagctaatcttgtacttcaagaggaggaatcacgctcggaaac tggagcgcatcgaaaacaacccgcgccggcgggccaaggagagagcaaggtgcgcgagtact 2126 AGGATGAGCAG-----GAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGG ccccgcacactgaccctgagctggagctggtgccgccacggctgtccaaggaggagctga aatggaagcagaagttctgccagcgctatgaccagctcatggaaggccttggaaaaaagg AGCAGGAGTTAGAGGAGCAGGAGCAGGAGTTAGAGGAGCAGGAGCTTAGAGGAGC

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2720 AAGAGCAGGAGCAGCAGGAGTTAGAGGAGGTGGAAGAGCAGGAGCAGCAGGGGGTGGAAC 2779
  ---gcctgatcgcatcattcctggaggaggaagacagtggctgagtgcgtcctctattact 1412
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                                         2480 ACCAGGAGCAGGAGTTAGAGGAGCAGGAGCAGGAGTTAGAGGAGCAGGAGGTGGAAGAGC
                                                                                         acctgactaagaagaatgagaactataagagcctggtgagacggagctatcggcgccgcg
                                                                                                                           2540 AAGAGCAGGAGGTGGAAGAGCAAGAGCAGGAAGAAGAAGAGGAAGTTAGAGGAGGTGG
                                                                                                                                                                         PatentIn Release #1.0, Version #1.30
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APPLICANT: Bohenzky, Roy A.
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Gellman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: POLYPEPTIDES FROM KA
TITLE OF INVENTION: PERPESVIRUS, DNA BNC
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
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SYSTEM: PC-DOS/MS-DOS
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TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-05.25
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
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ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Length 32207;

DB 2;

Score 107.8; DB 2; Pred. No. 8.3e-11;

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Query Match Best Local Similarity

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                                    agcccgggaatgaacggtcccaggagctccacctgcggccagagtcccactcatacctgc 278
                                                                                                            ccgagetgggggaagtcagagatggagttcattgaaagcaagcgccetcggetagagetgc 338
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792;
Mismatches
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Conservative
Matches 631;
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1299 gigagcaggagaaggagccttccgggagaagttcaigcagcaicccaagaactitg---
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APPLICANT: BOHDENZKY, ROY A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Gelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS TITLE OF INVENTION: SEQUENCES AND USES THEREOF WUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/757,669.
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Patent No. 6183751
GENERAL INFORMATION:
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NAME: White, John P.
REGISTATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4518:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 278-040
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: New York
COUNTRY: U.S.A.
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                                           Gaps
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Ouery Match 1.3%; Score 107.8; DB 4; Best Local Similarity 43.8%; Pred. No. 8.3e-11; Matches 631; Conservative 0; Mismatches 792;
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                                  1239 acgggcttatggccgaccccatgaaggtgtacaaagaccgccaggtcatgaacatgtgga 1298
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APPLICANT: Lao, Ying
APPLICANT: Hang, Betty
APPLICANT: Payan, Don
TITLE OF INVENTION: Mammalian Protein Interaction Cloning
TITLE OF INVENTION: System
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rclease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,863
FILING DATE: 30-MAR-1998
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ATTORNET SALVA, ROBID M.
NAME: SALVA, ROBID M.
REGISTRATION NUMBER: 38,304
REFRENCE/DOCKET NUMBER: A-656
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 949-8711
INFORMATION FOR SED ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2580 base pairs
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ZIP: 94111-4187
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APPLICANT: Horlick, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes TITLE OF INVENTION: From Multiple Transfected Episomes FILE REFERENCE: 0867/ID903US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
                                                                                                                                           Indels
                                                                                                      Score 96.2; DB 3;
Pred. No. 5.6e-09;
0; Mismatches 353;
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                                                                                                        1.1%;
                                                                                                        Query Match 1.1
Best Local Similarity 48.2
Matches 331; Conservative
                unknown
                               MOLECULE TYPE: DNA
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STRANDEDNESS:
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                                   ; MOLECULE T
US-09-050-863-2
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Emeryville California

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                                                                                                      Length 5452;
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APPLICANT: Zuckermann et al.
TITLE OF INVENTION: Compositions and Methods for TITLE OF INVENTION: Polynucleotide Delivery NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
                                                                                                    1.1%; Score 96.2; DB 2;
Similarity 48.2%; Pred. No. 6.7e-09;
31; Conservative 0; Mismatches 353;
SOFTWARE: FastSEQ for Windows Version 3.0
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                                   ; TYPE: DNA
; ORGANISM: VEBNA
US-09-130-114-1
                                                                                                    Query Match
Best Local Simil
Matches 331; C
          SEQ ID NO 1
LENGTH: 5452
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US-08-910-647-1
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STREET: 4560 Horton Street

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                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,647
                                                                                                                                                                                                                                               1218.002
                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/CDCKET NUMBER: 1218
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
                                                                IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                           TELEFAN. (510) 655-3542
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                  LENGTH: 9600 base pairs
                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: sing
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N: U.S.A. 94608-2916
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Matches 331; Conserv
                                                                                                                                                       FILING DATE:
CLASSIFICATION:
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COUNTRY:
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2076 aggaggetgeattecegecegtggtggaggatgaggagatggaggegtegggegtgageg 2135
                              1476 agagecageageacaacaacageageageageageageageageageageageageageege 1535
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                                                                                                                                                                                                                            APPLICANT: Godowski, Paul J. Lokker, Nathalie A. Mark, Melanie R. TITLE OF INVENTION: SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS NUMBER OF SEQUENCE: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
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Pred. No. 7.9e-09;
0; Mismatches 353; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                             2136 gaaatgaggagagatggtggaggg 2162
                                                                                             1365 AGCAGGAGGGGCCAGGAGCAGGAGG 1391
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/884,811
                                                                                                                                                                              Sequence 15, Application US/07884811
Patent No. 5316921
GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 48.29
Matches 331; Conservative
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REGISTRATION NUMBER: 3
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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TYPE: NUCLEIC ACID
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US-07-884-811-15
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GENERAL INFORMATION:

APPLICANT: Godowski, Paul J. Lokker, Nathalie A. Mark, Melanie R.
TITLE OF INVENTION: HEPATOCYTE GROWTH FACTOR PROTEASE DOMAIN VARIANTS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STREET: California
1716 ccaacagccagggaagacgcaaaggccgcatcaccgctcaatggctaatgaggccaaca 1775
                                               2480 GGAGGGGCAGGAGCAGGAGGAGGGCCAGGAGGGCAGGAGCA-GGAGGAGGGCCAGGAGG 2538
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FR PC-DOS/MS-DOS
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19920518
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; Patent No. 5328837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: patin (Generach)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885
FILING DATE: 19920518
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/OOCKET NUMBER: 779
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/25-3216
TELEFA: 415/95-981
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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TYPE: NUCLEIC ACID
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US-07-885-971-15
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TELEFAX: 415/952-9881
TELEX: 910/371-7168
INPORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
LENGHH: 10596 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.1%;
Best Local Similarity 48.2%;
Matches 331; Conservative (
                                                                                                                                                                                                                                                                                                                                                      415/952-9881
 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Linear
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TOWNER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUWTRY: USA

ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1956 tetaetteaaetaeaagaagaaggeagaaeetegatgagatettgeageageaeagetga
                                                                              Score 96.2; DB 1; Length 10596;
Pred. No. 7.9e-09;
0; Mismatches 353; Indels 3;
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                                                                                  Ouery Match 1.1%;
Best Local Similarity 48.2%;
Matches 331; Conservative
STRANDEDNESS: single
               ; TOPOLOGY: linear
US-07-885-971-15
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US-08-087-783A-15
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1536 tgccccgcagcagccaggaggagaaaagatgagaaaggagaaaggaaaaggagagagaagg 1595
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Pred. No. 7.9e-09;
0; Mismatches 353;
vE: 3.5 inch, 1.44 Mb floppy disk
IBM PC compatible
                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,783A
FILING DATE: 13-U1-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/884811
FILING DATE: 18-MAY-92
PRIOR APPLICATION NUMBER: 07/885971
FILING DATE: 18-MAY-92
ATTORNEY GENT INFORMATION:
NAME: MASCRAMY DATA:
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: 35,600
REFERENCE/DOCKET NUMBER: 90755779P1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         P0755779P1
              COMPUTER: IBM PC COMPALLALL
OPERATING SYSTEM: PC-DOS/MS-DOS
COFFWARE: WinPatin (Genentech)
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SEQUENCE CHARACTERISTICS:
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APPLICANT: GOGOWSK1, Paul J. Lokker, Nathalie A. Mark, Melanie R.
TITLE OF INVENTION: SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                2076 aggaggetgeattecegecegtggtggaggatgaggaggatggaggegteggegtgageg
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48.2%; Pred. No. 7.9e-09;
tive 0; Mismatches 353; Indels 3;
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: DEAD FOR SOFTWARE:
COMPUTER: DATIN (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 09-FEB-1994
                                                                                                                 2136 gaaatgaggagagatggtggaggagg 2162
                                                                                                                                                 2899 AGCAGGAGGAGGGCAGGAGCAGGAGG 2925
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Patent No. 5580963
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PRIOR APPLICATION DATA:
PAPPLICATION NUMBER: 07/884811
FILING DATE: 18-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gallegos, R. Thomas
REGISTRATION NUMBER: 32,692
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELERAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 331; Conservative
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US-08-194-088B-15
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Sequence 15, Application US/08194087
Patent No. 5879910
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J. Lokker, Nathalie A. Mark, Melanie R.
TILLE OF INVENTION: HEPATOCYTE GROWTH FACTOR PROTEASE DOMAIN VARIANTS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
2422 GGCAGGAGGGCAGGAGGAGGAGGGCCAGG--AGGGGCAGGAGGGCAGGAGCAGGA 2479
                                                                                  ccaacagccagggaagacgcaaaggccgcatcacccgctcaatggctaatgaggccaaca 1775
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                                                                                                                               2480 GGAGGGCCAGGAGCAGGAGGAGGGCCAGGAGGAGCA-GGAGGAGGGCCAGGAGG
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,087
FILLING DATE: 18-MAY-1992
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
TELEX: 910/371-716
INFORMATION FOR SEQ ID NO: 1
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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1956 tctacttcaactacaagaagaggcagaacctcgatgagatcttgcagcagcacaagctga
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TELEPHONE: 415/225-3216
                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                         TELERA: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: NUCLEIC ACID
STRANDEDNESS: single
                COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 in
                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                             COMPUTER: IBM POPERATING SYSTEM
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PCT-US93-04648-15
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NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Genericch, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 10596,
                                                                                                                                 0; Mismatches 353; Indels
                                                                                                    1.1%; Score 96.2; DB 2; 48.2%; Pred. No. 7.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2136 gaaatgaggaggagatggtggaggagg 2162
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                                                                                                                                 Matches 331; Conservative
LENGTH: 10596 bases
TYPE: nucleic acid
STRANDEDNESS: single
US-08-194-087-15
                                                                                                                    Best Local Similarity
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                                                                                                      Query Match
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1896 gcaactggtcggccatcgcccggatggtgggctccaagactgtgtcgcagtgtaagaact 1955
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1.1%; Score 96.2; DB 5;
Best Local Similarity 48.2%; Pred. No. 7.9e-09;
Matches 331; Conservative 0; Mismatches 353;
3: 5.25 inch, 360 Kb floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                       SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04648
FILING DATE: 19930517
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/884811
FILING DATE: 18-MAY 92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/885971
FILING DATE: 18-MAY 92
ATTORNEY/AGENT INFORMATION:
NAME: DISSERTION NUMBER: 07/885971
REGISTRATION NUMBER: 07/885971
REGISTRATION NUMBER: 07/885971
REGISTRATION NUMBER: 07/885971
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GENERAL INFORMATION:
APPLICANT: Horlick, Robert A.
APPLICANT: Horlick, Robert A.
APPLICANT: Banad, Bassam B.
APPLICANT: Bundad, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/1D903US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT APPLICATION NUMBER: 19500/6
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.1%; Score 90; DB 2; Length 1931; 54.1%; Pred. No. 6.8e-08;
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Patent No. 5976807
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Best Local Similarity 54.1%
Matches 183; Conservative
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; ORGANISM: EBNA
US-09-130-114-2
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US-09-130-114-2/c
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em\_esthum14: em\_esthum16: \* em\_esthum18:

em\_esthum26

em\_estin4

em\_estov2

em\_estov1

em\_estpl3

em\_estp14

em\_estpl7

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
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Perfect score:
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em\_estpl10

em\_estro3

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gb\_est43: gb\_est44: gb\_est45: gb\_est46: gb\_est46:

gb\_est41: gb\_est42:

gb\_est32

gb\_est31

gb\_est110:\*
gb\_est111:\*
gb\_htc:\*
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em\_gss\_hum1:\*
em\_gss\_hum2:\*

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em\_gss\_pro2:\*
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em\_gss\_rod2:\*
em\_gss\_rod3:\*

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1172   17   17   17   17   17   17   17	0000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

9b\_gss28:\*
9b\_gss29:\*
9b\_gss30:\*
9b\_gss31:\*
9b\_gss31:\*
9b\_gss32:\*
9b\_gss34:\*
em\_gss\_inv4:\*
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Email: cgapt Tissue Proct CDNA Libran CDNA Libran CDNA Cone distr Cone distr found throughttp://image Plate: LLAM High quality FEATURES Source 1.	/ ADD COLOR TO BE A DOLLE OF THE BASE COUNT 188 a DOLLE OF THE BAS	Query Best Match 32 33	DD 91 TCTGCCAAGCACCC QY 3392 gtccagctccacgt DD 121 GTCCAGCTCCACGT QY 3452 gggctgcccctgcc QY 3452 gggctgccccrgcC QY 3512 cagctgtccccacg QY 3512 cagctgtccccac	Db 241 CAGCTGTCCCACC Qy 3572 gaggcgtccgtgct Qy 3572 gaggcgtccgtgct Db 301 GAGGCGTCCGTGT Qy 3632 ggcattcccagcac	3692 421 3752 481 3812 541
Description BG252161 602366028 BG25257 602365136 BB73487 601588114 BE728145 601563413 BE900740 601673910	BE22916.2 00.2044007 BE291091 601286040 BE391091 601286040 BE390324 602071630 BG117169 602346448 A1830862 wj61b09.x BE795997 601591169 BE764455 601191770 BG301632 602191770 BG301632 60219770 BF058781 7834907.x AR877713 ob11b07.x BR487513 ob11b07.x BR487551 7006641.x AW488580 xx82610.x	A1523558 th08c09.x BE542336 601067079 BE675456 7f09d11.x AW674918 bb30f04.y BF475570 mac46e06. BG119261 602349134 A1373205 qz13h02.x BG420527 602452582 BF062632 7h62h12.x AW674586 bb34f04.y BE839873 Q000-FN018	AA437468 GAGUEGUS S BEE903379 6016/6011 A1499095 to04f05.x BEE4249 60111857 AWB50948 EST363018 A1812033 tw466d3.x A1761007 wh97d05.x A1761007 wh97d05.x BEE27658 602040636 BGG25574 602274985 AA42197 zuga8402.s	AW95613 EST38683 BF528779 602041380 BE548650 601074545	Sapiens CDNA clone IMAGE:4473271 5', sapiens cDNA clone IMAGE:4473271 5', craniata; Vertebrata; Euteleostomi; catarrhini; Hominidae; Homo. ib, Mammalian Gene Collection (MGC) Ph.D.
Length D 876 1087 1787 1700 1111	~	21 136 138 119 149 174 1194 1194	122 102 102 102 102 103 173 173	558 122 AW956613 642 150 BF528779 526 137 BE548650 ALIGNMENTS	H_MGC_90 mRNN H_MGC_90 Homo :12761977 azoa; Chordate eria; Primates 876; /mgc.nci.nih.g tutes of Healt 1999;
% Ouery Match Match 7.9	6330.4 6330.4 6238.2 623.2 619.4 619.8 77.2 609.2 77.1 599.4 77.0 594.8 699.4 700 594.8 699.4 700 594.8 699.4 700 594.8 699.4 700 594.8 699.4 700 594.8 699.4 700 594.8 699.8 700 594.8 699.8 700 599.8 700 700 700 700 700 700 700 700 700 70			503 5	
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/tab_host="bH10B (phage-resistant)
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dr primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NHH MGC Library."
a 322 c 257 g 109 t
cgapbs-r@mail.nih.gov

by Courement: ATCC
ibrary Preparation: Life Technologies, Inc.
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quencing by: Incyte Genomics, Inc.
distribution: MGC clone distribution information can be
through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov
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ality sequence stop: 711.
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DEFINITION

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

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3810 acgaaggcaagaagggccacgtcttgtcctatga-gggtggcatgtctgtgacccagtgc 3868
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                      at-gggccgtgccatcccgccggagcgacacagccccaccaccacagagcagcacca 4050
                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapbz-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM10295 row: h column: 09
High quality sequence stop: 641.
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                       718 ATGGGGCCGTGCCATCCCCGCGGAGGCGAAAAGCCCC--ACACTACAAAGAAGCGGACC- 774
                                                                                                                   601 AAGGAGGACGCCAGAAGCAGCTCACGACCCCCCCATGAGACGG-CGCCCCCAAGCGCA-C 658
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.9%; Score 679.6; DB 175; Length 1087;
89.7%; Pred. No. 2.6e-117;
iive 0; Mismatches 79; Indels 16;
                                                                                                                                                                mRNA sequence.
BG252257
BG252257.1 GI:12762073
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 787)
NIH-MGC http://mgc.nci.nih.gov/. BE793487 787 bp mRNA EST 20-SEP-2000 601588814F1 NIH\_MGC\_7 Homo sapiens CDNA clone IMAGE:3943059 5

BASE COUNT ORIGIN

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242 gagctccacctgcggccagagtcccactcatacctgcccgagctggggaagtcagagatg 301
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AUTHORS
TITLE
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/clone=lin="MIH_MGC_7"
/tissue_type="small cell carcinoma"
/tissue_tone ing; Vector: pOTBF; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5/
adaptor: GGCACGAGGG) Size=selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
87 a 248 c 231 g 121 t
              L Unpublished (1999)
Contract: Robert Strausberg, Ph.D.
Email: cgapbs remail.nh, gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM797 row: 1 column: 04
High quality sequence stop: 762.
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Pred. No. 2.6e-116;
0; Mismatches 28;
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Best Local Similarity 95.5'
Matches 748; Conservative
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/issue_type="melanotic melanoma"
//lab.host="briton proper resistant)
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S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: capabs-rémail.nih.gov

Tissue Procurement: ArcC/ACT/DCTP

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

High quality sequence stop: 716.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                gagttcattgaaagcaagcgccctcggctagagctgctgcctgaccccctgctgcggaccg
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/db\_xref="taxon:9606"
/clone="InAGE:395667"
/clone="InAGE:295667"
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/lab\_host="BHIOB:(phage-resistant)"
/note="Organ: placenta: Vector: pOTBD: Site\_1: XhoI;
Site\_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAGGG). Size-selected >500bp for average insert size 1:8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Callifornia, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM833 row: c column: 04 High quality sequence stop: 698.

Location/Qualifiers
1. 700

source

cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution car

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                                                                              ctgcttaccgttcaagaggcgtgtgcaggccgacagtcggtgaccccatcactcgcagga 8390
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 Score 661; DB 141; Length 700;
Pred. No. 7.6e-114;
0; Mismatches 15; Indels 2
Query Match 7.7%;
Best Local Similarity 97.6%;
Matches 682; Conservative (
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 700)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

AUTHORS TITLE JOURNAL

COMMENT

REFERENCE

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mRNA EST 29-SEP-2000 Homo sapiens cDNA clone IMAGE:3956667

BE900740 700 bp 601673910F1 NIH\_MGC\_21 mRNA sequence. BE900740 BE900740.1 GI:10389217

LOCUS DEFINITION

BE900740

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Homo sapiens human.

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/db_xref="taxon:9606"
/clone="IwAGE:4123770"
/clone="IwAGE:4123770"
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/lab_host="Dayan: muscle: Vector: poTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXAhoI sites using the following 5' adaptor: GGACGAGGG): Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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NIH WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                   BF307042 1111 bp mRNA EST 21-NOV-2000 601889875F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123770 5',
                                                                                                                                                                                                                                                                                                                                              mational institutes of meatin, manufating using Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nh,gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM1009 row: e column: 19
High quality: sequence stop: 629.
Location/Qualifiers
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Pred. No. 4.8e-113;
3; Mismatches 77;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                     8129
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Contact: Robert Strausberg, Ph.D.
Email: Gapbs-Temail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM9495 row: e column: 17
High quality sequence.stop: 712.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/lab_host="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Location/Qualifiers
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/clone_lib="NIH_MGC_17"
/tissue_type="rhabdomyosarcoma"
/tissue_type="rhabdomyosarcoma"
/lab_host="lubtlob (phage-resistant)" site_1: EcoRI;
/note="Organ: muscle; Vector: poTB7; site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGAG(6). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZaPe-DNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The L.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM86 row: p column: 08
High quality sequence stop: 641.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
A EST 20-JUL-2000 sapiens cDNA clone IMAGE:3028471
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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98.3%; Pred. No. 2.1e-108;
tive 0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3028471"
   mRNA
                               Homo
BE298158 660 bp
601118532F1 NIH_MGC_17
                                                                                                                   BE298158.1 GI:9181745
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BE298158
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E I (bases 1 to 688)
S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
L Onpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCAMSPS row: p column: 10
High quality sequence start: 8
High quality sequence start: 8
High quality sequence start: 8
Location/Qualifiers
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/note="Corgan: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
Callfornia, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
213 c 208 g 99 t
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                                                                                   8040 cccagtgcgctcgttccggtccccacagactgccccagccaacgagattgctggaaacca 8099
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BE391091. GI:9336456
                          agtcaggccaggtggggggacaaaagggccaggtgcggcctggggggaacggatgctccg
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="twAcE:3607929"
/clone=lib="NIH_MGC_44"
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Gaps

Score 630.4; DB 167; Length 688; Pred. No. 4.1e-108; 0; Mismatches 1; Indels 4;

7.48;

Query Match 7.4 Best Local Similarity 99.3 Matches 675; Conservative

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Eukaryotacia Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 657)

NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF530324 657 bp mRNA EST 11-DEC-2000 602071630F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4214551
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BF530324
BF530324.1 GI:11617698
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. (bases 1 to 920)

NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L. Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs.remail.nih.gov
Tissue Procurement: ATCC

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LiAM10212 row: p column: 12
                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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/note="Organ: liver; Vector: pCWV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally: oligo-dT primed.
Average insert size 1.7 kb Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC_Library."
/d a 277 c 266 g 173 t
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       602346448F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4441595
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Pred. No. 1.2e-106;
0; Mismatches 54;
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Location/Qualifiers
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                                                  BG117169.1 GI:12610675
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Matches 778; Conservative
                        mRNA sequence.
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                                                                                                                                                                        /los_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; cloned unidirectionally. Primer: Oligo dr.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                    1. .657
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/clone="INAGE:4214551"
/tissue_type="anaplastic oligodendroglioma with lp/19q
loss"
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found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLMB9788 row: 1 column: 08
High quality sequence stop: 657.
Location/Qualifiers
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Lumbul June Aurora
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Prayade By: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2006 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 465.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 622)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                    8060 ccccacagactgccccagccaacgagattgctggaaaccaagtcaggccaggtgggggg
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/clone_lib="NCI_CGAP_Lu19"
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/db_xref="taxon:9606"
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               /note="Organ: lung; Vector: pT7T3D-pac (Pharmacia) with a modified polylinker; lst strand cNRA was prepared from pooled lung tumor tissue, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to ECO RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and ECO RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Patima Bonaldo.
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601591169F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945305 5'
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/lab_host="DH10B (phage-resistant)"
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BE795997
BE795997.1 GI:
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             Euteleostomi;
                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM803 row: i column: 18
High quality sequence stop: 629.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
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         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 629)
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Pred. No. 5.3e-105;
0; Mismatches 2; Indels
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/db_xref="taxon:9606"
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Best Local Similarity 99.5%;
Matches 626; Conservative
                                                                    Unpublished (1999)
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ORGANISM
                                            AUTHORS
TITLE
JOURNAL
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Mammalia, Eutheria, Prímates, Catarrhini, Hominidae, Homo.
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NIH WGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 3.9e-104;
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Plate: LLCM216 row: 1 column: 17
High quality sequence stop: 649.
Location/Qualifiers
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/clone_lib="NIH_MGC_92"
/tissue_type="embryonal carcinoma, cell line"
/tab_host="DHIOB (phage-resistant)"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                     ggaaggaaaggcagatgtaaatga-tgtgtttggtttacagggtatatttttgataccttc
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information car
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM10462 row: i column: 23
High quality sequence stop: 623.
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
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AF113003 Homo sapi AF125672 Homo sapi U37146 Humann silen AF125671 Mus muscu AF113001 Mus muscu AF113002 Mus muscu BC004326 Homo sapi S83390 T3 receptor

Description

// Aluction="transcriptional co-repressor"  // Anote="hemr" alpha: longer isoform than previously reported" // Anote="hemr" alpha: longer isoform than previously reported" // Codon_start=1 // Codon_start=1 // Codon_start=1 // Pyroduct="silencing mediator of retinoic acid and thyroid hormone receptor alpha   // Landalation="MacSTOLYDRENEWEDLENEPERPREPERPRESSIVE REVERLINEPERPRELIAPOPAGEDLINESCHENESCHENEPERPREPERPRESSIVE REVERLINEPERPRELIAPOPAGEDLINESCHENESCHENEPERPRESSIVERIE RESKREMICHONINDENDERSPLIATOGOPAGEDLINGKENGENESCHENEPERPRESSIVERIE RESKREMICHONINDENDERSPLIATOGOPAGEDLINGKENGENESCHENEPERPRESSIVERIE RESKREMICHONINDENDERSPLIATOGOPAGEDLINGKENGENESCHENEPERPRESSIVERIE RESKREMICHONINDENDERSPLIATOGOPAGEDLINGKENGENESCHENEPERPRESSIVERIE RESKREMICHONINDENDERSPLIATOGOPAGEDLINGKENGENESCHENEPERPRESSIVERIE RESKREMICHONINDENDERSPLIATOGOPAGEDLINGKENGENESCHENESCHENEPERPRESSIVERIE RESKREMICHONINDENDERSPLIATOGOPAGENERKENGENESCHENESCHENESTRENGENESCHENE REKLITYFERRHARKORNOGENETRYNDENGENERKENERSPRESSIVERIE ROOPETIRGKENENGENERGENERGENERGENENGENERGENESCHENESTRENGENER REKLITATERRYNDENGENERGENERGENERGENENGENERGENERGENERG	FLAKEPARGELEPASSPEKGESPERDLYBYGGHATHARPARMATAPHARGLPRHAE SASDPHREKTGERFASTOELELASLGYHGSSYEPEGYEPVSPWSSPSTTHAPHARGLPRHL ESLDKSHLEGELRPKOPGPVKLGGEAAHLPHLRPLPESOPSSPSLLGTAPGCHQRY VTLACHISEVTTORPTRHIPOGLSAPLEAPEGASCPVLLGTRPFESDLYLEPPDH GAPARGSPHSEGGRREPENWTSVLGGGEDGIEPVSPPEGWTEPGHSSAVY PLLYRD GEOTEPSRMGSKSPGNTSOPPAFFSKLTESNSAWYKSKKOEINKKLNTHNRNEPEYNI SOPCTETENMAATTGTGLANTYRSOAVOENSTATASLAKKVSCRPSSRAKSPPLS ANAFNPLNASASLPAAMPITAADGRSDHTLTSGGGGKAKVSGRPSSRRAKSPPCLA SGDRPPSVSSVHSGGONRRTPLTNRWHDEPSSAGSTPPPYNPLIMRLQAGVWASPP BASE COUNT 1862 a 3033 c 2525 g 1141 t ORIGIN	Query Match         99.6%: Score 8541; DB 89; Length 8561;           Best Local Similarity 99.9%: Pred. No. 0;         No. 0;           Matches 8560; Conservative 1; Mismatches 0; Indels 10; Gaps 1;           Qy 1 catglegggctccacacagcttgtggcacagacgtggagggcactgagccccgtaccc 60           Iniiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii
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32.4 13.2 209594 75 AC073916 48.4 11.1 161970 71 AC027706 32.8 8.5 79494 73 AC06887 53.6 6.5 560 97 HSU80750 09.4 4.8 AC068837 55.6 8.3 0.161970 71 AC027706 52.2 229816 69 AC025685 82.6 2.1 184815 69 AC025685 82.7 1 184815 69 AC025685 82.8 209594 75 AC069201 82.8 1.5 209594 77 AC087390 82.8 1.6 303091 77 AC084799 83.8 1.5 220469 75 AC074344 83.8 1.5 220469 75 AC074342 83.8 1.5 220469 75 AC073424 83.8 1.5 220487 75 AC033490 83.8 1.5 220487 75 AC033490 83.8 1.5 220488 75 AC033490 83.8 1.5 220488 81 ALS89767 83.8 1.5 220488 81 ALS89767 83.8 1.5 220488 81 ALS89767	AF113003 8561 bp mRNA Hormone sapiens silencing mediator of reti hormone receptor alpha mRNA, complete c AF113003.1 GI:4454551 human. Homon sapiens EUKaryota; Metazoa; Chordata; Craniata; Mammalia: Eutheria; Primates; Catarrhin 1 (bases 1 to 8561) Grdentlich, P., Downes, M., Xie, W., Genin	Unique forms of human and mouse nuclear Proc. Natl. Acad. Sci. U.S.A. 96 (6), 26 917891.  2 (bases 1 to 8561) Downes, M.R., Ordentlich, P. and Evans, R.M. Direct Submission Direct Submission Institute for Biological Studies, 10010 Jolla, CA 92037, USA I. 8561 Corganism="Homo sapiens" //db_arsef="taxon:9606" //chromosome="12" //map="12924" //msp="12924"

RESULT 1
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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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Homo sapiens Butazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 8686) Finances; Catarrhini; Hominidae; Homo.

2 (bases 1 to 8686) Finance, D.J., Yang, M., Li, H., Li, L. and Chen, J.D. SMRTe, a silencing mediator for retinoid and thyroid hormone receptors-extended isoform that is more related to the nuclear 8100 8040 8160 8150 8340 8400 8460 8390 8450 2 (bases 1 to 8686) Chen, J.D. Direct Submission Submitted (03-FEB-1999) Pharmacology and Molecular Toxicology, AF125672 8686 bp mRNA PRI 04-APR-1999 Homo sapiens silencing mediator of retinoic acid and thyroid hormone receptor extended isoform (SMRTE) mRNA, complete cds. AF125672.1 GI:4559297 acacaggoggccagggccagggacccaaagcaggatgaccacgcactccacgccac tgcctccccgaatgcatttggaaccaaagtctaaactgagctcgcagccccgcgccct coctococtoccatcccgcttagcgctctggacagatggacgcaggccctgtccagccc ttacgcaaggaaggacttacccagtattactgctgctgtgcttttgatcttgcttaccg ttcaagaggcgtgtgcaggccgacagtcggtgaccccatcactcgcaggaccaaggggggc receptor corepressor Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3519-3524 (1999) 99199215 human ACCESSION VERSION KEYWORDS SOURCE ORGANISM 7 DEFINITION 7851 7911 7981 7971 8041 8031 8101 8091 8221 8211 8281 8341 JOURNAL MEDLINE REFERENCE AUTHORS TITLE JOURNAL 7861 7921 AUTHORS TITLE RESULT AF125672 LOCUS REFERENCE g οy g οy g δ g οy 셤 ŏ q ζ g δ ద ò 셤 δ a ð 용 a ò

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δ á	2461	tgtggtccccaaggagagagaggaggaggagaccgcagcagcgcccccagtggaggagg 2520
2 6	2	GIGGICCCCAAGGAAGAAGAAGGAAGAACAACCGCAGCACCCCCC
දු දු	2521	ggaggagcagaagcccccgeggctgaggagctggcagtggacagagggaaggccgagga 2580 
οy	58	cccgtcaagagcgagtgcacggaggaagccgagggaggggccggcc
qq	2682	GCCCGTCAAGAGCGAGTGCACGGAGGAAGCCGAGGGGCCGGCC
Οy	2641	cgctgaggccacggccgaggggcgctcaaggcagagaagaaggagggcgggag 270
QQ	2742	GAGGCCGCTGAGGCCACGGCCGAGAGGCCCTCAAGGCAGAAAGAA
Qy	0	76
Q O	2802	GGCAGGGCCACCACAGGCCAAGAGCTCGGGCGCCCCCAGGACAGCGACTCCAGTGCCAC 28
ογ		82
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ΟŊ	3001	aggaagcacccg 306
Dp	3102	CCACCGCAAAACTIGCAGCGGAGAGCGACGCCCTCAGCAGCCTGGCAGCAGCCCCC
οχ	3061	agcccggcacccccgccgacaaggag310
QQ	3162	GGCAAGAGCAGGCCCGGCACCCCCCGCCGACAAGGAGGCAGAAA
Οy	3101	cottcgcagccgaggcccagaagctgcctggggacccccttgctggacttccgg 315
q	3222	CHILLING CONTROLL CONTROL CONTROLL CONTROL
Qy	3157	ccttcccgtgccccccgtgaggtgatcaaggcctcccgcatgcccggaccc 321
qq	3282	CCTTCCCCGTGCCCCCCGTGAGGTGATCAAGGCCTCCCCGCATGCCCCGGACCC 33
Οy	3217	ctcagccttctcctacgctccacctggtcacccactgcccctgggcctccatgacactgc 3276
QQ	3342	casccrictrocracerceaecrescraceceaerseceressecres 34
δλ	3277	ccggcccgtcctgccgcgcccaccaccatctccaacccgcctccctc
qa	3402	GGCCGTCCTGCCGCCCCACCATCTCCAACCGCCTCCCTCATCTCTCTC

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4417 cgtacc               4542 CGTACC   4477 gatggc   4602 GATGGG   4537 agggac   4662 AGGCAA		4717 cagcc1 4842 CAICH 4842 CACCC 4777 cgccac 4777 cgccac 4902 cGcCACC 4837 gcacct 1	4897 cgaccc               5022 CGACCC   4957 ccgacs   1           5082 CGACJ   5017 c ccGACJ   1		5257 caccgo 5382 CACCGG 5317 cagcac 5412 CAGCAC 5377 ctcgtc 5502 CTCGTG 5437 gtccat 5437 gtccat 5437 gtccat 5437 gtccat
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                      GCATCCTTGCCTGTCTAAAGCCTTAACTAAGACTCCCGCCCCGGGCTGGCCCTGTGCAGA
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GPPHETAARKRIYDMMEGRYGRAISSASIEGLMGRAIPPERHSPHHLKEOHHIRGSIT
GGIPRSYVEAQEDYLRREAKLLKREGTPPPPPSRDLTEAYKTQALGPLKLKPAHEGL
VATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGSITQGTPLKYDTGASTTGSKKHD
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PELGK ROGSPLTYEDHGAPPFAGHLPRGSSPTRALDFAPPTRALDFASSGGSIARGAPVIV
PREIAR KSPHSTYPEHHPHP ISPYEHLLRGVSSPYNREPPPRALDFAPPSIPEDDAA
AAYYLPRHLAPNPTYPHLYPPYLIRGYPDTAALENRQTIINDYITSQOMHHNTATAMA
ORADMIRGLSPRESSLALNYAAGPRGIIDLSQYPHLPVLVPPPFGTPATAMDRLAYLP
TAPOPFSRHSSPLSGPPHLITFWTTTSSSERERNDREBRESKILTSTTT
VEHAPIWRPGTEQSSGSGGGGSSSRFASHSHAHOHSPISPRTQDALQORPSYL
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LLPKEAPRVARPERPRADTGHAFLARPPARSGLEPASSPSKGSBPRPLVPPVSGHATI
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SLGVPTAQEASVLRGTALGSVPGGSITKGIPSTRVPSDSAITYRGSITHGTPADVLYK
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ASCPVLDLRRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEPNKTSVLGGGEDGIEPVS
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GKAKVSGRPSSRKAKSPAPGLASGDRPPSVSSVHSEGDCNRRTPLTNRVWEDRPSSAG
STPFPYNPLIMRLQAGVMASPPPPGLPAGSGPLAGPHHAWDEEPKPLLCSQYETLSDS
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                                                                                       interacts with nuclear hormone
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Primates; Catarrhini; Hominidae;
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/gene="SMRT"
/note="transcriptional co-repressor"
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Chen, J.D. and Bvans, R.M.
Direct Submission
Chen, G.D. Chen, Generation (27-SEP-1995) J. Don Chen, Generatitute, 10010 N. Torrey Pines Road, 1
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                                                                                       that
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1.5989
/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                       A transcriptional co-repressor
                                                                                                                                                   Nature 377 (6548), 454-457
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                                                        and Evans, R.M
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/gene="SMRT"
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Best Local Similarity 99.7%;
Matches 5477; Conservative
Eutheria;
1 to 5989)
                               (bases 1
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Chen, J.D.
Direct Submission
Submitted (03-FEB-1999) Pharmacology and Molecular Toxicology
University of Massachusetts Medical School, 55 Lake Avenue 1
Worcester, MA 01655, USA Natl. Acad. Sci. U.S.A. 96 (7), 3519-3524 (1999) /function="transcriptional corepressor" /note="SMRTe" receptor extended isoform (Smrte) mRNA, /organism="Mus musculus" /db\_xref="taxon:10090" Location/Qualifiers 1. .8544 /codon\_start=1 hormone receptor extend AF125671 AF125671.1 GI:4559295 /gene="Smrte" 'gene="Smrte" receptor corepressor Mus musculus Proc. Nat 99199215

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Institute for Biological Studies, 10010 North Torrey Pines Road, La
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KEAEKPAFFPAFPTEGPKLPTEPPRWSSGLPPPIPPREVIKTSPHAADPSAFSYTPPG
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HAKAPMGPLTMGLPLAVDPKKLGTALGSATSGSITKGLPSTRAADGPSYRGSITHGTP
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DGRSSSGPPHETAAPKRTYDMMEGRVGRTVTSASIEGLMGRAIPEQHSPHLKEQHHIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product-"silencing mediator of retinoic acid and thyroid
Apromone receptor alpha"
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                                                                                                                                                                                                                                                                                 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                    Unique forms of human and mouse nuclear receptor corepressor SMRT Proc. Natl. Acad. Sci. U.S.A. 96 (6), 2639-2644 (1999)
                                                                                                                                                                                AF113001 8388 bp mRNA ROD 20-MAR-1999 Mus musculus silencing mediator of retinoic acid and thyroid hormone receptor alpha mRNA, complete cds.
                         8404 ACGCCACTGTG----CCCTTCCCCACACCTTACTTCAGCGAAATGGACTTGATGCGTATTC
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Ordentlich, P., Downes, M., Xie, W., Genin, A., Spinner, N.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function="transcriptional co-repressor"
/note="mSMRT alpha"
/codon_start=1

    (bases 1 to 8388)
    Downes, M.R., Ordentlich, P. and Evans, R.M.

Direct Submission
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626. .8047
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SOURCE
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AUTHORS
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GIPLERAAAAAYYLPRHIAPSPTYPHLYPPYLIRGYPDTAALENRQTIINDYITSQQH
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TTVBHAPINREQTDSSSGAGGSSRPASHTHOHSPISPRTODALQQRESYLHNTSMKGV
VTSVBEGTPTVLRWARSTSTSSPVRPAATFPPATHCPLGGTLEGVYPTLMEPVILLPKE
                                                                                                                                                                                                               TSRVARPERARVDAGHAFLTKPPGREPASSPSKSSEPRSLAPPSSSHTAIARTPAKUL
APHHASPDPPAPTSASDLHREKTQSKPFSIQELELRSLGYHSGAGYSPDGVEFISPVS
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PSSRKAKSPAPGLASGDRPPSVSSVHSEGDCNRRTPLTNRVWEDRPSSAGSTPFPYNP
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2762 c 2285 g 1306 t 7 others
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Pred. No. 0;
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· 6		AAGAGGCAGAGAAACCCGCATTCTTTCCGACTTCCCAAAGCTACCGA 3776	q	4677 CA
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ò	3192 aggeet	occogoatgooccogaccottcaqcottctacgacctagtcacccac 3251	δλ	4260 ag
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ò	3312 accede	ngagagasaatagatg 33	δ	4380 ac
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musil (bases 1 to 7465)
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Proc. Natl. Acad. Sci. U.S.A. 96 (6), 2639-2644 (1999)
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teccagegagecacaggaacggeectgeagagegggggggggeggeteececeaacea 7661
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Downesy.R.W. Ordentlich,P. and Evans,R.M.
Direct Submission
Submitted (11-DEC-1998) Gene Expression Laboratory, The Salk
                                                                                                                                      aggaaggagcccttgagtccgccttccatc....---catctgtccg
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NDEKEAVASKGRKTANSGGRRKGRITRSMARZANHEETATPQGSSELASMEMRESSRW
TEEEMETAKKGLLEHGRNWSAIARMVGSKTVSQCKNFYFNYKKRQNLDEILQQHKLKM
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PSYLHMTRMKGVTYSVEDGTPVLRMARSTSTSSPVRRPATFPPATHOPLGGTLEGVY
PTLMEPVLLPKETSRVARPERARVDAGHAFLTKPPGREPASSPSKSSEPSSS
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RQYHENIKINOAMRKKLILYFKRRNHARKQWEQRFCQRYDQLMEAWEKKVERIENNPR
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GTPLKYDSGAPSTGTKKHDVRSIIGSPGRPFPALHPLDIMADARALERACYEESLKSR
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LVPPTPGTPATAIDRLAYLPTAPPPFSSRHSSSPLSPGGPTHLAKPTATSSSERERER
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SSAGSTPFPYNPLIMRLQAGVMASPPPPGLAAGSGPLAGPHHAWDEEPKPLLCSQYET
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hormone receptor beta"
/protein_id="AAD20945.1"
/db_xref="GI:4454550"
for Biological Studies, 10010 North Torrey Pines Road, 92037, USA
Location/Qualifiers
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); Mismatches 1164; Indels 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                            function="transcriptional co-repressor"
                                                                                                                                                                                                                                                                                                                              /tissue_type="spleen; brain"
363. .7124
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	aaaaaaagtggagcgcatcgaaaacaacccgcgccggcgggccaaggagagcaaggtgc 9  	gcgagtactacgaaaagcagttccctgagatccgcaagcagcggggctgcaggagcgca 1 	tgcagagcagggtgggccagcgggggcagtgggctgtccatgtcggccgccgcagcagc 11 	acgaggtgtcagagatcatcgatggcctctcagagcaggagaacctggagaagcagatgc 11 	gccagctggccgtgatcccgcccatgctgtacgacgctgaccagcagcatcaagttca 1	tcaacatgaacgggcttatggccgaccccatgaaggtgtacaaagaccgccaggtcatga 1: 	acatgtggagtgagcaggagaaggagaccttccgggagaagttcatgcagcatcccaaga 1 	actttggcctgatcgcatcattcctggagaggaagacagtggctgagtgcgtcctctatt 14 	actacctgactaagaagaatgagaactataagagcctggtgagacggagctatcggcgcc 14 	goggcaagagccagcaacaacagcagcagcagcagcagcagc	agcccatgcccgcagcagcagcaggagaaagatgagaaaggagaaaggaaaaggaggcgg 1 	agaaggaggaggagaagccggaggtggagaacgacaaggaagacctcctcaaggagaaga 1 	cagacgacacctcaggggaggacaacgacgagaaggaggctgtggcctccaaaggccgca 17 	aaactgccaacagccagggaagacgcaaaggccgcatcaccgctcaatggctaatgagg 17 	ccaacagcgaggaggccatcaccccagcagagcgccgagctggctccat	atgagagttctcgctggacagaagaaatggaaacagccaagaaaggtctcctggaac 18 	acggccqcaactggtcggccatcgccqgatggtgggctccaagactgtgtcgcagtgta 19.	agaacttctacttcaactacaagaagaggcagaacctcgatgagatcttgcagcagcaca 20
574	930	990	1050 754	1110	1170	1230 934	1290 994	1350	1410	1470	1530	1590	1650	1710	1770	1830	1890	1950
qq	Oy Db	9. Pb	oy B	QQ Dp	QY Dp	QY Db	Oy Db	Oy Op	Qy Dp	QY Db	oy D	Qy Dp	QQ Dp	QY Db	Qy Dp	QY Db	oy Db	δ

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Oy 30 Oy 31. Oy 31. Oy 32. Oy 32.		<i>~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~</i>	Oy 38 Oy 39

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                                                                                                                                 choriocarcinoma"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2842)
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Submitted (01-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Homo sapiens, clone IMAGE:3629785, mRNA, partial cds.
BC004326.1 GI:13279241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nlh.gov
Contact: Robert Strausberg, Ph.D.
TTB1: (301) 496-1550
Email: Robert_Strausberg@nlh.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg, R.
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DEFINITION

BC004326

RESULT

ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

TITLE JOURNAL AUTHORS REFERENCE

REMARK COMMENT

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GPLAGAHHAWDEEPKPLLCSQYETLSDSE"
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Identification of TRACs (T3 receptor-associating cofactors), a family of cofactors that associate with, and modulate the activity of, normone receptors
MOI. Endocrinol. 10 (7), 813-825 (1996)
                                                                                                              fetal liver, mRNA, 2930
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/note="This sequence comes from Fig. 4; Authors report
detecting several TRAC alternative transcripts; TRAC-1"
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                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
GenBank staff at the National Library of Medicine created this entry (NCBI glabsq 1/9975) from the original journal article. This sequence comes from Fig. 4.

Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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qa	2403		2402
Qy	7185	gtggcggcggaaggccaaggtctctggcagacccagcagcagaaaagcc	7244
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Qy	24	agteceeggecegggeetggeatetggggaceggecaceetetgtetecteagtgeaet	30
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REFI A(	REFERENCE AUTHORS	Muzny, D.W., Addans, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S. L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J.	,C., ia,J.,
		Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay.	
		<pre>ButCh,F., ButKetL,C., ButTell,N.L., bytd,N.C., Catron,T.F., Carter,M., Chavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,G., Chen,G., Chen,L., Chuytty,T., Christopoulos,C., Cleveland,C.D., Cox.</pre>	n, R.,
		Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederitch,D.A., Delaney,K.R., Delgado,O., Denn a.T. Ding V. Dink H. H. Douthwaite K.I. Draner H.	
		Dugan Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Fore	, C.C., d, J.,

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Foster, P., Frantz, P., Gabisi, A., Gac, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J. H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Harri, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hudgson, A., Houloway, C., Harrison, E., Jacobson, A., Holloway, C., Jackson, L. B., Jacobson, B., Jis, Y., Johnson, R., Jolivet, S., Hume, J., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J. Liu, M., Liu, M., Loulseged, H., Lozado, R. J., Lideu, C., Liu, J., Liu, R., Lua, R., Martines, E., Mabhari, M., Martine, P., Maclor, R., Lua, R., Lua, R., Martine, E., Mawhiney, E., Mcicod, M. P., Meador, M., Marsey, E., Mcicod, M. P., Meador, M., Moyen, N., Moyen, N., Noyen, R., Noyen, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Ressey, E., McChed, M., Shooshari, N., Rayen, N., Royen, N., Noyedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Pinmus, E., Pu, L.L., Quiles, M., Ren, Y., Ressey, E., Royen, R., Soluokon, I., Shooshari, N., Stanley, H., Tansey, J., Taylor, C., Taylor, C., Taylor, C., Taylor, C., Taylor, C., Taylor, C., Taylor, S., Warien, R., Washington, C., Walliamson, A., Wallezyk, R., Wooden, S., Walliamson, A., Wallezyk, R., Wall, R
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NOTE: This is a 'working draft' sequence It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: M13; L08821

Chemistry: Dye-primer Bodipy: 24 of reads

Chemistry: Dye-terminator B1g Dye: 76% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 209115 bases at least Q40

Consensus quality: 213878 bases at least Q30

Consensus quality: 216310 bases at least Q20

Estimated insert size: 205541; sum-of-contigs estimation

Quality coverage: 0.x in Q20 bases; sum-of-contigs estimation

Quality coverage: 5.x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (05-JUL-2000) Human Genome Sequencing Center, Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Mar 10, 2001 this sequence version replaced g1:12965246.
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49756: gap of unknown length
104158: contig of 54402 bp in length
104258: gap of unknown length
148912: contig of 44654 bp in length
149012: gap of unknown length
172642: contig of 23630 bp in length
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Web site: http://www.hgsc.bcm.tmc.edu/
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Center clone name: RP11-408118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---- Genome Center
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Unpublished
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Direct Submission
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49757
104159
104259
148913
149013
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COMMENT

TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

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90599 CCGCAGGTTCCACGCCATTCCCCTACAACCCCCTGATCATGCGGCTGCAGGCGGGTGTCA 90540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8088 tgctggaaaccaagtcaggccaggtgggcggacaaaagggccaggtgcggcctgggggga 8147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90539 TGGCTTCCCCACCCCACCGGGCCTCCCCGGGGCAGCGGGCCCCTCGCTGGCCCCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 209594;
                                                                                                                                                                                                                                                                                                                                                                                                                  7368 ccgcaggttccacgccattcccctacaacccctgatcatgcggctgcaggcgggtgtca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90251 TGTCTAAAGCCTTAACTAAGACTCCCGCCCCGGGCTGCCCTGTGCAGACCTTACTCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggatgtttacctggtgctcgggaagggaagggaaggggccggggaggggggcacggcaggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ccctgtccagccccagtgcgctcgttccggtccccacagactgccccagccaacgagat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7488 acgeetgggaegaggageceaagecactgetetgetegeagtaegagaeactetecgaea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7548 gcgagtgactcagaacagggcgggggggggggggggteuersperlugtcaggtcccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tgtctaaagccttaactaagactcccgcccgggctggccctgtgcagaccttactcagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90311 GAGCCCCTGAGTCCGCCTGCGCCTCCATCTGTCCGTCCAGAGCCGGCATCTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gtgtggcagccacacacaggcggccagggcggccagggacccaaagcaggatgaccacgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                    813 others
                   of 27343 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                11; Indels
                                                                                                                                      unknown length
of 1100 bp in length.
                                                                                                                      of 1360 bp in length
                                                                                                                                                                                                                                                                                                                                            DB 75;
gap of unknown length contig of 27343 bp in 1 gap of unknown length contig of 5472 bp in le gap of unknown length gap of unknown length gap of unknown length contig of 1360 bp in le
                                                                     length
                                                                                                       length
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Pred. No. 1.8e-159;
3; Mismatches 11;
                                                                                                                                                                                                                                                                              58364 c 60674 g 47056 t
                                                                                                                                                                                        1. .209594
/organism="Homo sapiens"
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                                                                                                                                                                                                                                          /chromosome="12q"
/clone="RP11-408118"
                                                                                                                                                       5 209594: contig or Location/Qualifiers
                                                                                                                                         gap of
                                                                                                                                                                                                                                                                                                                                            13.2%;
97.7%;
                                                                                    206934:
                                                                                                                                       208494:
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205657:
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                   172743
200086
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ORIGIN
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us-09-522-753-4.rge

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NOTE: This is a 'working draft' sequence. It currently consists of 49 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                     Contact sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Conter project Information
Center clone name: 665_C_13
Center clone name: 665_C_13
Center clone name: 665_C_13
Sequencing vector: M13: M77815; 100% of reads
Sequencing vector: M13: M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 140943 bases at least Q30
Consensus quality: 154599 bases at least Q30
Consensus quality: 104020 bases; agarose-fp
Quality coverage: 3.1 in Q20 bases; sum-of-contigs
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1053 1152: gap of 105 bp in length 1053 1152: gap of 100 bp 1153 2378 contig of 1226 bp in length 2379 2478: gap of 100 bp 2479 3812: contig of 1334 bp in length 3813 3912: gap of 100 bp 2459 2468: gap of 100 bp 24688: gap of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14007 14106: gap of 100 bp
14107 15358: contig of 1252 bp in length
15359 15458: gap of 100 bp
17559 17152: contig of 1694 bp in length
17153 17252: gap of 100 bp
17253 18800: contig of 1548 bp in length
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21889: contig of 1498 bp in length
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21990 24355: contig of 2366 bp in length
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26757: contig of 2302 bp in length
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    COMMENT
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91130 91229; contig of 4832 bp in length 91130 91229; gap of 100 bp 94475; contig of 3246 bp in length 94575; gap of 100 bp 94575; gap of 100 bp 94576; gap of 100 bp 94576; gap of 100 bp 9483 98482; gap of 100 bp 98383 98482; gap of 100 bp 98383 98482; gap of 100 bp 103992 103991; contig of 5409 bp in length 103892 109749; contig of 5588 bp in length 109750 109849; gap of 100 bp 100950 116075; contig of 6226 bp in length 116076 116176 1122437; contig of 6262 bp in length 116176 1122437; contig of 6262 bp in length 112238 122537; gap of 100 bp 122538 112392; contig of 9389 bp in length 132393 132492; gap of 100 bp 132493 132492; gap of 100 bp 132493 141881; contig of 9389 bp in length 141882 141981; gap of 100 bp 141882 161970; contig of 19989 bp in length 156270; contig of 19989 bp in length 161670; contig of 19980 bp in length 161670; contig of 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 bp
of 3592 bp in length
100 bp
of 4852 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                           54867: gap of 100 bp
57938: contig of 3071 bp in length
58038: gap of 100 bp
60538: contig of 2500 bp in length
                                                                                                                                                                                                                                                                        47365: gap of 100 bp
49847: contig of 2482 bp in length
49947: gap of 100 bp
52474: contig of 2527 bp in length
52574: gap of 100 bp
54767: contig of 2193 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63422: contig of 2784 bp in length
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77598: contig of 2258 bp in length
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                            in length
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                                                                                              3643 39742: gap of 100 bp 39743 41978: contig of 2236 bp in 41979 42078: gap of 100 bp 44964 45063: gap of 100 bp 4564 45063: gap of 100 bp 4566 47265: contig of 2202 bp in 47266 47365: gap of 100 bp 47366 49847: contig of 2482 bp in 49848 49947: gap of 100 bp
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3913. 5368
/note="assembly_fragment"
5469. 6519
14: gap of 100 b<sub>l</sub>
37181: contig of 1867
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/clone_lib="RPCI-11 Human
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/note="assembly_fragment"
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6 86177: contig of 3:
8 86277: gap of 10
8 91129: contig of 4
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/chromosome="12"
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                                                                                                                            11.1%; Score 948.4; DB 71 ilarity 97.6%; Pred. No. 3.8e-132; Conservative 4; Mismatches 19;
                                           vector_side:left"
855. 10347
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10448. 12145
/note="assembly_fragment"
12246. 14006
/note="assembly_fragment"
14107. 15358
     6620. .7852
/note="assembly_fragment"
7953. .8464
/note="assembly_fragment
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/note="assembly_fragment"
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1 (bases 1 to 956)
Glienke, J., Hinzmann, B., Pilarsky, C. and Thierauch, K.H.
61419 TGCAGGCCGACAGTCGGTGGACCCCATCACTCGCAGGACCAAGGGGGCGGGGACTGCTGGC 61478
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PILARSKY CHRISTIAN (DE) ; THIERAUCH KARL HEINZ (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                  PAT
                                                                                                                                                                                                                                                                                                                                                                                                                          10.5%; Score 898.4; DB 9;
99.1%; Pred. No. 6.9e-124;
ive 0; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                 Patent: WO 0053734-A 43 14-SEP-2000;
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                                                                                                                                                                                         Sequence 43 from Patent W00053734.
AX035226
AX035226.1 GI:11190973
                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
288 c 287 g 18'
                                                                                                                       8533 taaaaagcgaattatactccaaaaaaaa 8561
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Sirren B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Bouklagalter, B., Brown, A., Burkett, G., Eampopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Colgagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Grand Pierre, N., Grant, G., Langos, B., Heaford, A., Horton, L., Klein, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Murphy, T., Mihova, T., Mihova, T., Mihova, T., Mihova, T., Mihova, T., Mihova, T., Wellin, J., Meneus, L., Mihova, T., Miranda, C., Monnell, P., O'Connor, T., O'Donnell, P., O'Neil, D., Ollvar, T.M., Ollver, J., Peterson, K., Plerre, N., Stantos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Tralamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J.,
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8106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGGAAGGACTTACCCAGTATTACTGCTGTGCTTTTGATCTCTGCTTACCGTTCAAG 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC068837 79494 bp DNA HTG 13-JUL-2000
Homo sapiens clone RP11-339B19, LOW-PASS SEQUENCE SAMPLING.
AC068837
cyctcyttccygtccccacagactyccccagccaacgagattyctygaaaccaagtcagg
                            ccaggtgggcggacaaaagggccaggtgcggcctggggggaacggatgctccgaggactg
                                                                                                                                                  aaggaaggacttacccagtattactgctgctgtgcttttgatctctgcttaccgttcaag
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 79494)
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in length

COMMENT

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38745: gap of 100 bp 39754: contig of 1009 bp in length 39854: gap of 100 bp 40828: gap of 100 bp 40928: gap of 100 bp 100 bp 40928: contig of 974 bp in length 41925: contig of 975 bp in length
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44097: contig of 962 bp in length
44197: gap of 100 bp
45179: contig of 982 bp in length
45279: gap of 100 bp
46245: contig of 966 bp in length
                                                                                                                                                                                                                               oof 100 bp contig of 1033 bp in length
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                                                                                                                                                                                   36: gap of 100 bp
29940: contig of 1004 bp in length
                                                14: gap of 100 bp 26685: contig of 971 bp in length 875 gap of 100 bp 100 bp 66: gap of 100 bp 100 bp 28836: contig of 970 bp in length 28836: contig of 970 bp in length
                                                                                                                                                                                                                                                                                                               32263: gap of 100 bp
3325: contig of 992 bp in length
3355: gap of 100 bp
3443: gap of 100 bp
34443: gap of 100 bp
35421: contig of 978 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                              221: gap of 100 bp 36507: contig of 986 bp in length 37558: contig of 986 bp in length 37558: contig of 951 bp in length 558: gap of 100 bp 10
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6 47341: contig of 996 bp ir
2 47441: gap of 100 bp
48397: contig of 956 bp ir
8 48497: gap of 100 bp
8 49441: contig of 944 bp ir
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Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Submitsed (10-MAY-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:

Simit, A.F. A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center for Genome Research
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* sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
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93.3%; Pred. No. 4.8e-100;
ive 3; Mismatches 49;
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      64536: gap of 10
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Wang, J. and Liu, J.M.
Direct Submission
Submitted (22-JAN-1998) Hematology Branch, National Heart, Lung and Blood Institute, Bldg. 10, Rm. 7C103, 9000 Rockville Pike,
Bethesda, MD 20892, USA
Location/Qualifiers
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ESTYREYY PEKOPPETRKOREOOERFORVGORGAGLSATIARSEHEISEIIDGLSEOEN
NEKOMROLSVIPPMMEDAEORRVKFINMGLMEDPMKVYKDROPMNVWTDHEKEIFKD
KFIGHPKNIEGLIASYLERKSYDEDEVLYYYTYKKNEWYKALYRRNYGERRGRNOOIARP
SQEEKVEEKEEDKAEKTEKKEEEKKDEEEKDEKEDSKENTKEKDKIDGTAEETEEREO
ATPRORKTENNSOGRRKGTITREMTNEAAASAAAATEEPPPPLPPPPPEPISTEPVE
KOKTSKRPREENDSOCESVARTYSAQEDEDIEASNEENPEDSEVEAVKPSEDSPEN
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DDQEHSAEEGSVCDPPPATKADSVDVEVRVPENHASKVEGDNTKERDLDRASEKVEPR
LVSSPLKPNPLDLPQLQHRAAVIPPNVSCTPCNITGTPVSGYALYORHIKAMHESAL
LEEDRORORDIDLEKRSSTSPCGTSKSPNREMEVLOPAPHOLITNLPEGVRLPTRPT
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ASKGHVIYEGKSGHILSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRE
SPVSAPLEGILCRALPRGSPHSDLKERTVLSGSIMQTPRATTESFEDGLKYPKQIKR
ESPPIRAFEGAITKGRYDGITTIKEMGRSIHEIPRODILTQESRKTPEVVQSTRPII
EGSISQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVERGKYE
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SGQPCGDDQNASPSKLSKEELIQSMDRVDREIAKVEQQILKLKKKQQQLEEEAAKPPE
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1 (bases 1 to 7940)
Wang,J., Hoshino,T., Redner,R.L., Kajigaya,S. and Liu,J.M.
ETO, fusion partner in t(8:21) acute myeloid leukemia, represses transcription by interaction with the human N-CoR/mSin3/HDAC1
                                    co-repressor N-CoR mRNA, complete
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AATAATGAGAAACAAATGCGGCAGCTCTCTGTGATTCCACCTATGATGTTTGATGCAGAA 1473

1414

Mus musculus Sukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 7780) 2118 1653 1450 1765 1825 1750 1998 1780 1900 2119 CGATGGACAGAAGAAGAAGATGGAAGTTGCTAAAAAAGGTCTAGTAGAACATGGTCGTAAC 2178 tggtcggccatcgcccggatggtgggctccaagactgtgtcgcagtgtaagaacttctac 1960 ttcaactacaagaagaggaagcctcgatgagatcttgcagcagacaaagctgaaga 2018 19-0CT-1996 Mus musculus nuclear receptor co-repressor mRNA, complete cds 1631 gacetecteaaggagaagacagacgacaceteaggggaggacaacgacgagaaggagget GCCACACCCCGGGGGCGAAAAAAACTGCCAACAGTCAGGGCCGCGTAAGGGCCGGATCACC cgctggacagaagaagaaatggaaacagccaagaaaggtctcctggaacacggccgcaac TGGGCAGCAATTGCTAAAATGGTGGGAACGAAAAGTGAAGCTCAATGTAAAAACTTCTAT cagcagcaccaagttcatcaacatgaacgggcttatggccgaccccatgaaggtgtac 1766 CGCAAGAAGAAAAGTAGAAGAAAAAGAAGAAGATAAAGCAGAAAAAAG gtggcctccaaaaggccgcaaaactgccaacagccagggaagacgcaaaggccgcatcacc ----ggccaacagcgag AGGTCCATGACAAACGAAGCTGCAGCTGCCAGTGCTGCAGCCGCAGCGGCTACTGAAGAG aaagaccgccaggtcatgaacatgtggagtgagcaggagaaggagaccttccgggagaag cagcagcagcagcagcagcccatgccccgcagcagccaggaggagaaagatgagaag 1571 gagaaggaaaaggaggcggaggaggaggaggagagagccggaggtggagaacgacaaggaa <u> Aataccaaggaaaaggacaagatagatggtacagcagaagaaactgaggaaagagggaa</u> cgctcaatggctaatga-------**MRNA** 7780 bp U35312, GI:1022717 house mouse. MMU35312 DEFINITION 1999 2179 14 ACCESSION VERSION KEYWORDS SOURCE ORGANISM 1961 2239 1331 1879 1751 1211 1474 1271 1534 1594 1391 1654 1451 1714 1511 1826 1691 1939 1781 2059 1841 1901 RESULT 1, MMU35312 LOCUS REFERENCE AUTHORS qq οχ g δ g q ò qq ò q ò Dp δ g ò 셤 δ q g δ 셤 ò g δy 셤 ò οχ δ

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                                                                                                                                                                             Horlein, School of Medicine,
CA 92093-0648, USA
                                                                                                    Horlein, J. T., Neer, A.M., Heinzel, T., Torchia, J., Gloss, B., Kurokawa, R., Kamai, Y., Ryan, A., Glass, C.K. and Rosenfeld, M.G. Direct Submission
Submitted (O2-5EP-1995) Andreas J. Horlein, School of Medicin UCSD, 9500 Gilman Drive, La Jolla, CA 92093-0648, USA Location/Qualifiers
  Ligand-independent repression by the thyroid hormone receptor
                                                                                                                                                                                                                                                                                                                                                                                                   co-repressor"
                      mediated by a nuclear receptor co-repressor
Nature 377 (6548), 397-404 (1995)
96008539
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DASE COUNT 2314 a 1974 c 1896 g 1593 t 3 others
ORIGIN

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Homo saplens CTG26 alternate open reading frame mRNA, complete cds.
U80761
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1 (bases 1 to 56).

Margolis, R.L., Abraham, M.R., Gatchell, S.B., Li, S.H., Kidwai, A.S., Breschel, T.S., Stine, O.C., Callahan, C., McInnis, M.G. and Ross, C.A. Chols with long CAG trinucleotide repeats from human brain Hum. Genet. 100 (1), 114-122 (1997)
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                                                                                                                            1830 CGAAAGACTGCTAACAGCCAAGGCCGCGGAAGGCCCGGGTCACCAGGTCGATGACAAGT 1889
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                                                                                              Length 560;
                                                                                             6.5%; Score 554.8; DB 97; Length 99.3%; Pred. No. 7.8e-73; Live 1; Mismatches 3; Indels
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         Compugen Ltd
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                              8, 2001, 09:38:43;
                                                                              412676 seqs, 60623988 residues
                     protein search, using sw model
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## ALIGNMENTS

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticovulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coaqulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; antianament; gene therapy; cancer; proliferative disorder; hypertension; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; caters proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinutia; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; Human ORFX ORF338 polypeptide sequence SEQ ID NO:676. contraceptive 08-FEB-2001 thrombosis; AAB40574; 

Homo sapiens

05-OCT-2000.

31-MAR-2000; 2000WO-US08621

WO200058473-A2.

99US-0127607. 31-MAR-1999;

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database

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Minimum DB Maximum DB

Perfect score:

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OM protein

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Scoring table:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Retinoid X recepto Human ORFX ORF2255 Human SRCAP, Homo Human OYCG27 gene Human ORFX ORF995 Human SRCAP, Homo Human ORFX ORF338 Transcriptional co HNRCR protein sequ Human HNRCR protei Rat p3103 protein Description AAB40574 AAW18226 AAB12454 AAB12453 AAB99738 AAB42491 AAB50362 AAB3408 AAB41231 AAB4000 8 2518 1495 2453 2343 2343 619 3266 3118 2971 2972 Length Query Match 7866 4187 4043 718 565.5 477.5 469.5 456 456 Score ٠ 9 Result

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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as cytostatic; hepatotropic; vulnerary; antiparatic antipornian; nootropic; neuroprotective; categoralic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coaqulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; proteins and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autinifiammatory disease; to enhance nocturnal haemoglobinuria, antinifiammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                           frame
                                                                                                                                                                                                                                                                        Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 784-790; 5507pp; English
                       05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
99US-0127636
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 21; Length 2518;
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99.7%; Score 13178.5; 99.8%; Pred. No. 0;
                  1; Mismatches
                   Conservative
         Best Local Similarity
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and thyroid hormone receptor;

acid

Silencing mediator for retinoic ac SMRT; transcriptional co-repressor Pranscriptional co-repressor SMRT

Homo sapiens

Region

Key

Region Region Region

AAW18226;

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/note="alternatively spliced insert not present in the original two-hybrid clone"

STUDIES

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95US-0522726

01-SEP-1995;

/label= glutamine-rich region 1201..1495

/label= C-terminal\_region

1330..1376

Peptide Region

WO9709418-A1

1..160 /label- N-terminal\_region /note= "proline-rich domain" 773..790

ERDR\_region

/label=

/label= SG\_region

1061..1132 .827

Location/Qualifiers

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A novel receptor interacting factor (AAW18226) is designated SWRT, i.e. silencing mediator (co-repressor) for retinoic acid receptor (RAR) and thyroid hormone receptor (RR). Its association with RAR and TR both in solution and on DNA response elements is destabilised by ligand. The interaction of SMRT with mutant receptors correlates with the transcriptional silencing activities of receptors. In vivo, SMRT functions as a potent co-repressor. A call DNA binding domain fusion of SMRT behaves as a frank repressor of a GAL4-dependent reporter. These data identify a novel class of cofactor which is believed to represent an important mediator of cofactor which is believed to represent an important mediator of a HeLa library in a two-hybrid screen using a GAL4 DNA binding domain/RXR fusion protein as bait.
                                                           New co-suppressor of steroid-thyroid hormone receptor activity - also methods for identifying compounds that relieve its suppressant
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                             Claim 2; Page 40-45; 71pp; English.
                                                                                                                    effect and/or activate receptors
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                                         EKSILTSTTTVEHAPIWRPGTEQSSGSSGGGGGSSSRPASHSHAHQHSPISPRTQDA
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                                 GLPLPMDPKKLAPFSGVKQEQLSPRGQAGPPESLGVPTAQEASVLRGTALGSVPGGSITK
                                                                  GIPSTRVPSDSAITYRGSITHGTPADVLYKGTITRIIGEDSPSRLDRGREDSLPKGHVIY
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                                                                                                                                                The present invention describes a human homologue of nuclear receptor coreceptor (HNRCR). The present sequence represents an HNRCR protein sequence used in comparison with the human HNRCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 EPRYPPHSLSYPVQIARTHTDVGLLEYQ - HHSRDYASHLSPGSIIQPQRRRPSLLSEFQ 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          series
MGKYDQWEESPPLSANAFNPLNASASLPAAMPITAADGRSDHTLTSPGGGGKAKVSGRPS
                                                                                                           NKKLNTHNRNEPEYNISQPGTEIFNMPAITGTGLMTYRSQAVQEHASTNMGLEAIIRKAL
                                                                                                                                      SRKAKSPAPGLASGDRPPSVSSVHSEGDCNRRTPLTNRVWEDRPSSAGSTPFPYNPLIMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coding
                                                                                                                                                                                   LQAGVMASPPPGLPAGSGPLAGPHHAWDEEPKPLLCSQYETLSDSE 2517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human kernon acceptor co-repressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.7%; Score 4187; DB 21;
llarity 41.0%; Pred. No. 1.6e-227;
Conservative 348; Mismatches 796;
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                                                                                                                                                                                                                                                                                                                nuclear receptor coreceptor
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                                                                                                                                                                                                                                        standard; Protein; 2453
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Best Local Similarity
Matches 1103; Conserv
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                                                                                                                                                                                                                                                                                                                                 Unidentified
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δ	305 L	MEALEKKVERIENNPRRRAKESKVREYYEKQFPEIRKQRELQERMOSRVGQRGSGLSMS	364
QQ	314 1	:        :	372
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qq	373 1	iarseheiseildglsegennekqmrqlsvippmmfdaeqrrvkfinmnglmedpmkvyk	432
οy	425 DI	RQVMNMWSEQEKETFREKFWQHPKNFGLIASFLERKTVAECVLYYYLTKKNENYKSLVR	484
qq	433 d:	drgfmnvwtdhekeifkdkfighpknfgliasylerksvpdcvlyyyltknenykalvr	492
οy	485 R	SY-RRRGKSQQQQQQQQQQQQQQPMPRSSQEEKDEKEKEAEK-	541
Q D	493 ri	nygkrigrnggiarpsgeekveekeedkaektekkeeekk	544
οy	542 KI	EDLLKEKTDDTSGEDNDEKEAVASKGRKTANSQGRRKGRITRSMANE	598
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qq	665 y		716
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QQ	717 ne	eeenpedsegeenssdtesapspyeaak	756
οy	769 PI	PATLGADGPPPGPPTPPRRTSRAPIEPTPASEATGAPTPPPAPPSPSAPPVVPKEEKE	828
QQ	757	rgntepvaeleattdpapcaspssav	794
0y	829 EI	ETAAAPPVEEGEEQKPPAAEELAVDTGKA	871
qq	795 ve	oeqytdsasaetaepmdydheecgaegssyldppaptkadsydpemgy-pentaskg	851
٥y	872 EC	SPAKGKDAEAAEATAEGALKAEKKEGGSGRATTAKSSGAPQDSDSSATCSADEVD	928
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δ	929 AE	GGDKNRLLSPRPSLLTPTGDPRANASPQKPLDLKQLKQRAAIPPI	926
οp	903 g€	-pergrvfpmdakpslltppgsili-sspikpnl	096
οy	116	AAPTKPAPPAPPPONLQPESDAPQOPGSSPRGK	1022
qo	961 pt	gtpvsgyalygrhikamhesalleegrgrgegvdlecrsstspcst	1008
0y 1	.023 SF	SPAPPADKEAFAAEAQKLPGDPPCWTSGLPFPVPPREVIKASPHAPDPSAFSYAPPGH	1082
DP 1	(s 600	pnreqvitnlpegv	1034
0y 1	083	PLPLGLHDTARPVLPRPPTISNPPPLISSAKHPSVLERQIGAISQGMSVQLHVPY	1137

TALGSVPGGSITKGIPSTRVPSDSALTYRGSITHGTPA------DVLYKGTITRI-IG 1248 EDSPSRLDRGREDSLPKGHVIYEGKKGHVLSYEGGMSVTQCSKEDGRSSSGPPHETAAPK 1308 1361 1313 1421 GRSIHEIPREEL----RHTPELPLAPRPLKEGSITQGTPLKYDTGASTTGSKKHDVRSL 1476 1417 1584 1525 1585 LTSTPRE----IAKSPHSTVPEHHPHPISPYEHLLRGVSGVDLYRSHIPLAFDPTSIPRG 1640 : |: || | : | :||| | | | | | | ataesfedgl-kypkqikres-----ppirafegai-----tkgkp-ydg-ittikem 1358 IGSPGRIFPPVHPLDVMAD-ARALERACYE-----ESLKSRPGTASSSGGSIARGAPVIV 1530 1641 IPLDAAAAYYLPRHLAPNPTYPHLYPPYLIRGYPDTAALEN-RQTIINDYITSQQMHHNT 1699 ||| | :|| ::|: | :| psvfggtngtsvitpldptaglrimplpsggpsisgglpasryntaada-laalvdaaas 1846 1700 ATAMAQRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAMDRLA 1759 1760 YLPTAPQPFSSR-HSSSPLSPGGPTHLTKPTTTSSSERERDRDRERDRDREREKSILTST 1818 1819 TTVEHAP---IWRPGTEQSSGSSGSSGGGGSSSRPASHSHAHQHSPISPRTQDA-LQQR 1874 1875 PSVLHNTGMKGIITAVEPSKPTVLRSTSSPV----RPAATFPPATHCPLGGTLDGVYP 1930 1847 apqmdvsktkeskheaarleenIrsrsaavseqqqleqknlevekrsvqcvctssalpsg 1906 GSEPRPLV------PPVSGHATIARTPAKN--LAPHHASPDPPAPPASASDPHRE 2024 2025 KTQSKPFSIQELELRSLGYHGSSYSPEGVEPVSPVSSPSLTHDKGLPKHLEELDKSHLEG 2084 gsgssdss----sslsshryetasdalevispasspappqekpgayqpdmvkanqaen 2020 ELRPKQPGPVKLGGEAAHLPHLR-----PLPESQPSSSPLLQT--APGVKGHQRVVTLAQ 2137 1138 SEHAKAPVGPVTMGLPLPMDPKKLAPFSGVKQEQLSPRGQAGPPESLGVPTAQEASVLRG RTYDMMEGRVGRAIS-----SASIEGLMGRAIPPERHSPH-HLKEQHHIRGSITQGIPR SYVEAQEDYLRREAKLLKREGTPPPPPPPPSRDLTEAYKTQALGPLKLKPAHEGLVATVKEA 1531 PELGKPRQSPLTYEDHGA----PFAGHLPRGSPVTMREPTPRLQEGSLSSSK-ASQDRK 1931 TLMEPVLLPKEAPR------VARPERPRADTGHAFLAKPPARSGLEPASSPSK 1205 1362 1314 1146 1249 1309 1422 1359 1477 1198 1634 1788 1978 1967 2085 δ g οŽ g Ω g οχ qq à g Óλ qq ò 셤 οy Dp δλ QQ δý q δy qq δ qq ογ g QD δý ΩĎ qq g δ οy δ

Indels 444; Gaps 104;

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Mismatches

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                                                                      --HGAPA-RGSPH-----SEGGKRSPEPNKTSVLGGGEDGIEPVSPPEGMTEPG-HSRSA 2240
                                                                                   2124 vlhprpgprvspenlvdksrgsrpgkspershi---psepyepisppqg---pavhekqd 2177
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                                                                                                                                                                                                                                                                AKSPAPGLA--SGDRPPSVSSVHSEGDCNRRTPLTNRVWEDRPSSAGSTPFPYNPLIMRL 2471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence represents a human homologue of nuclear receptor coeptor (HNRCR).
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                                                                                                                                                                                hicqiitqdfarnqvpsqaststfqtspsalsstp-----vrtktssryspesqsqt
                                                                                                                    VY PLLY RDGEQTEPSRMGSKSPGNTSQPPAFFSKLTESNSAMVKSKKQEINKKLNTHNRN
                                                                                                                                 ----SPPLSANAFNPLNASASLPAAMPITAADGRSDHTLTSPGGG-GKAKVSGRPSSRK
                                                                                                                                                                   EPEYNISQPGTEIFNMPAITGTGLMTYRSQAVQEHASTNMGLEAIIRKALMGKYDQWEE-
                        HISEVITQDYTRHH-PQQLSAPL----PAPLYSFPGASCPVLDLRRPPSDLYLPPPD---
                                                                                                                                                                                                                                                                                                                            2472 QAGVMASPPPPGLPAGSGPL--AGPH---HAWDEEPKPLLCSQYETLSDSE 2517
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                                                                                                                                                                                                                                                                                                                                                                                                AAB12453 standard; Protein; 2343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein SEQ ID NO:20
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N-PSDB; AAA60629.
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Length 2343;

Score 4043; DB 21; Pred. No. 2.1e-219;

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Query Match Best Local Similarity

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RPVLPRPPTISNPPPLISSAKHPSVLERQIGAISQG-----MSVQLHVPYSEHAKAP-VG 1146
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                                                    LYNQPSDTRQYHENIKINQAMRKKLILYFKRRNHARKQWKQKFCQRYDQLMEALEKKVER 315
                                                                                                                               IENNPRRRAKESKVREYYEKQFPEIRKQRELQERMQSRVGQRGSGLSMSAARSEHEVSEI 375
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                                          KQQQLEEEAAKPPEPEKPVSPPPIESKHRSLVQIIYDENRKKAEAAHRILEGLGPQVELP
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 PVTMGLPLPMDPKKLAPFSGVKQEQLSPRGOAGPPESLGVPTAQEASVLRGTALGSVPGG 1206
                                                                                  1107
                                                                                                            REDSLPKGHVIYEGKKGHVLSYEGGMSVTQCSKEDGRSSSGPPHETAAPKRTYDMMEGRV 1318
                                                                                                                                                                                                                                          1432 EL----RHTPELPLAPRPLKEGSITQGTPLKYDTGASTTGSKKHDVRSLIGSPGRTFPP 1486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reeaaskghviyegksghilsydnikna----regtrsprtaheisl-krsyesvegni 1161
                                                                                                                                                                  GRAIS-----SASIEGLMGRAIPPERHSPH-HLKEQHHIRGSITQGIPRSYVEAQEDYL 1371
                                                                                                                                                                                                                                                                                                                                                                                            1541 LTYEDHGA----PFAGHLPRGSPVTMREPTPRLQEGSLSSSKA-SQDRKLTSTPRE--- 1591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tpldptaq1rimplpaggpsisqglpasryntaada-laalvdaaasapqmdvsktkesk 1747
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                                                                                                                                                                                                                                                                                                 :: | |||: : ||: ||||||||||| | : ||:|||| | : diltqesrktpevvqstrpiiegsisqgtpikfdnn-sgqsaikhnvkslitgpsklsrg
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                                                                                                                                                                                                                                                                                                                                      VHPLDVMAD-ARALERACYE-----ESLKSRPGTASSSGGSIARGAPVIVPELGKPRQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SR-HSSSPLSPGGPTHLTKPTTTSSSERERDRDRERDRDREREKSILTSTTTVEHAPIWR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1644 pgseq------pgrpgshgyvrspsp-svrtgetmlggrpsvfggtngtsvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1888 TAVEPSKPTVLRSTSTSSPV----RPAATFPPATHCPLGGTLDGVYPTLMEPVLLPK---
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                                                       SITKGIPSTRVPSDSAITYRGSITHGTPA------DVLYKGTITRIIGEDSPSRLDRG
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Mouse retinoid X receptor (RXR) interacting protein RIP13 (AAR99738) is a candidate transcriptional co-activator. It was identified using an in vivo interaction trap system for the isolation of proteins that physically interact with RXRs, esp. with the ligand binding domain of human RXR alpha. Recombinant RIP13 can be obtd. using a cDNA clone (AAT31931) obtd. from a mouse liver library. RIPs (see also AAR99735-37 and AAR99739) can be used to modulate or mediate RXR function, and may be used therapeutically or to raise antibodies.
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                                                                                                                 -SPPLSANAFNPLNASASLPAAMPITAADGRSDHTLTSPGGG-GKAKVSGRPSSRKAKSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Retinoid X receptor (RXR) interacting protein (RIP) - useful to modulate or mediate RXR function, anti-RIP antibodies can be used determine RIP subcellular distribution patterns
                                                 GAP-ARGSPH----SEGGKRSPEPNKTSVLGGGEDGIEPVSPPEGMTEPGHSRSAVYPL
                                                                         qrpgsrvspenlvdksrgsrpgkspershv---ssepyepisppq--vpvvhekqdslll
                                                                                                   LYRDGEQTEPSRMGSKSPGNTSQPPAFFSKLTESNSAMVKSKKQEINKKLNTHNRNEPEY
                                                                                                                                                   NISOPGTEIFNMPAITGTGLMTYRSQAVQEHASTNMGLEAIIRKALMGKYDQWEE----
                                                                                                                                                                                                                                                         AP--GLASGDRPPSVSSVHSEGDCNRRTPLTNRVWEDRPSSAGSTPFPYNPLIMRLQAGV
ITQDYTRHH-----PQQLSAPLPAPLYSFPGA--SCPVLDLRRPPSDLYLPPPD-
                                                                                                                                                                                                                                                                                                         2476 MASPPPPGLPAGSG-PLAGPH---HAWDEEPKPLLCSQYETLSDSE 2517
                                                                                                                                                                                                                                                                                                                       Retinoid X receptor interacting protein; RXR; RIP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor interacting protein RIP13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 51-52; 90pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                  standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95WO-US16311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-0372652
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N-PSDB; AAT31931.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-SEP-1996
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determine RJ
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                                                                                                                                                                                                                                                                                                                    2135 LAQHISEVITQDYTRHHPQQLSAPLPAPLYSFPGA--SCPVLDLRRPPSDLYLPPPD--- 2189
                                                                                                                                                                                                                                                                                                                                                                                                2190 --HGAPA-RGSPH----SEGGKRSPEPNKTSVLGGGEDGIEPVSPPEGMTEPG-HSRSA 2240
                                                                              1975 PSKGSEPRPLV-----PPVSGHATIARTPAKN--LAPHHASPDPPAPPASASDP 2021
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                                                                                                                                                            HREKTQSKPFSIQELELRSLGYHGSSYSPEGVEPVSPVSSPSLTHDKGLPKHLEELDKSH 2081
                                                                                                                                                                                                                                        2082 LEGELRPKQPGPVKLGGEAAHLPHLR-----PLPESQPSSSPLLQT--APGVKGHQRVVT 2134
                                                                                                                                                                              184 aenestrgyegp-----lhhyrsqqespspqqqpplppssqsegmgqvprthrlit 234
                                                                                                                                                                                                                                                                                                                                                                                                                          290 vlhprpgprvspenlvdksrgsrpgkspershi---psepyepisppgg---pavhekqd 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    462 hgvvmshpv---gimpgsastsv----vtssearrdegepsphagvckpklinksnsrk 513
                                                                                                                   70 psgkaqphasvvyseagkdkgpppksryeeelrtrgkttitaanfidvtitrqiasdkda 129
                                                                                                                                                                                                                                                                                                                                                         235 ladhicqiitqdfarn--qvpsqpststfqtspsalsstpv---rtktssryspesqsqt 289
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                                         90;
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                                           Indels
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5.4%; Score 718; DB 17; I
36.0%; Pred. No. 1.5e-32;
ive 76; Mismatches 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB42491 standard; Protein; 3266 AA
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                                         Conservative
                    Best Local Similarity
Matches 213; Conserv
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    Query Match
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osteopathic, antiparkinsonian; nootropic; neuroprotective; osteopathic; antiparkinsonian; nootropic; neuroprotective; osteopathic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antilaflammatory; antibacterial; antiviral; antifungal; antirheumatic; antinflammatory; antibacterial; antiviral; antifungal; antiantenery; antibacterial; antiviral; antifungal; antiantanemic. The sequences can be used to determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, rythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic aneamia, burns, wounds, home and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 3700-3708; 5507pp; English.
                                                                                                                                                                              31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                                                   31-MAR-2000; 2000WO-US08621
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                                                                                                                                                                                                                                                                                                   (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                              Leach
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                                           WO200058473-A2
                                                                                                                                                                                                                                                                                                                                            Shimkets RA,
  Homo sapiens
                                                                                        05-OCT-2000
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Query Match 4.3%; Score 565.5; DB 21; Length 3266; Best Local Similarity 19.5%; Pred. No. 5.5e-23; Matches 567; Conservative 350; Mismatches 973; Indels 1011; Gaps 71 EFQPGNERSQELHLRPE-----SHSYLPELGKS-----EMEFIESKR---PRLELLP 114

137;

266 YHENIKINQAMRKKLILYFKRRNHARKQWKQKFCQRYDQLMEALEKKVERIENNPRR--- 322

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δλ	VIYEGKKGHVLSYEGGMSVTQCSKEDGRSSS 129	98
QQ		30
δy	EGLMGRAIPPERHSPHHLKEQHHIRGSI 135	55
qq		99
ΟŸ	REGTPPPPPPSRDLTEAYKTQALGPLKLKPAHEGLV 141	15
QQ	tppgsctsdlskipster 200	90
Qy	1416 ATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGSITOGTPLKYDTGASTTGSKK 1470	20
qq	r 204	44
Οy	1471 HDVRSLIGSPGRIFPPVHPLDVMADARALERACYEESLKSRPGTASSSGGSIARGAPV 1528	28
QQ	2045 fryhsilesdpytppsdpsipitlpsvtaaklsppvasg 2086	84
ΟŸ	HGAPFAGHLPRGSPVTMREPTPRLQEGSLSSSK 157	8.
qq	2085giphgspptkvtewitrgeepragstpspalppdtkasdvdts 2127	27
δy	HLLRGVSGVDLYR 162	25
QQ	2128 sstlrkilmdpkyvsatsvtstsvttaiaepvsaapclheappppvdskkplee 2181	81
οy	YPHLYPPYLIRGYPDTAALENROTI 168	92
q	2182 ktappvtnnselgasevlvaadkekvapviapkitsvisrmpvsidlensgki 2234	34
δy	ALNYAAGPRGIIDLSQVPHLPVLVP 174	45
QQ	226	29
Qy	YLPTAPQPFSSRHSSSPLSPGGPTHLTKPTTTSSSERERDRDRERD 180	05
ф	pagpvnvlkgpv229	94
οy	184	41
qq	2295nvltgpvnvlttpvnatvgtvnaapgivnaaasavnatasavtvtagavtaas 234	47
οy	1842 GGGGSSSRPASHSHAHQHSPISPRTODALQQRPSVLHNTGMKGIIT 1888	88
QQ	kckqrasanensrfhpgsmpviddrpadag-sgagl 240	03
οy	-TFPPATHCPLGGTLDGVYPTLMEPVLLPKEA 194	42
QQ	gqktegpqrisakisqippasamdiefqqsvsksqvkpds 245	23
ογ	1943 PRVARPERPRADIGHAFLAKPPARSGLEPASSPSKGSEPRPL 1986	84
q	hls 251	15
δλ	199	66
qq	2516 vstpvtgggtvkvltggintppvlvhnglvltpsivttnkkladpvtlkietkvlgpanl 2575	75
. Оу	2000 -KNLAPHHASPDPPAPPASASDPHREKTQSKPFSIQELELRSLGYHGSSYSPEGVE 2054	54
QQ	lpsklptevnhvpsgpsipadr	31
δλ	2055 PVSPVSSPSLTHDKGL	32
QQ	2632 sfprashpsstastalstnatvmlaagipvpqfissihpegsvimpphsitgtvslshls 2691	91
δy	ESQPSSSPLLQTAPGVKGHQRVVTLAQH 213	88
qq	2692 ageyrmntotlositysirpealhspr-aplgpagievra 2730	000

Sep 10

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2269
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2139 ISEVITQDYTRHHPQQLSAPLPAPLYSFPGASCPVLDLRRPPSD---LYLPPPDHGAPAR 2195
               2434 HSE-GDCNRRTPLTNRVWEDRPSSAGSTPFPYNPLIMRLQAGVMASPPPGLPAGSGPLA 2492
                                                                                                                                                                                                                                                                                                                                                      3020 gaetgptsfpspvsvsmkpdlpvslptgtapkgplfvpttsg-----pstppg---lv 3069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; SRCAP; Snf2 related CBP activator protein; antiviral; CREB; cAMP regulatory element; CREB binding protein; CBP; APPase; transcription activation; Dabb box NNA dependent helicase; adenoviral DBP protein; beta-actin; nuclear receptor; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    binding protein (CBP)
CREB binding protein,
affecting viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is an Snf2 related CREB (CAMP regulatory element)
                                                                                                                          2772 sevlvmgseyrlhpytvprdvrimvhphvtavseqpraadgvvkvppaskap----qqpg
                                                                                                                                                                              2328 RSQAVQEH----ASTNMGLEAIIRKALMGKYDQWEE-SPPLSANAFNPLNASASLPAAMP
                                                                                                                                                                                                                                                                       2383 ITAADGRSDHTLTSPGGGGKAK---VSGRPSSRKAKSPAPGLASG--DRPP----SVSSV
                                                     ----PH-----SEGGKRSPEPNKTSVLGGGEDG
                                                                                                         2222 IEPVSPPEGMTEPGHSRSAV-----YPLLYRDGEQTEPSRMGSKSPGNTSQ----PP
                                                                                                                                                             2270 AFFSKLTESNSAMVKSKKQEINKKLNTHNRNE--PEYNISQPGTEIFNMPAITGTGLMTY
                                                                                                                                                                                                                                   Snf2 related cAMP regulatory element (CREB) activator protein, capable of co-activating useful for modulating transcription and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 77-86; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB50362 standard; protein; 3118
                                                                                                                                                                                                                                                                                                                                                                                                 3070 lphtefqpapkqdssphltsq 3090
                                                                                                                                                                                                                                                                                                                                                                                 GPHHAWDEEPK----PLLCSQ 2509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAY-1999; 99US-0136620.
25-MAY-2000; 2000US-0579181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAY-2000; 2000WO-US14719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYSL-) UNIV SAINT LOUIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chrivia J, Yaciuk P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-061545/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAC89859
                                                    2196 GS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human SRCAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-DEC-2000
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                          2731
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binding protein (CBP) activator protein (SRCAP) polypeptide. It has APPase activity and is capable of activating transcription. SRCAP polypeptides are useful for activating transcription in a cell, for enhancing CREB (CAMP requiatory element) binding protein (CBP) mediated activation of transcription in a cell, for treating a patient having a disease involving a function such as insufficient transcription of a gene, e.g. a gene mediated by CBP co-activation, DEAD box RNA dependent helicase, adenoviral DBP protein, beta-actin or a nuclear receptor as antibodies, antisense molecules, polynuclectides or ribozymes, are useful for treating diseases mediated by SRCAP-activated transcription, for example, infection by adenovirus, hepatitis C virus, human immunodeficiency virus type-1, Epstein Barr virus, cytomegalovirus or ellrslppqllegpsspsqtpsshd-sdtrdg--peegaeeeppqvleikppp--savt 336 137 KDRSLTGKLEPVSPPSPPH--TDP------ELELVPPRLSKEEL-IQNMDRVDREI 183 184 TMVEQQISKLKKKQQQLEEEAAKPPEPEKP------VSPPPIESKH-----R 224 ---etriaelrkegfwslkrlpkvpepprpkghwdylceemgwlsadfagerrwkrgvar 112 SLVQII ---YDENRKKAEAAHRILEGLGPQVELPLYNQPSDTRQYHENIKINQAMRKKLI 281 QERMQSRVGQRGSG-LSMSAARSEHEVSEIIDGLSEQENLEKQMRQ-LAVIPPMLYDADQ 404 QRIKFINMNGLMADPMKVYKDRQVMNMWSEQEKETFREKFWQHPKNFGLIASFLERKTVA 464 -----ECVLYYYL-----TKKNENYKSLVRRSYRRRGKSQQQQQQQQQQQQQQQ regelsmeellqqyagayapgsgssededevdanssdcepegpveaeeppgedsssqs 446 dsvedrsedeedehseeetsgssaseesesesedaqsqsqadeeeedddfgveyllar 506 vmlnwemelkrwcpsfkiltyygaqkerklkrqgwtkpnafhvcitsyxlvlqdhqafrr 686 222 ssppppasrlddedgdfqpqedeeeddeetieveeqqegndaeaqrreiellrregelpl 281 LYFKRRNHARKQWKQKFCQRYDQLMEALEKKVERIENNPRRRAKESKV------QPMPRSSQEEKDEKEKEKER-----EKEEEKPEVENDKEDLLKEKTDDTSG-----E deeqseadagsgpptpgpttlgpkkeitdiaaaaeslqpkgytlattqvktpiplllrgq RNWSA1ARWGSKTVSQCKNF-----YFNYKKR------QN-----L Indels 1169; Length 3118; ---RITRSMANEANSEEAI-TPQQSAELA--Score 477.5; DB 22; Pred. No. 4.8e-18; 0; Mismatches 1109; ----ANSOGRRKG--------REYYEKQFPEIRKORE-----TEEEMETAKKG-Conservative 330; 3.6%; 18.6%; DNDEKEAVASKGRKT - - - - - - -3118 AA; Best\_Local Similarity Matches 597; Conserv MELN --- ESSRWhepatitis B virus Sequence Query Match 7 225 282 162 347 282 405 465 387 510 207 687 26 337 447 557 581 607 627 632 \$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$ 셤 ò δ g g Op g g g οy g οy δ à ò ŏλ g δ g δ g ò 8 셤 ò

683 802 740 853 777	787 965 836 1023	895 1081 950 1137	980 1197 1028 1257	1069 1311 1129 1360	1186 1396 1232 1456	1284 1516 1337 1576	1397 1604 1456 1651 1512 1704
DEILQOH	qeg: KEE	VEEGEECKPPA-AEELAVDTGKAEEPVKSECTEEAEEGPAKGKDAEAAEATAEGALKAEK ::     :	qlaslaqrpvanaspqKpLDLKOLKQRAAAIPPIQVTK qlaslaqrpvanaggskpltfqiqgnkltltgaqvrqlavgqprplqmpptmvnntgvvkVHEPPREDAAPTRPAPPAPPPQNLQPESDAPQQPGSSPRGKSRSPAP   :	PADKEAFAAEAQKLPGDPPCWTSGLPFPVPPREVIKASPHA   : : :	SVQLHVPYSEHAKAPVGPVTMGLPLPMDPKKLAPFSGVKQEQLSPRGQAGPPESLGV  :	TPADVLYKGTITRIIGEDSPSRLDRGREDSLPKGHVIYEGKKGHVLSYEGGM     :   :     :     :     :	ERHSPHHLKEQHHIRGSITQGIPRSYVEAQEDYLRREAKLLKRECTPPPPPPSRDITEAY
663 743 684 803 741 854	778 906 788 966	837 1024 896 1082	951 1138 981 1198	1029 1258 1070 1312	1130 1361 1187	1233 1457 1285 1517	1338 1577 1398 1605 1457
oy oy ob	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	oy oy	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Oy Oy Oy	oy Oy Ob	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

ζ	1513	GTASSSGGSTARGAPVIVPELGKPROSPLTYEDHGAPFAGHLPRGSPV 1560
QΩ	1705	sqasslvvsasgaaplpvtmvsrlpvskdepdtltlrsgppsppstatsfggprprrqp- 1763
δλ	1561	LQE
QQ	1764	pppprspfyldsleekrkrqrserlerifqlseahgalapvygtevldfctlpqpva 1820
δy	1594	KSPHSTVPEHHPHPISPYEHLLRGVSGVDLYRSHIPLAFDPTSIPRGI 1641
Dp	1821	spigprspgpshptfwtyteaahravlfpggrldglseiierfifvmppvea 1872
Οy	1642	PLDAAAAYYLPRHLAP1675
QQ	1873	pppslhachpppwlaprqaafqeqlaselwprarplhrivcnmrtqfpdlrliqydcgkl 1932
ō	1676	-TAALENRQTIINDYITSQQMHHNTATAMAQRADMLRG- 1712
qq	1933	qtlav1lrq1kaeghrv1iftqmtrm1dv1eqf1tyhghly1r1dgstrveqrqa1merf 1992
δλ	, 1713	LSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAMDR 1757
qq	1993	nadkrifcfilstrsggvgvnltgadtvvfydsdwnptmdagagdrchrig 2043
οy	1758	1770 POPESS 1770
g	2044	qtrdvhiyrlisertveenilkkanqkrmlgdmaieggnfttayfkqqtirelfdmplee 2103
δλ	1771	RHSSS-PLSPGGPTHLTKPTTTSSSERERDR1800
QQ	2104	
ογ	1801	DRERDREREKSILTSTTTVEH1823
qq	2164	fpagegeeagrpgaedeemsraegelaalvegltpieryamkfleasleevsreelkgae 2223
οy	1824	APIWR-PGTEQSSGSSGSSGGGGSSSRPASHSHAHQHSPIS 1864
QQ	2224	desscotgogthrrskkakaperpotrv
Qy	1865	ITAVEPSKPT
qq	2284	erlrgaraetgganhtpvisahgtrstttpprcsparervprpaprprpt 2333
οy	1922	GGTLDGVYPTLMEPVLLPKEAPRVARPERPRADTGHAFLAKPPARSGLEPASSPSKGSEP 1981
qq	2334	pasapaaipalvpvpvsapvpisapnpitilpvhilpsppppsqippcsspactp 2388
δλ	1982	RPLVPPVSGHATIARTPAKNLAPHHASPDPPAPPASASDPHREKTQSKP 2030
qq	2389	ppactpppahtpppaqtclvtpssplllgppsvpisasvtnlplglrpeaelcagal 2445
οy	2031	LRSLGYHGSSYSPEGVEPVSPV
qq	2446	:       : . :       : :
δŏ	2073	HLEELDKSHLEGELRPKQPGPVKLGGEAAHLPHLRPLPESQPSSSPLLQTAPGV 2126
qq	2506	gqeqeapdsaegttltvlpegeelplcvsesnglelppsaasdeplqeplead 2558
δλ	2127	KGHQRVVTLAQHISEVITQDYTRHHPQQL-SAPLPAPLYSFPGASCPVLDLRRPPSDLYL 2185
g G	2559	rtseelteaktptsspekpgelvtaevaapstsssatssp 2598
οy	2186	PPPDHGAPARGSPHSEGGKRSPEPNKTSVLGGGEDGIEPVSPPEGMTEPGHSRSAVYPLL 2245
qq	2599	
οy	2246	YRDGEQTEPSRMGSKSPGNTSQPPAFFSKLTESNSAMVKSKKQEINKKLNTHNRNEPE 2303
QQ	2609	rrtsadveirgggfgrpgqppgpkvlrklpgrlvtvveekelvgrrr 2655
è	2304	VNTSOBETETEMMENTTERSTMTVDSOAVORHASTNMCLRATTRKATMCKVDOWRRSDDL 2363

135;

991; Gaps

Indels

22; 982;

Local Similarity

paqpkpgvaappevapa-----pkswasnkqgqqgdgiqvnsqfqqefpslqa 150

103

17

ò g

PRYPPHSLSYPVQIARTHTDVGLLEYQHHSRDYASHLSPGS-----IIQPQRRRPSLLS 70

511 690 603 642 367 441 501 554 631 643 tpvvh-etepesgsq-prpavlsgyfkqfqkslpprfqrqqeqmkqqqwqqqqqgvlpq 700 | | | | :: ::: | :: | | :: pihpgmippkplmrrdqmegspnssesfehiarsardhaislseprmlwgsdpyphaepq 820 SGAPQ------DSDSSATCSADEVDEAEGGDKNRLLSPRPSLLTPT-GD 950 124 404 464 MPRSSQEEKDEKEKEKEREREEKPEVENDKEDLLKEKTDDTSGEDNDEKEAVASKGRKT 571 h-----grpgpfpskqqva | :: : : : : : | |: :|| : :-|:: :-|| : :-|| 442 dedeiwkgrrrggseisaaverarkrreeeerrmeegrkaacaeklkrldeklgilekgp 572 ANSQGRRKGRITRSMANEANSEEAITPQQSAELASMELNESSRWTEEEMETAKKGLLEHG :| : | :: | | ::|||| :| -----ekekelgkmkegekecelekerekleek----1e LAVDIGKAEEP - - VKSECTEEAEEGPAKGKDAEAAEATAEGALKAEKKEGGSGRATTAKS -----pgpslrppnvacwrdgg -ATGOPAGSEDLTKDRSLTGKLEPVSPPSPPHTDPELELVPPRLSKEELIQNMDRVDREI TMVEQQI-----SKLKKKQQQLEEE--AAKPP---EPEKPVSPPPIESKHR---SLVQI 230 IYDENRKKAEAAHRILEGLGPQVELPLYNQPSDTRQYHENIKINQAMRKKLILYFKRRNH 290 ARKOW--KOKFCORYDOLMEALEKKVERIENNPRRRAKE---SKVREYYEKOFPEIRKOR 317 adegwagaqmevdyteql--nfsdddeggsnspkennsedggskasenne-----nkk ELQERMQSRVGQRGSGLSMSAARSEHEVSEIIDGLSEQENLEKQMRQLAVIPPMLYDADQ etdevsntk----sssqipaqpsvakvpygkgpsfnqergtsshlppppkll-aqq **QRIKFINMNGLMADPMKVYKDRQVMNMWSEQEKETFREKFMQHPKNFGLIASFLERKTVA** 465 -ECVLYYYLTKKNENYKSLVRRSYRRGKSQQQQQQQQQQQQQQQQ------QQQP 632 RNWSAIARWVGSKTVSQCKNFYFNYKKRQNLDEILQQHK-LKMEKERNARRKKKKAPAAA 691 SEEAAFPPVVEDEEMEASGVSGNEEEMVEEAEALHASGNEVPRGECSGPATVNNSSDTES 701 tvpsqpssstvpppphrplyqpmqphpqhlasmgfdprwlmmqsymvprmmsgrpamdip PAPPSPSAPPPVVPKEEKEEETAAAPPVEE--------GEEQKPPAAEE qattpkateepedvrseaaldgeg-----itaaysvehngleahpk----adfire | | | | | | | : | :: seaqyqkflsrsvedvrphhtdanngsac-----feapdqktlsapqeerisavesq PRANAS-----PQKPLDLKQLKQRAAAIPPI-----QVTKVHEPPREDA---AP 185 kaagspsssd---qdeklpgqdestagts------eqndilk------vvekriacgppqaklngqqaalasqyrammppymfqqyprmtypplhgpmrfppslse-------remekerkgek------ekelergk-----IPSPHTEAAKDTGQNGPKP------TLGADGPPPGPPTPPRRTSRAPIEPTPASEA. ---agdgekkeketnddnyg----951 606 921 δy g ŏ

,		
a	1039	ekaekgppa 1071
οy	1097	PRPPTISNPPLISSA-KHPSVLERQIGAISQGMSVQLHVPYSEHAKAPVGPVTMGLPLP 1155
qq	1072	
ò	1156	MDPKKLAPFSGVKOROLSPRGOAGPPSLGVPTAORASVLRGTALGSVPGGSTTKGTP8 1215
· 6	1103	ditek - bleboxtvovensyktvnortmannvykeekonekyikiklive 1151
}		
ογ	1216	RVPSDSAITYRGSITHGTPADVLYKGTITRIIGEDSPSRLDRGREDSLPKGHVIYEG 1272
qq	1152	6
ογ	1273	GGMSVTQCSKEDGRSSSGPPHETA
Ω	1209	trdypqyrdnkpraehips
ογ	1321	SIEGLMGRAIPPERHSPH-HLKEO
qq	1263	rgsetdtdseihesasdkdslskgklpkreerpenkkpvkphssfkpdnhvrid-nrlle 1321
δ	1361	SYVEAQEDYLRREAKLLKREGTPPPPP
q	1322	
ογ	1407	PLKEGS
g	1382	: :
ογ	1462	RSLIGS
g	1413	rkfdparerprigrptrpprgdkpprfrrlrereaasksnevva 1456
δ	1516	ARGAPVIVPELGKPROSPLTYE
Q	1457	:   ::
δ	1558	SPVTMREPTPRLQEGSLSSSKASQDRKLTSTPREIAKSPHSTVPEH 1603
qq	1517	knadlnagtvvkvgenvlppkrelakrsfssgrpvdrgnrrgnngppksgrnfsgprner 1576
δ	1604	EHLLRGVS
q	1577	
ογ	1658	RQTIINDYITSQQMHHNTA
QQ	1612	
δ	1717	TPGTPAT
qq	1643	ekvdalsgfdlnnyasvviiddhpevtviedp
ŏ	1771	TKPTTTSSSERERDRDRERDI
g	1675	gsnlnddgftevskkgqkrlqdeerrkkeeqvigvwnkk 1714
ογ	1831	TEOSSGSSGSGGGGSSSRPASHSHAHQHSPISPRTODALQORPSVLHNTGMKGI 1886
Ωp	1715	nanekgrsgtsklpprfakkqatgiqqaqssasvppl 1751
ογ	1887	ITAVEPSKPTVLRSTSTSSPVRPAATFPPATHCPLGGTLDGVYP-TLMEPVLLPKEAPRV 1945
qq	1752	:    :
ŏ	1946	ARPERPRADIGHAFLAKPPARSGLEPASSPSKGSEPRPLVPPVSGHAII 1994

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antiporiatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosupressant; cardiant; immunostimulant; thrombolytic; coagulant; vasctropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antidiantemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; 2039 2259 cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive. 2147 2208 tkmedtlvnnvplpntlplpkretiggsssltsvpptt-----fsltfkmesarkawe 2260 -----ARTPAKNLAPHHASPDPP---APPASASDPHREKTQSKPFSIQELELRSLGYHG 2045 SSYSPEGVEPVSPVSSPSLTHDKGLPKHLEELDKSHLEGELRPKQPGPVKLGGEAAHLPH 2105 ----pappapaqtqaq-thkpv 1942 1943 gnplqttsgsskgpppsirlpsagtpng------tdyvasgksigtpgshgt 1988 gakngge----sgleigtdtiqfgapasngne----nevvpvlseksadkipepkegrg 2090 KSPGNTSQPPAFFSKLTESNSAMVKSKKQ-EINKKLNTHNRN------EPEYN---- 2305 -----ISQPGTEIFNMPAITGTGLMTYRSQAVQEHASTNMGLEAIIRKAL 2350 2351 MGKYDQWEESPPLSANAFNP---LNASASLPAAMPITAADGRSDHTLTSPGGGGKAKVS 2406 LSAPL-----PAPLYSFPGASCPVLDLRRPPSDLYLPPPDHGAPAR-----GSPHSE 2201 GRPSSRKAKSP-----APGLASGDRPPSVSSVHSEGDCNR-RTPLINRVWEDRPSSA 2457 1989 ltaelwdnkvappavlndiskklgpi----sppq----psvsawnkpltsfgsapsse GGKRSPEPNKTSVLGGGEDGIEPVSPPEGMTEPGHSRSAVYPLLYRDGEQ--TEPSRMGS kqp---ragpikaqklpdlspvenkehkpgpigkerslknrkvkdaqqvepeggekpspa LRPLPESQPSSS-----PLLQTAPGVKGHQRVVTLAQHISEVITQDYTRHHPQQ---1865 ilasalastsaptpapaasspaapvitaptipasap----tasvpla-----Human ORFX ORF995 polypeptide sequence SEQ ID NO:1990 2458 GSTPFPYNPLIMRLQAGVMASPP-----PPGLPAGSGPLA 2492 gt----yttsslstkstttsdppnickvkpqqlqtsslpsa 2357 AAB41231 standard; Protein; 2971 AA asasapapap-tpvsapn------(first entry) Homo sapiens 08-FEB-2001 AAB41231; 1805 1995 1909 2106 2155 2202 2040 2260 2091 2306 2407 2321 οy qq qq g QQ δ g qq Qγ δy à δ g ò Dp qq δ ò

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344 deeeedddfavevllardeeaseadaasanntnanttlankkeitdiaaaaeslankavt 403
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; sequences have activities such as: cytostatic; hepatotropic; vulnerary; osteopathic; antiparkinsonian; nocitopic; neuroprotective; catalant; thrombolytic; cagulant; vasotropic; nmunostimulant; cardiant; thrombolytic; cagulant; vasotropic; antidabetic; hypotensive; dermatological; immunosuppressive; antidabetic; hypotensive; dermatological; or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, virai, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anneamia, burns, wounds, bone and cartilage damage, coaqulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 3.5%; Score 456; DB 21; Length 2971;
Best Local Similarity 19.6%; Pred. No. 7.4e-17;
Matches 596; Conservative 305; Mismatches 1141; Indels 1006; Gaps 134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 LLATGQPAGSEDLTKDRSLTGKLEPVSPPSPPHTDPELELVPPR---LSKEELIQNMDRV 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DREITMVEQQISKLK ---KKQQQLEEEAAKPPEPEKPVSPPPIESKHRSLVQIIY ----
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                                                                                                                                                  31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                         31-MAR-2000; 2000WO-US08621
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05-0CT-2000
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ογ	392	PMLYDADQQRIKFI43
QQ	404	lattqvktpiplllrgqlreyqhigldwlvtmyekklngilademglgktigtisllahl 463
οy	432	WS
g	464	acekgnwgphliivptsvmlnwemelkrwcpsfkiltyygaqkerklkrqgwtkpn 519
δy	466	CVLYYYLTKKNENYKSLVRF
qq	520	afhvcitsyklvlqdhqafrrknwryllldeaqniknfksqrwqsllnfnsqrrllltgt 579
οy	508	
qq	580	plqnslmelwslmhflmphvfqshrefkewfsnpltgmiegsqeyneglvkrlhkvlrpf 639
Qy	537	EVENDKEDLLKEKTDDISGEDNDEKEAVASKGRKTANSQGRR 578
qq	640	
δ	579	KGRITRSMANEANSEEAITPQQSAELASMELNESSRWTEEEMETAKKG 626
qq	691	msvinilmqlrkvcnhpnlfdprpvtspfitpgicfstaslvlratdvhplqridmgrfd 750
δ	627	LLE-HGRNWSAIARMVGSKTVSQCKNFYFNYKRQNLDEILQQHKLKMEKERNARRKKK 685
qq	751	glegrsryeadtflprhrlsr
δλ	989	APAAASEEAAFPPVVEDEEMEASGVSGNEEEMVEEAEALHASGNEVPRGECSGPAT
qq	780	vatapdppprpkpvkmkvnrmlqpypkqegrtvvvvnnp 818
οy	746	KDTGONGPKP PATLGADGPPP
Q	819	raplgpvpvrpppgpelsagptpgpvpqvlpaslmvsaspagppllpasrppgpvllp 876
γ	793	PPAP
q	877	vrlspa
δλ	839	EGEEGKPPAABELAVDTGKAEEPVKSECTEEAEEGPAKGKDAEAAEATAEGALKAEKKEG 898
ор	927	pssllkpltvppgytfpp944
QΫ	899	GSGRATTAKSSGAPQDSDSSATCSADEVDEAEGGDKNRLLSPRPSLLTPTGD 950
QQ	945	aaatttstttatatttavpaptpapqrlilspdmqarlpsgevvsiggla 994
Qy	951	RANASPQKPLDLKQLKQRAAA
qq	995	slagrpvanaggskpltfgiggnkltltgagvrqlavggprplgmpptmvnntgvvkivv 1054
δy	982	PPREDAAPTKPAPPAPPPQNLQPESDAPQQPGSSPRGKSR
qq	1055	
δλ	1029	DKEAFAAEAQKLPGDPPCWTSGLPFPVPPREVIKA
g	1115	
Qγ	1073	FSYAPPGHPLPLGLHDTARPVLPRPPTISNPPPLISSAKHPSV
qq	1169	sstvsvplssslpisvpttlpapasapltipisapltvsasgpall1214
δy	1133	LHVPYSEHAKAPVGPVTMGLPLPMDPKKLAPFSGVKQEQLSPRGQAGPPESLGVPTAQ 1190
Q	1215	tsvtpplapvvpaapgppslap-sgaspsasaltlglatapsl 1256
οy	1191	BASVLRGTALGSVPGGSITKGIPSTRVPSDSALTYRGSITHGTP 1234
qq	1257	sssqtpghplllaptsshvpglnstvapacspvlvpasalaspfpsapnpapaqasllap 1316

ADVLYKGTITRIIGEDSPSRLDRGREDSLPKGHVIYEGKKGHVLSYEGGMSVTQCS 1290   :  :  :    assasqalatplapmaapqtailapspapplaplpvlapspgaapvlassqtpvpvmaps 1376	PHETAAPKRTYDMMEGRVGRAI-SSASIEGL-MGRAIPPERHSPH 1343	143	ninegalitatitatikaivenyelyinekan kantan kant	PLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPR-PLKEGSITGGTPLKYDTG 1462 	TFPPVHPLDVMADARALERACYEESLKSRPGTASSS 151		:   :  vvsasgaaplpvtmvsrlpvskdepdtllrsgppspstatsfggprprrqpppp 1620	PRLQESPH 1597     :   :	FDPTSIPRGIPLDAAA		168	eqiaseiwprarpinrivcnmrtqipdiriiqydcgKlqtlavi	NRQ	LSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAMDR 1757	.tgadtvvíydsdwnptmdagagdrchriggtrdvh 1903		iyrlisertveenilkkanqkrmlgdmaieggnfttayfkqqtirelfdmpleepssssv 1963	GGPTHLTKPTTTSSSERERDR1800	hilegalcraedeediraatgakaegvaelaefnendgfpageg 2023	SKEREKSILTSTTTVEH1823		APIWR-PGTEQSSGSSGSSGGGGSSSRPASHSHAHQHSPISPRTQDA 1870	rkdldqakeevfrlpqeeeegpgagdesscgtgggthrrskkakaperpgtrvserlrga 2143	ITAVEPSKPTVLRSTSTSSPVRPAATFPPATHCPLGGTLDG 1927			-vpvpvsapvpisapnpitilpvhilpsppppsqippcsspactpppactp 2248	PHHASPDPPAPASASDPHREKTQSKPFSIQEL 2036	ppaqtclvtpssplllgppsvpisasvtnlplglrpeaelcagalaspesl 2305
	KEDGRSSSGP-				ASTTGSKK	GGSIARGAPVIV	:   :   vvsasgaaplpvtmvsrlpvskde		STVPEH		-	-		-	fcfilstrsggvgvnltgadtvvfydsdw-			PLSP	psapeeeeetvaskqthilegalcra	DRERDRDREREKSI	-			LOORPSVLHNTGMKG	raetgganhtpvisahg	VYPTLME 	aipal	VSGHATI I	ppahtp-
1235	1291	1377	1432	1404	1463	1519	1565	1567	1598	1681	1648	1/33	1681 1793	1713	1853	1758	1904	1776	1964	1801	2024	1824	2084	1871	2144	1928	2194	1988	2249
oy op	Óγ	q i	8 3	Qy Dp	δο d	g &	q	ço q	οy	Q	ò	9	G G	ογ	q	οχ	q	ò	q	οy	g	ò	a	Qγ	g	Qγ	අ	ογ	QQ

2556 sslptppqqpfiarrhielgvtgggspengdgallaitppavkrrrgrppkknrspadag 2615 2133 VTLAQHISEVITQDYTRHHPQQL-SAPLPAPLYSFPGASCPVLDLRRPPSDLYLPPPDHG 2191 2192 APARGSPHSEGGKRSPEPNKTSV-----LGGGEDGIEPVSPPEGMTEPGHSRSAVYPLL 2245 2500 ----eekelvrrrrqqrgaastlvpgvsetsaspgspsvrsmsgpessppiggpceaaps 2555 2616 rgvdeapsstlkgktngadpvpgpetlivadpvlepglipgpgplgpgpvhrpnpllsp- 2674 ELRSLGYHGSS----YSPEGVEPVS----PV-----SSPSLTHDKG-LPKHLEELD 2078 2246 YRDGEQTEPSRMGSKSPGNTSQ-PPAFFSKLTESNSAMVKSKK-QEINKKLNTHNRNEPE 2303 2304 YNISQPGTEIFNMP-----AITGTG------LMTYRSQAVQEH------ASTN 2339 2399 GGGKAKVSGRPSSRKAKS-PAPGLASGDRPPSVSSVHSEGDCNRRTPLTNRVWEDRPSSA 2457 Snf2 related cAMP regulatory element (CREB) binding protein (CBP) activator protein, capable of co-activating CREB binding protein, useful for modulating transcription and for affecting viral infection Human; SRCAP; Snf2 related CBP activator protein; antiviral; CREB; cAMP regulatory element; CREB binding protein; CBP; ATPase; transcription activation; DEAD box RNA dependent helicase; adenoviral DBP protein; beta-actin; nuclear receptor; viral infection. 2414 --tseelteaktptsspekpqelvtaevaapstsssats-----spegp 2079 KSHLEGELRPKQPGPVKLGGEAAHLP-----HLRPLPESQPSSSPLLQTAPGVKGHQRV 2366 pdsaegttltvlp----egeelplcvsesnglelppsaasdeplgepleadr----2340 MGLEAIIRKALMGKYDQWEESP-PLSANAFNPLNASASLPAAMPITAADGRSDHTLTSPG 2458 GSTPFPYNPLIMRLQAGV------MASPP-----PPGLPAGSGP 2490 AAB50363 standard; protein; 2972 AA 27-MAY-1999; 99US-0136620. 25-MAY-2000; 2000US-0579181. 25-MAY-2000; 2000WO-US14719. (first entry) (UYSL-) UNIV SAINT LOUIS. ď. WPI; 2001-061545/07. N-PSDB; AAC89860. Chrivia J, Yaciuk WO200073467-A1. Homo sapiens. 12-MAR-2001 Human SRCAP. 07-DEC-2000. AAB50363; 10 셤 ò a ò g ò q ò g ò g ò g ò g ò g

The present sequence is an Snf2 related CREB (cAMP regulatory element)

Dinding protein (CBP) activator protein (SRCAP) polypeptide. It has
Dipperides are useful for activating transcription. SRCAP

DOLYPEPERIOR (CAMP regulatory element) binding protein (CBP) -mediated
activation of transcription in a cell, for rectivating protein (CBP) -mediated
activation of transcription in a cell, for treating a patient having a
disease involving a function such as insufficient transcription of a
gene, e.g. a gene mediated by CBP co-activation, DEAD box RNA dependent
helicase, adenoviral DBP protein, beta-actin or a nuclear receptor
affected by SRCAP protein. Compounds that modulate SRCAP function, such
as antibodies, antisense molecules, polynucleotides or ribozymes, are
useful for treating diseases mediated by SRCAP-activated transcription,
for example, infection by adenovirus, hepatitis C virus, human
immunodeficiency virus type-1, Epstein Barr virus, cytomegalovirus or Claim 1; Page 86-94; 103pp; English. hepatitis B virus. 

2972 AA; Sequence

151 sspsqtpsshdsdtrdgpeegaee----eppqv---leikpppsavtgrnkgpwhpded 202 123 LLATGQPAGSEDLTKDRSLTGKLEPVSPPSPPHTDPELELVPPR---LSKEELIQNMDRV 179 304 691 msvinilmqlrkvcnhpnlfdprpvtspfitpgicfstaslvlratdvhplgridmgrfd 750 DREITMVEQQISKLK---KKQQQLEEEAAKPPEPEKPVSPPPIESKHRSLVQIIY---- 231 deeftaneeeaedeedtiaaeeqlegevdhamelselaregel----smeellqqyaga 257 282 LYFKRRNHARKQWKQKFCQRYDQLMEALEKKVERIENNPRRRAKESKVREYYEKQFPEIR 341 ------drsedeedehseeeetsgssaseeseedagsgsga 343 : | | | : | : | | | 344 deeeedddfgveyllardeeqseadagsgpptpgpttlgpkeitdiaaaaeslgpkgyt 403 431 -----WS--------EQEKETFREKFMQHPKNFGLIASFLERKTVAE----- 465 acekgnwgphliivptsvmlnwemelkrwcpsf----kiltyygaqkerklkrggwtkpn 519 -----KEKEAEKEEE-----KP- 536 ---EVENDKEDLLKEKTD------DISGEDNDEKEAVASKGRKTANSQGRR 578 579 KGRIT-----RSMANEAN-----SEEAITPQQSAELASMELNESSRWTEEEMETAKKG 626 EFQPGNERSQE----LHLRPESHSYLPELGKSEMEFI--ESKRPRLELLPD--PLLRPSP 122 342 KORE-----LQERMQSRVGQRGSGLSMSAARSEHEVSEIIDGLSEQENLEKQMRQ 391 ------DENRKKAEAAHRILEGLGP-QVELPLYNQPSDTRQYHENIKINQAMRKKLI 258 yapgsgssedededevdanssdcepegpveaeep---pqedsssgsdsve-----LAVIP----PMLYDADQQRIKFI------NMNGLMADPMKVYKDRQVMNM--------CVLYYYLT-----KKNENYKSLVRRSYRRGKSQQQQQQQQQQQQQ Query Match 3.4%; Score 452; DB 22; Length 2972; Best Local Similarity 19.0%; Pred. No. 1.2e-16; Matches 587; Conservative 296; Mismatches 1107; Indels 1092; 180 203 208 232 305 392 464 466 537 ò g g ò qq ŏ qq ò g ò g δŏ g ò a οy g

ΟŊ	627	E-HGRNWSAIARWVGSKTVSQCKNFYFNYKKRQNLDEILQQHKLKMEKERNARRKKK 	685
QQ	751	liglegrsrrvlle	779
δy	989	APAAASEEAAFPPVVEDEEMEASGVSGNEEEMVEEAEALHASGNEVPRGECSGPATVNNS	745
QQ	780	vnrml	818
οy	746	SDTESIPSPHTE-AAKDTGONGPKPPATLGADGPPGPPTPPRRTSRA	792
QQ	819	aqptpqpvpqvlpaslmvsaspa	876
Qy	793	ATGAPTPppAp	838
Q	877		926
٥y	839	EGEEQKPPAAEELAVDTGKAEEPVKSECTEEAEEGPAKGKDAEAAEATAEGALKAEKKEG	868
qq	927	ssslkpltvppgytfpp	944
οy	668	GSGRATTAKSSGAPQDSDSSATCSADEVDEAEGGDKNRLLSPRPSLLTPTGD	950
qq	945	aaatttstttatatttavpaptpapqrlilspdmqarlpsgevvsigqla	994
οy	951	PRANASPQXPLDLKQLKQVRAAAIPPIQVTKV	981
Op	995	slagrpvanaggskpltfgiggnkltltgagvrqlavgqprplgmpptmvnntgvvkivv	1054
ΟŸ	982	HEPPREDAAPTKPAPPAPPPQNLQPESDAPQQPGSSPRGKSRSPAP	1028
qq	1055	rqaprdgltpvpplapaprppssglpavlnprptltpgrlptptlgtarapmptptlvrp	1114
δy	1029	PADKEAFAAEAQKLPGDPPCWTSGLPFPVPPREVIKASPHAPDP	1072
qq	1115		1168
δλ	1073	SAFSYAPPGHPLPLGLHDTARPVLPRPPTISNPPLISSAKHPSVLERQIGAISQGMSVQ	1132
qq	1169		1214
δŏ	1133	Td.	1189
qq	1215	tsvtpplapvvpaapgppslqpsg-aspsasaltlglata	1253
δλ	1190	QEASVLRGTALGSVPGGSITKGIPSTRVPSDSAITYRGSITHG	1232
qq	1254	slsssqtpghplllaptsshvpglnstvapacspvlvpasalaspfpsapnpapagasl	1313
οy	1233	-TPADVLYKGIITRIIGEDSPSRLDRGREDSLPKGHVIYEGKKGHVLSYEGGMSVT	1287
q	1314	lapassasqalatplapmaapqtailapspapplaplpvlapspgaapvlassqtpvpvm	1373
٥y	1288	QCSKEDGRSSSGPPHETAAPKRIYDWMEGRVGRAI-SSASIEGL-MGRAIPPERH	1340
qq	1374	apsstpgtslasaspvpaptpvlapsstgtmlpapvpsplpspastgtlalapalapt	1431
δλ	1341	SPHHLKEQHHIRGSITQGIPRSYVEAQEDYLRREAKLLKREGTPPPPPPSRDLTEAYKTQ	1400
qq	1432	lggsspsqtlslgtgpppfptqtls	1458
οy	1401	ALGPLKLRPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPR-PLKEGSITQGTPLKY	1459
qq	1459	ltpa-sslvptpaqtlslapgpplgptqtlslapapplapaspvgpapaht	1508
δž	1460	DTGASTTGSKKHDVRSLIGSPGRTFPPVHPLDVMADARALERACYEESLKSRPGTA	1515
qq	1509	ltlapasssasllapasvqtltlspapvptlgpaaaqtlalapastqspasqa	1561
ΟŊ	1516	SSSGGSIARGAPVIVPELGKPRQSPLTYEDHGAPFAGHLPRGSPVTMR	1563
d d	1562	sslvvsasgaaplpvtmvsrlpvskdepdtltlrsgppsppstatsfggprprrqp	1617

ŏ	1564	EPTPRGEGSLSSSKASQDRKLTSTPREIAK	
අ	1618	pppprspfyldsleekrkrqrserlerifqlseahgalapvygtevldfctlpqpvaspi 1677	_
οy	1595	SPHSTVPEHHPHPISBYEHLLRGVSGVDLYRSHIPLAFDPTSIPRGIPLD 1644	
g	1678	gprspgpshptfwtyteaahravlfpqqrldqlsellerflfvmppveappp 1729	_
δ d	1645	AAAAYYLPRHLAPNPTYPHLYPPYLIRGYPDTA	
2	1/30	sınacnpppw.taprqaarqeq.taselwprarpinrivcnmrtqrpdiriiqydcgkiqti 1/89	_
δ	1678		
qq	1790	avllrqikaeghrvliftqmtrmldvleqfityhghlylrldgstrveqrqalmerfnad 1849	
ΟŊ	1713	LSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAMDR 1757	
qq	1850	krifcfilstreggvgvnltgadtvvfydsdwnptmdagagdrchrigqtr 1900	
δý	1758	POPFSSRHS 1773	
a a	1901	dvhiyrlisertveenilkkanqkrmlgdmaleggnfttayfkqqtirelfdmpleepss 1960	
ΟŊ	1774	SS-PLSPGGPTHLTKPTTTSSSERENDR	
셤	1961	ssypsapeeeeetvaskqthilegalcraedeediraatgakaegvaelaefnendgfpa 2020	
οy	1801	DRERDRDREREKSILTSTTTVEH	
g	2021	gegeeagrpgaedeemsraegeiaalvegltpieryamkfleasleevsreelkgaeegv 2080	
οy	1824		
g	2081	eaarkdldga	
οÿ	1868		
qq	2141	rgaraetgganhtpvisahgtrstttpprcsparervprpaprprptpas 2190	
δý	1925	LDGVYPTLMEPV	
qq	2191		
δ	1985	VPPVSGHATIARTPAKNLAPHHASPD	
g	2246	ctpppahtpppaqtclvtpssplllgppsvpisasvtnlplg1rpeaelcaqalasp 2302	
ογ	2034	QELELRSLGYHGSSYSPEGVEPVSPV	
q	2303	eslelasvassetsslslyppkdllpvaveilpvseknlsltpsapsltleagsipngge 2362	
ò	2076	ELDKSHLEGELRPKQPGPVKLGGEAAHLPHLRPLPESQPSSSPLLQTAPGVKGH 2129	
qq	2363		_
οy	2130	QRVVTLAQHISEVITQDYTRHHPQ	
Q	2414	:: ::    : :     :    :   :	
δy	2189	DHG	
q	2453	:	_
οy	2249		
QQ	2466	:             sadveirgggtgrpg	
ογ	2307	SQPGTEIFNMPAITGTGLMTYRSQAVQEHASTNMGLEAIIRKALMGKYDQWEESPPLS 2364	
qq	2510		-
è	2365	2000 FIRHOSCOMART CMARGINES AND INDIVIDUAL AND	

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84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents rat p3103 protein, also referred to as Synamon in the title of the specification. The p3103 protein contains both an SH3 domain and a PDZ domain, and was identified as being able to interact with the protein SAPAPl via the yeast two-hybrid system. P3103 protein is therefore thought to be involved in neuronal function, and may be useful for the study of the human nervous system, and for the diagnosis, prevention and treatment of various neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                        Rat; p3103 protein; Synamon; SH3 domain; PDZ domain; SAPAP1 interaction; neuronal function; nervous system; neurological disorder.
                                                                   2610 spadagrgvdeapsstlkgktngadpvpgpetlivadpvlepglipgpgplipgpgpvh--- 2666
:| | : | | : | | 2550 ceaapssslptppqqpfiarrhielgvtgggspengdgallaitppavkrrrgrppkknr 2609
                                                                                                                                 2667 ---rpnpllspvekrrrgrppkardlpip-----gtissagdgnsesrtqppphp 2713
                                           -----LASGDRPPSVSSVHSEG 2437
                                                                                                   2438 DCNRRIPLINRVWE---DRPSSAGSTPFPYNPLIMRLQAGVMAS-----PPPPGLP 2485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               593 EEAI---TPQQSAEL--ASMELNESSRWTE-EEMETAKKGLLEHGRNWSAIARWVGSKTV 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.2%; Score 429; DB 21; Length 2091; ilarity 20.8%; Pred. No. 1.6e-15; Conservative 140; Mismatches 627; Indels 694;
                                           SPGGGGKAKVSGRPSSRKAKS----PAPG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               554..613
/note= "SH3 domain"
654..749
/note= "PDZ domain"
                                                                                                                                                                                                                                                                    AAB12000 standard; Protein; 2091 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 5-10; 13pp; Japanese.
                                                                                                                                                               2486 AGSGPLAGPHHAWDEEPKPLLC 2507
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2714 spltpl------ppllvc 2725
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                                                                                                                                                                                                                                                                                                                            19-DEC-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2091 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 384; Conserv
                                                                                                                                                                                                                                                                                                                                                             Rat p3103 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A protein Synamon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAA62000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Domain
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SQCKNFYENYKKRONLDEILGOHKLKMEKERNARRKKKAPAAASEBAAFPPVVEDBEME 706 	ASGVSGNEEEMVEBARALHASGNEVPRGECSGPATVNNSSDTESIPSPHTEAAKDTGONG 766 :	DGPPPGPPTPPRRTSRADIEPTPASEATGAPTPPPAPPSPSA 817			KDAEAAEATAEGALKAEKKEGGSGRATTAKSSGAPQDSDSSATCSADEVDEAE 930 	GGDKNRLLSPRPSLLTPTGDPRANASPQKPLDLKQLKQRAAAIPPIQVTKVHEPPRE 987     : :	-APPAPPPQNLQPESDAPQQPGSSPRGKSRSPAPPA 103	happpqphhhhahpphppemetggspddppprlalgpqpslrgwrgggpsptsgapspsh 1065	DKEAFAAEAQKLPGDPPCWTSGLPFPVPPREVIKASPHAPDPSAFSYAPPGH 1082 : :	PLPLGLHDTARPVLPRPPTISNPPLISSAKHPSVLERQIGAISQGMSVQL 1133 			TPADVLYK		GTITRIIGEDSPSRLDRGREDSLPKGHVIYEGKKGHVLSYEGGMSVTQCSKEDGRSSGP 1300 	AISSASIEGLM GRAIPPER 1339	aftsflpprplvhpltgkaldpasplglalaareralkessegggtpgpppppppry 1380		udppptillinisplisplisplialiepvillamguparieigyragigsgekaltasppaaris 1440 VIBBbaritabpropobobosonimesvemonionivinusplismuseso 1430	1	RSIHEIPREELRHTPE-LPLAPRPLKEGSITQGTPLKYDTGASTTGSKKHDVRSLIGSPG 1481	: 	RTFPPVHPLDVMADARALERACYEESLKSRPGTASSSGGSIARGAPVIVPELGKPRQSPL 1541	ptsptsprgneenglpllvlpppaps 1550	TYEDHGAPFAGHLPRGSPVTMREPTPRLQEGSLSSSKASQDRKLTSTPREIAKSPHSTVP 1601	166
		PKPPATLGA  :  ydrpsfl	PPPVVPKEE				DAAPTKP																			
647	707	767	818	926	878 938	931	886	1006	1031	1083	1134	1178	1181	1730	1241	1301	1323	1340	1370	1441	1423	1479	1482	1515	1542	1602
Qy	çy G	Oy Op	Οy	QQ	oy Dp	δ P	δy	Op	OY DP	6 64 64	δλ	qq	8	a	Oy Dp	δλ	Op	oy d	3 8	S 8	δy	q	οy	q	Qy Dp	δy

qa	1583	:   puppp			1602
QY	1662		PHLYPPYLIRGYPDTAALENRQTIINDYITSQQMHHNTATAMAQRADMLRGLSPRESSLA	OMLRGLSPRESSLA	1721
qa	1603	,	:	: : dseva	1629
λŏ :	1722		SQVPHLPVLVPPTPGTPATAMD 	FSSRHSSSPLSPGG	1781
qq 	1630	tltqgapaapgd-	apapgppapaapappapdb-	6	1661
å å	1782		PTHLTKPTTISSSERERDRDRERDRDREREKSILISTTTVEHAPIWRPGTEQSSGSSS	RPGTEQSSGSSGSS	1841
A (	7007		pupppg rasgressamprerissastrssi	>	1/03
ර් සි	1710		GGGGGSSSRPASHSHAHQHSPISPRTQDALQQRPSVLHNTGMKGIITAVEPSKPTVL 	TAVEPSKPTVL       :: 	1898
3 (	0 + 0 +	, , ,	5655185501 {p, {1975.		3011
oy G	1899	2	RSISISSPVRPAATFPPATHCPLGGTLDGVYPTLMEPVLLPKEAPRVARPERPRAD	EAPRVARPERPRAD	1954
3 8	17.73		TI babada TI aborbr	sprvsvrgagr	16/1
y do	1955		TGHAK-LAKPPAKSGEEFASSPSKGSEFRPLVPPVSGHATIAKTPAKNLAPHHASPDPPAP 	NLAPHHASPDPPAP 	2014 1846
QY	2015		-PASASDPHREKTQS-KPFSIQELELRSLGYHGSSYSPEGVEPVSPVSSPSLTHDKG	PVSSPSLT HDKG	2069
QO .	1847			 rggsggstdshhgg	1905
Qy	2070	;	-LPKHLEELDKSHLEGELRPKQPGPVKLGGEAAHLPHLRPLPESQPSSS	JPSSSSSS-C	2117
qa	1906		: :	:      kpsssifqnwpkpp	1945
Qy	2118		-PLLQTAPGVKGHQRVVTLAQHISEVITQDYTRHHPQQLSAPLPAPLYSFPGASCPVLDL	LYSFPGASCPVLDL	2176
d d	1946		lpplptgsgvssstaaapgatspsassasastr-hlggvefemrppl	[]	1992
ΟŊ	2177		RRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEPNKTSVLGGGEDGIEPVSPPEGMTEPGH	EPVSPPEGMTEPGH	2236
q	1993	rrapspsllpasdh	kvspaprpssl	-pilp	2021
Qy	2237			2277	
<b>a</b> .	2022	sgpiypglf-d	-sgpiypglf-dirslgpegrearltpslpslchhtpgylgvlee	2064	
RESI	RESULT 12	8			
ID AAK	AAKZOU49 ID AAR26049	5049 standard;	; Protein; 1404 AA.		
¥ ¥	AAR26049	5049;			
Y L	02-FI	02-FEB-1993 (first	st entry)		
YX DE	MSF I	MSF precursor.			
KW KW	Mega)	Megakaryocyte col stability; protec	te colony stimulating factor; secretion sign proteolytic cleavage; adhesion; alternative	signal; meg-CSF ive splicing.	<u>;</u> .
X SO X	Synt	Synthetic.			
FT	Key Region		Location/Qualifiers 126		
FT	Region		19051- EXCIL_1		
F F	Region		label= Exon_II 7 .107		
H	Region		/label= Exon_111 107.157		
FT	Region		19061		

126 sqtiksttkrspkppnkkktkkvieseeiteehsvsenqessssssssssstiwkikss 185

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The sequence given is a full length translation from the megakaryocyte stimulating factor (MSF) precursor. The sequence covered by exons II, stimulating factor (MSF) precursor. The sequence covered by exons II, III and IV encodes megakaryocyte stimulating factor (MSF). This sequence is modified by the addition of an Vterminal sequence encoding a secretory leader, an initiating methionine proceeding exon II and a terminating codon following exon IV. The cDNA sequence given contains sequences derived from human megakaryocyte cochony stimulating factor. (meg-CSF). Exon I contains the initiating methionine, and encodes a classical mammalian protein secretion signal sequence. The sequence of classical mammalian protein secretion signal sequence. The sequence cochony the original meg-CSF includes exons II-IV and is thought to this gene may be cleaved in different ways to yield a family of mRNA's each encoding a different wisp protein. Exons V and VI are thought to be related to the activity of the factor and are also implicated in the stability, folding and processing of the complement of MSF with other cytokines. Exons V = XII are believed to be implicated in the processing or folding of the appropriate structure of the resulting factor, ie. one or more of these exons may contain sequences which direct proteolytic cleaves, adhesion, organisation of the cellular matrix or extracellular matrix processing. Both naturally various combinations of alternatively spliced exons from this sequence, with the exons spliced together in differing orders to form different members of the MSF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human mega-karyocyte stimulating factors - for treating immune deficiencies, cancer, exposure to radiation or drugs. bacterial and viral infections, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Turner K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jacobs K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          RM,
                                                                                 /label= Exon_XI
1373..1404
/label= Exon_XII
                                                                  /label= Exon_VII
                                 /label= Exon_VI
1411..1166
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'label= Exon_V
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91US-0757022
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                    .1141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAQ27223
                                                                                                                                                                                                                                                                                                                                     17-JAN-1992;
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REDA--APTKPAPPAPPPPQNLQPESDAPQQPGSSPRGKSRSPAPPADKEAFAAEAQKLP 1043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDPP----CWTSGLPFPVPPREVIKASPHAPDPSAFSYAPPGHPLPLGLHDTARPVLPRP 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTISNP-PPLISSAKHPSVLERQIGAISQGMSVQLHVPYSEHAKAP-----VGPVTMGLP 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1211 GIPSTRVPSDSAITYRGSITHGTPADVLYKGTITRIIGEDSPSRLDRGREDSLPKGHVIY 1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1271 EGKKGHVLSYEGGMSVTQCSKEDGRSSSGPPHETA--APKRTYDMMEGRVGRAISSASIE 1328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLMGRAIPP---ERHSPHHLKEQHHIRGSITQGIPRSYVEAQEDYLRREAKLLKREGTP- 1384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----PPPPPSRDLTEAYKTQALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPE-L 1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HDVRSLIGSPGRTFPPVHPLDVMADARALERACYEESLKSRPGTASSSGGS-IARGAPVI 1529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            992 ittteimnkpeet-----akpkdratnskattpkpgkptkapkkptstkkpkt 1039
                        566 kepapttpkkpapttpkepapttpkepaptttkkpaptapkepapttpketapttpkklt 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               papttpkepapttpkepa------pttpketapttpkgtapttlkep 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      525 KEKEAEKE-EEKPEVENDKEDLLKEK-----TDDT-SGEDNDEKEAVASKGRKTANSQ 575
                                                                                                                304 ttsaketqsiektsakdl-----aptskvlakptpkaetttkgpalttpkeptpttpk 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 930 EGGDKNRLLSPRPSLLTPTGDPRANASPQKPLDLKQLKQRAAAIPPIQVTKVHEP----P 985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----sptttkepapttpkep-----sptttkepapttp 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alenspkepgvpttkt-----paatkpe---mtttakd-----ktterdlrttpett 931
                                                                                                                                                                                                                                                      EEAAFPPVVEDEEMEASGVSGNEEEMVEEAEALHASGNEVPRGECSGPATVNNSSDTESI 751
                                                                                                                                                                                                                                                                                               -----kept----pttiksapttpke 380
                                                                                                                                                                                                                                                                                                                                                                                   paptttksapttpkepapttt-----kepapttpkepaptttkepaptt-tksapttpke 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEEGPAKGKDAEAAEATAEGALKAEKKEGGSGRATTAKSSGAPQDSDSSATCSADEVDEA 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     apkkpapttpkepapttpkepaptttke----pspttpkepaptttksaptttkep---- 537
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                                                                                   GRRKGRITRSMANEANSEEAITP-QOSAELASMELNESSRWTEEEMETAKKGLLEHGRNW
                                                                                                                                                                                                                                                                                                                                           PSPHTEAAKDTGQNGPKPPATLGADGPPPGPPTPPRRTSRAPIEPTPASEATGAPTPP--
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The invention relates to a method of treating osteoarthritis via the administration of a composition comprising the camptodactyly-arthropathycoxa vara-perioarditis (CACP) protein.

The composition may be administered via intra-articular or intravenous of the invention may be administered via intra-articular or intravenous injection. The human CACP protein is identified in the invention as being megakaryocyte stimulating factor (MSF). The gene encoding CACP protein (MSF) is located on chromosome 1q25-31, and mutations in this gene are responsible for the heritable disorder camptodactyly-arthrough coxa vara-pericarditis, in which patients have synovial hyperplasia without evidence of inflammation. CACP protein (MSF) acts as a synovium lubricant, and can be used to lubricate tissue and contract in the treatment of setbearthritis. The composition may be applied to reduce the symptoms of osteoarthritis (e.g., joint pain, loss of range of movement or joint damage). The present sequence correspond to the symptom of osteoarthritis (e.g., joint pain, loss of range of movement or joint damage). The present sequence is not given in its entirety in figure 4 of the specification, although a GenBank accession number was given. This sequence was therefore obtained from GenBank (U70316).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; CACP protein; camptodactyly-arthropathy-coxa vara-pericarditis;
MSF; megakaryocyte stimulating factor; synovial lubricant;
chromosome 1q25-31; osteoarthritis; joint lubrication; osteopathic;
                      ----STPREIAKSPHSTVPEHHPH----PISPYEHLLRGVSGVDLYRS 1626
1530 VPELGKPRQSPLTYEDHGAPFAGHLPRGSPVTMRE--PTPRLQEGSLSSS---KASQDRK 1584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New composition comprising the camptodactyly-arthropathy-coxa vara-pericarditis protein in combination with an anesthetic, us treating osteoarthritis, or as lubricants of tissue and joints
                                                                                                                                                                                                                                                                                                                                                                                                             Human megakaryocyte stimulating factor (MSF, CACP).
                                                                                                                                                                                                                                                                                          AAB60568 standard; Protein; 1404 AA.
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19-JUL-2000; 2000US-0145328
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1040 mprvrkpkttp---
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                                                                                -----QQQQQQQQQQQQQQQQPMPRSSQEEKDEKE 524
                                                                                                             stlkstkrspkppnkktkkvieseeiteehsvsengesssssssssstiwkikss 185
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3.2%; Score 428; DB 22;
20.8%; Pred. No. 1e-15;
ive 136; Mismatches 516;
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us-09-522-753-5.rag

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Human MSF; megakaryocyte stimulating factor; tribonectin; datternative splicing; joint boundary lubricant; 0-linked oligosaccharide; osteoarthritis; tribosupplementation; tissue adhesion inhibition; friction coefficient reduction; gene therapy; antiarthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alternative splicing of the human MSF (megakaryocyte stimulating factor) agene. The tribonectin has at least one O-linked oligoaaccharide lubricating molety and has a polypeptide sequence comprising 1-76 repeats of a moit having at least 50% identity to the sequence KEPAPTT (AAB29774). The invention also relates to a nucleic acid encoding a human MSF-derived tribonectin, a blocompatible composition comprising a human mSF-derived tribonectin, a blocompatible composition and a method of diagnosing osteoarthritis or a predisposition to osteoarthritis by measuring the amount of MSF or its fragment in a biological sample of a mammal, wherein an increased amount of MSF compared to a control indicates the presence of or predisposition to developing osteoarthritis. The tribonectin and DNA encoding it are useful in the
   ---TTGSKK 1470
                                                                        1471 HDVRSLIGSPGRTFPPVHPLDVMADARALERACYEESLKSRPGTASSSGGS-IARGAPVI 1529
                                                                                                           992 ittteimnkpeet-----akpkdratnskattpkpgkptkapkkptstkkpkt 1039
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                                   932 taapkmtketatttektteskitatttgvtstttgdttpfkittlktttlapkvtttkkt 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a human tribonectin which is a product of
                                                                                                                                                                                   1040 mprvrkpkttp------tprkmtstmpelnptsriaeamlqtttrpnqtpnsk
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   QGTPLKYDTGAS ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel tribonectin polypeptide useful as lubricant for osteoarthritis, comprises O-linked lubricating moiety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human megakaryocyte stimulating factor (MSF), SEQ ID
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                                                                                                                                                                                                                                                                                                 1627 HIPLAFDPTSIPRGIPLD 1644
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1440 PLAPRPLKEGSIT
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treatment of osteoarthritis, where they may be used for lubricating mammalian joints, such as articulating joints of humans, dogs or horses. The tribonectin, when formulated as a membrane, foam, gel or fibre, is useful for inhibiting adhesion between two surfaces such as the injured tissues of a mammal, where the injury is caused by a surgical insertion or trauma, or an artificial device e.g., an orthopaedic implant. In particular, one of the surfaces is pericardial tissue. DNA encoding a tribonectin may be used in gene therapy. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        986 REDA--APTKPAPPAPPPPPQNLQPESDAPQQPGSSPRGKSRSPAPPADKEAFAAEAQKLP 1043
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Matches 266;
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                                                                                                           ----PPPPPSRDLTEAYKTQALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPE-L 1439
                                                                                                                                                                                                                     HDVRSLIGSPGRTFPPVHPLDVMADARALERACYEESLKSRPGTASSSGGS-IARGAPVI 1529
                                                                                                                                                                                                                                                                                              Shankla; Shank2; Shank3a; glutamate receptor; glutamate toxicity; memory disorder; learning disorder; stroke; epilepsy; schizophrenia; Alzheimer's disease; tissue degeneration; brain development; cardiac disorder; vasculature disorder; neurological disorder;
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                                                                                                                                                                1440 PLAPRPLKEGSIT-----TTGSKK
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                                                   GLMGRAIPP---ERHSPHHLKEQHHIRGSITQGIPRSYVEAQEDYLRREAKLLKREGTP-
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/note= "SH3 domain"
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The present sequence represents a rat Shankla polypeptide. The specification also describes Shank2 and Shank3a. The Shank polypeptides have an ankyrin domain, PDZ domain, proline-rich domain, and SAM domain. SH3 domain, PDZ domain, proline-rich domain, and SAM domain. Shank polypeptides play a significant role in the post synaptic density cytoskeleton. Compounds that modulate Shank proteins are useful for treating a disorder associated with glutamate receptors such as epilepsy, glutamate toxicity, disorders of memory, disorders of learning, stroke, schizophrenia, Alzheimer's disease, tissue degeneration and disorders of brain development. A disorder associated with Shank protein activity such as cardiac disorder, disorder of musculature disorder, neurological disorder, psordaric disorder, renal disorder, unterine disorder or a disorder of bronchial tissue is also treated by a compound that modulates Shank protein
                                                                                                                                                            New Shank polypeptide for identifying Shank protein modulator compounds used to treat Alzheimer's disease and stroke, comprises an ankyrin domain, SH3 domain, PDZ domain, proline-rich domain, and SAM domain
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Pred. No. 3.8e-15;
1; Mismatches 619;
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                                                              Sheng M;
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g G	1214 eg	ygssggygayaags	1241
oy O	1291 KE : 1242 ra	KEDGRSSSGPPHETAAPKRTYDAMEGRVGRAISSASIEGLM	1335
δy	1336 PP	GSITQGI	1359
ą	1300 pp		1359
οy	1360 PR	GPLKLKPAHE	1412
ą	1360 ta	pptapgvgplllqlg-pepptphpgvskawrtaa	1407
οy	1413 GL	SITQGTPLKYDTGASTTGSKKH	1471
a	1408	ppagtrgsste	1439
οχ	1472 DV	DARALERACYEESLKS	.531
g G	1440 d-	gpgvpppsprrvlptsptsprgneenglpllv-	1472
δy	1532 EL	ASQDRKLTSTPRE	1591
q	1473		.505
λά	1592 IA	AAYYL	1651
g	1506		1531
λ	1652 PR	TSQQMHHNTATAMAQRADMLR	1711
g	1532	:      : :   pppavaaapptldstassltsy	1553
λα	1712 GE	LSQVPHLPVLVPPTPGTPATAMDRLAYLPTAPQPFSSR	1771
g	1554	:  :	1589
λά	1772 HS	SERERDRDRERERSILTSTTTVEHAPIWRPGT	1831
a	1590		1628
λά	1832 EQ	SGSSGGGGSSSRPASHSHAHQHSPISPRTQDALQQRPSVLHNTGMKGIITAVE	1891
ą	1629 eg	egggntggvagggagvangtelldtyvayldgqafggsgtpgp	1671
δy	1892 PS	ATFPPATHCPLGGTLDGVYPTLMEPVLLPKEAPR	1944
q	1672 py		1712
λά	1945 VA		2004
g	1713 vs	: 	1765
à	2005 нн		2061
q	1766 we	plygplsgpqasalatvkasiiselssklgqfggss-taggalpwarggs	1824
ķ	2062 PS	LRPKOPGPVKLGGEAAHLPHLRPLPESOPSS	2116
ą	1825 99		1864
λ	2117 S-	AQHISEVITQDYTRHHPQQLSAPLPAPLYSF	2166

1920	2214	1958	2256	2006			
1865 sifqnwpkpplpplptgsgvssstaaapgatspsassasastr-hlqgvefemrppl 1920	APARGSPHSEGGKRSPEPNKTSV			1959 fdirssptggaggstdpfapvfvpphpgisgglggalsgasrslsptr 2006	2257 MGSKSPGNTSQPPAFFSK 2274	2007 lisippdkpígakpigfwrk 2026	Search completed: September 8, 2001, 14:34:13 Job time: 17730 sec
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Scoring table:

Searched:

Minimum DB Maximum DB

Database :

Result

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                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08372652
Patent No. 5932699
GENERAL INFORMATION:
APPLICANT: Moore, David
APPLICANT: Secl. Wongi
APPLICANT: Choi, Hueng-Sik
TITLE OF INVENTION: RETINOID X RECEPTOR-INTERACTING
TITLE OF INVENTION: POLYPEPTIDES AND RELATED MOLECULES AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 5.4%; Score 718; DB 2; Length 619; Best Local Similarity 36.0%; Pred. No. 1.5e-33; Matches 213; Conservative 76; Mismatches 212; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: MA
COUNTRY: USA
ZUP: 02110-2804
COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPA: DC-DOS/MS-DOS
SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/372,652
US-08-728-323A-2
US-08-931-820-1
US-08-931-820-4
US-08-931-820-4
US-08-953-825-21
US-08-397-633A-50
US-08-227-536-2
PCT-US95-0468-2
PCT-US95-0468-2
US-08-316-650-12
US-08-31-820-3
US-08-931-820-3
US-08-931-820-3
US-08-470-950-4
US-08-470-950-4
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RAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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LENGTH: 619 amino acids
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
  STRANDEDNESS: single
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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                                                                                                               2082 LEGELRPKQPGPVKLGGEAAHLPHLR----PLPESQPSSSPLLQT--APGVKGHQRVVT 2134
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                                     2022 HREKTQSKPFSIQELELRSLGYHGSSYSPEGVEPVSPVSSPSLTHDKGLPKHLEELDKSH 2081
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APPLICANT: Seol, Wongi
APPLICANT: Seol, Wongi
TITLE OF INVENTION: RELATED MOLECULES AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                     184 AENESTRQYEGP-----LHHYRSQQESPSPQQQPPLPPSSQSEGMGQVPRTHRLIT
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SKSPIPGQSYLGTERPSSVSSVHSEGDYHRQTP--GWAWEDRPSSTGSTQFPYNPLTIRM
                                                               2301 EPEYNISQPGTEIFNMPAITGTGLMTYRSQAVQEHASTNMGLEAIIRKALMGKYDQWEE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/16311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street, Suite 3100 CHTY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/372,652
FILING DATE: 13-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/246001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT/US95/1631
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Evans, Glen A.
APPLICANT: Djabali, Malek
APPLICANT: Djabali, Licia
APPLICANT: Selleri, Licia
APPLICANT: Parry, Pauline
TITLE OF INVENTION: CHARACTERIZATION OF A CHROMOSOME 11023
TITLE OF INVENTION: TRANSLOCATION BREAKPOINT ASSOCIATED WITH ACUTE LEUKEMIAS
TUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
                                                                                                                                                                                                                                                                                                                                                                        26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAQHISEVITQDYTRHHPQQLSAPLPAPLYSFPGA--SCPVLDLRRPPSDLYLPPPD--- 2189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2241 VYPLLYRDGEQTEPSRMGSKSPGNTSQPPAFFSKLTESNSAMVKSKKQEINKKLNTHNRN 2300
                                                                                                                                                                                                                                                                                                                                                                                                                           ------PPVSGHATIARTPAKN--LAPHHASPDPPAPPASASDP 2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2022 HREKTQSKPFSIQELELRSLGYHGSSYSPEGVEPVSPVSSPSLTHDKGLPKHLEELDKSH 2081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             290 VLHPRPGPRVSPENLVDKSRGSRPGKSPERSHI---PSEPYEPISPPQG---PAVHEKQD 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 PSGKAQPHASVVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVTITRQIASDKDA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 AENESTROYEGP-----LHHYRSOQESPSPQOOPPLPPSSQSEGMGQVPRTHRLIT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2190 --HGAPA-RGSPH-----SEGGKRSPEPNKTSVLGGGEDGIEPVSPPEGMTEPG-HSRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2301 EPEYNISQPGTEIFNMPAITGTGLMTYRSQAVQEHASTNMGLEAIIRKALMGKYDQWEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       462 HGVVMSHPV---GIMPGSASTSV----VTSSEARRDEGEPSPHAGVCKPKLINKSNSRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2414 AKSPAPGLA--SGDRPPSVSSVHSEGDCNRRTPLTNRVWEDRPSSAGSTPFPYNPLIMRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEGELRPKQPGPVKLGGEAAHLPHLR-----PLPESQPSSSPLLQT--APGVKGHQRVVT
                                                                                                                                                                                                                                                                                                                                                                        90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 619;
                                                                                                                                                                                                                                                                                                       5.4%; Score , ...,
36.0%; Pred. No. 1.5e-33;
...ive 76; Mismatches 212; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Pretty, Schroeder, Brueggemann & Clark
444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 5, Application US/08061376; Patent No. 6175000; GENERAL INFORMATION:
                                                                                                            619 amino acids
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 36.03
Matches 213; Conservative
                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 444 South
CITY: Los Angeles
                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: DNA PCT-US95-16311-5
                                                                                                                                                                                                                                                                                                                                                                                                                         1975 PSKGSEPRPLV--
                                                                                                            LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-061-376-5
                                                                                                                                                                                                                                                                                                                    Query Match
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Gaps 148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1018 TDK------RVASLLKKAKAQLC-----KIEKSKSL------1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           964 GRGNLEKTNLDLGPTAPSL----EKEKTLCLSTPSSSTVK-HSTSSIGSMLAQADKLPM 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | :::| |:::| |:::| |:::| |:::| |:::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |::::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 SHLSPGSIIQPQRRRPSLLS-EFQPGNERSQELHLRPESHSYLP----ELGKSEMEFIES 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 KRPRLELLPDPLLRPSPLLATGQPAGSEDLTKDRSLTGKLEPVSPPSPPHTDPELELVPP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 RLSKEELIQNMDRVDREITMVEQQISKLKKKQQQLEEEAAKPPEPEKPVSPPPIESKHRS 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              861 -RDADKSVEKDK------SRERDREREKENKRESRKEKR-----KKGSEIQSSSA 903
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                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/061,376
FILING DATE: 13-MAY-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9387
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)546-4737
TELEPHONE: (619)546-9392
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 3969 amino acids
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unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-061-376-5
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: unl
TOPOLOGY: unknown
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φ. 4	597	TPQQSAELASMELNESSRWTEEEMETAKKGLLEHGRNWSAIARWVGSKTVSQCKNFY 653
QC	114/	CPGCQVPEDCGVCINCLDKPKGGRN
δy	654	
qq	1188	CKMRKCQNLQWMPSKAYLQKQAKAVKKKEKKSKTSEKKDSKESSVVKN 1235
οy	714	EEEMVEEAEALHASGNEVPRGECSGPATVNNSSDTESIPSPHTEAAKD 761
QQ	1236	VVDSSQKPTPSAREDPAPKKSSSEPPPRKPVEEKSEEGNVSAPGPESKQATTPASRK 1292
δŏ	762	TSRAP
QQ	1293	SSKQVSQPALVIPPQPPTTGPPRKEVP-KTTPSEPKKKQPPPPESGPEQSKQK 1344
. Ох	817	APPPVVPKEEKEEETAAAPPVEEGE
QΩ	1345	KVAPRPSIPVKQKPKEKEKPPPVNKQENAGTLNILSTLSNGNSSKQKIPADGVHRIRVDF 1404
δλ	848	AEEEDVKSECTEEAEE 872
QQ	1405	KEDCEAENVWEMGGLGILTSVPITPRVVCFLCASSGHVEFVYCQVCCEPFHKFCLEE-NE 1463
Qy	873	GPAKGALKAEKKE 897
qq	1464	RPLEDQLENMCCRRCKFCHVCGRQHQATKQLLECNKCRNSYHPECLGPNYPTKPTKKKV 1523
Οy	868	
QΩ	1524	WICTKCVRCKSCGSTTPGKGWDAQWSHDFSLCHDCAKLFAKGNFCPLCDKCYDDDDYESK 1583
Οy	931	GDPRANASPQKPLDF 963
qq	1584	MMQCGKCDRWVHSKCENLSDEMYEILSNLPESVAYTCVNCTERHPAEWRLALEKELQISL 1643
0y	964	KQ
qq	1644	KQVLTALLNSRTTSHLLRYRQAAKPPDLNPETEESIPSRSSPEGPDPPVLTEVSK 1698
δy	1010	DAPQQPGSSPRGKSRSPAPPADKEAFAAEAQKLPGDPPCWTSGLPFPVPPREVIKASPHA 1069
qq	1699	QDDQQPLDLEGVKRKMDQGNYTSVLEFSDDIVKIIQAAINS 1739
Οy	1070	PDPSAFSYAPPGHPLPLGLHDTARPVLPRPPTISNPPPLISS 1111
qq	1740	DGGQPEIKKANSMVKSFFIRQMERVFPWFSVKKSRFWEPNKVSSNSGMLPN 1790
Qy	1112	AKHPSVLERQIGA-ISQGMSVQLHVPYSEHAKAPVGPVTMGLPLPMDFKKLA 1162
QQ	1791	AVLPPSLDHNYAQWQEREENSHTEQPPLMKKIIPAPKPKGPGEPDSPTPLHPPTPP 1846
Οy	1163	GVKQEQLSPRG
QQ	1847	ILSTDRSREDSPELNPPPGIEDNRQCALCLTYGDDSANDAGRLLYIGQNEWTHVNCAL 1904
οy	1193	TKGIPST
qq	1905	WSAEVFEDDDGSLKNVHMAVIRGKQLRCEFCQKPGAIVGCCLISCTSN 1952
οy	1231	HGTPADVLYKGTITRYEG 1272
qq	1953	YHEMCSRAKNCVFLDDKKVYCQRHRDLIKGEVVPENGFEVFRRVFVDFEG 2002
οy	1273	KKGHVLSYEGGMSVTQCSKEDGRSSSGPP 1301
QQ	2003	ISLRRKFLNGLEPENIHMMIGSMTIDCLGILNDLSDCEDKLFPIGYQCS 2051
δλ	1302	HETAAPKRIYDMMEGRVGRAISSASIEGLMGRAIPPERHSPHHLKEQHHIRGSITQGIPR 1361
qq	202	RVYWSTTDARKRCVYTCKIVECRPPVVEPDINSTVEHDENRTIAHSPT 2099

1362 SYVEAQEDYLRREAKLLKREGTPPPPPPSRDLTEAY------KTQALGPLKLKPAH 1411

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2100	1412	1472	1531	1578	1638	1676	1699	1720	1768	1816	1844	1856	1883	1907	1937	1979	2034	2093
đ	QQ QQ	97 PP	Q P	9 P	QY Db	Qy Db	OY Db	QY Db	OY D	b O	S G	Oy Dp	Qy Dp	\$ A	oy Ob	Qy Db	Oy Db	οy

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                                                                                                                                                                                                                                                        2215 LGGGEDGIEPVSPPEGMT-----EPGH-----SRSAVYPLLYRDGEQT--- 2252
                                                                                                                                                                                                                                                                                          3235 PSSTPSNIAPSDVVSNMTLINFTPSQLPNHPSLLDLGSLNTSSHRTVPNIIKRSKSSIMY 3294
                                                                                                                                                                                                                                                                                                                                                             -EPSRMGSKSPGNTSQPPAFFSKLTESNSAMVK-----SKRQEINKKLNTHNRNEPEYN 2305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2306 ISQPGTEIFNMPAITGTGLMTYRSQAVQEHASTNMGLEAIIRKALMGKYDQWEESPPLSA 2365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2366 NAFNPLNASASLPAAMPITAADG-----RSDHTLTSPGGGGK------AKV 2405
3055 PSQISNAAVQTTPPHLKPATEKLIVVNQNMQPLYVLQTLPNGVTQKIQLTSSVSSTPSVM 3114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 62, Application US/08642255;
Patent No. 5773249
GENERAL INFORMATION:
APPLICANT: CAPPELLO, Joseph
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: A Embarcadero Center, Suite 3400
CITY: San Francisco
CITY: CANTER: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTWARE: Patentin Release #1.0, Version #1.30
SOUTWARE: PATENTIN Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
FILING DATE:
FLING DATE:
FLING PATE:
ATORNEY/AGENT INFORMATION:
NAME: ROWIND, BETTAM I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A55556-3/BIR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3498 ---KALSSAVQASPTSPG-GSPSSPSSGQRSASPSVPGP 3532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2466 PLIMRLQAGVMASPPPPGLPAGSGPLAGPHHAWDEEPKP 2504
                                                  2144 TQDYTRHHPQ-----QLSAPLPAPLYSFPGASCPVL---
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
ACHIFFR: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 62
SEQUENCE CHARACTERISTICS:
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HAPDP----SAFSYAPPGHPLPLG----LHDTARPVLPRPPTISNPPPLISSAKHPSVL 1118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      964 KOLKORAAAIPPIQVTKVHEP-----PREDAAPTKP-APPAPPPQNLQPESDA 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1298 SGPP--HETAAPKRTYDMMEGRVGRAISSASIEGLMGRAIPPERHSPHHLKEQHHIRGSI 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1414 LVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGSITQGTPLKYDTGASTTGSKKHDV 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1474 RSLIGSPGRTFPPVHPLDVMADARALERACYEESLKSRPGTASSSGGSIARGAPVIVPEL 1533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PQQPG-SSPRGKSRSPAPP-ADKEAFAAEAQKLPGDPPCWTSGLPFPV--PPREVIKASP 1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1119 ERQIGAISQGMSVQLHVPXSEHAKAPVGPV-TMGLPLPMDPKKLAPFSGVKQEQLSPRGQ 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1178 AGPPESLGVPTAQEASVLRGTALGSVPGGSITKGIPSTRVPSDSAITYRGSITHGTPADV 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1238 LYKGTITRIIGEDSPSRLDRGREDSLPKGHVIYEGKKGHVLSYEGGMSVTQCSKEDGRSS 1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GAHGPAGPKGAHGPAGPKGAHGPAGPKGAHGPAGPKGAPGPAGPPGSRGDPGP 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  376 GAPGPAGPPGSRGDPGPPGAPGPPGSRGDPGPPGAPGP---AGPPG------- 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SRG------DPGPPGAPGPAGPPGSRGDPGPPG----AP------GP 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   575 APGPAGPPGS------RGDPGPPGAPGP-------AGPPGSR---- 603
                                                                                                                                                                                                                                                                                                                                                                                                                       APTP-----PPAPPSPSAP-----PPVVPKEEKEETAAAPPVEEGEEQKP 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 APGPAGPPGSRGDPGPPGAPGPPGSRGDPGPPGAP-----GPAGPPGSRG-DPGP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                846 PAAEELAVDTGKAEEPVKSECTEEAEEGPA--KGKDAEAAEATAEGALKAEKKEGGSGRA 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGAPGPAGPPGSRGDP----GPPGAPGPAGPPGSRGDPGPPGAPGPPGSRGDPGPP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            904 TTAKSSGAPQDSDSSATCSADEVDEAEGGDKNRLLSPRPSLLTPTGDPRANASPQKPLDL 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAPGPAGPP-----GSRGDPG----PGAPGPAGPBGSRGDPGP--- 267
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                                                                                                                                                                                                                                   694 AAFPPVVEDEEMEASGVSGNEEEMVEEAEALHASGNEVPRGECSGPATVNNSSDTESIPS 753
                                                                                                                                                                                                                                                                                                                             754 PHTEAAKDTGQNGPKPPATLGADGPP----PGPPTPPRRTSRAPIEPTPASEA---TG 804
                                                                                                                                                                                                                                                                                                                                                                      71 APGPAGPPGSRGDPGPPGAPGPPGSRGDPGPPGAP----GPAGP-PGSRGDPGPPG 124
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                                                                                                                                                                                        Indels 691;
                                                                                                                                            Length 1064;
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                                                                                                                                       2.9%; Score 377.5; DB 1;
21.7%; Pred. No. 8.7e-14;
live 40; Mismatches 545;
                                                                                                                                       Query Match 2.9%
Best Local Similarity 21.7%
Matches 353; Conservative
                     TOPOLOGY: linear
MOLECULE TYPE: protein
STRANDEDNESS: sir
TOPOLOGY: linear
                                                     ; MOLECULE TY
US-08-642-255-62
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                                                                                                                                                                                                                                                                                                                                                                                                                                           1881 TGMKGIITAVEPSKPTVLRSTSTSSPVRPAATFPPATHCPLGGTLDGVYPTLMEPVLLPK 1940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1941 EAPRVARPERPRADTGHAFLAKPPARSGLEPASSPSKGSEPRPLVPPVSGHATIARTPAK 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2119 LLQTAPGVKGHQRVVTLAQHISEVITQDYTRHHPQQLSAPLPA------PLYSFPG 2168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2169 ASCPVLDLRRPPSDLYLPPPDHGAPA-RGSPHSEGGKRSPEPNKTSVLG-GGEDGIEPVS 2226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001 NLAPHHASPDPPAPPASASDPHREKTQSKPFSIQELELRSLGYHGSSYSPEGVEPVSPVS 2060
1594 KSPHSTVPEHHPHPISPYEHLLRGVSGVDLYRSHIPLAFDPTSIPRGIPLDAAAAYYLPR 1653
                                                                                                                                                                                                                                                                                                                                                                                               803
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                                                                                                                                                                                                                                                                                                                                                   GTEQSSGSSGSGGGGSSSR----PASHSHA---HQHSPISPRTQDALQQRPSVLHN-
                                                                                       HLAPNPTYPHLYPPYLIRGYPDTAALENRQTIINDYITSQQMHHNTATAMAQRADMLRGL
                                                                                                                              683 --ApgpAgp---pg--SrgDpgppg--------
                                                                                                                                                                                                                     -----APGPAG-----PPGSRGDPGPPGA-----PGPAGPPG
                                                                                                                                                                                                                                                              1770 SRHSSSPLSPGGPTHLTKPTTTSSSERERDRDRERDRDREREKSILTSTTTVEHAPIWRP
                                                                                                                                                                                                                                                                                                            -----GPAGPP
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                                         655 GSRGDPGPPGAPGPAGP-----PGSRG------DPG--PPG--PPG-----
                                                                                                                                                                                                                                                                                                                                                                                               745 GSRGDPGPPGAPGPAGPPGSRGDPGPPGAHGPAGPKGAHGPAGPKGAHG-PAGPKGAHGP
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APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  804 AGPKG---APGPAGPPGSRG-DPGPPGAPGPAGPPGSRGDPG---
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                     SRGDPGP--PGAP-------
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
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US-09-041-886-23
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US/09/041,886
                        CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/POCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEFRAX: (619) 535-9001
TELEFRAX: (619) 535-901
TELEFRAX: (619) 535-943
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                       LENGTH: 1185 amino acids
                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-09-041-886-23
APPLICATION NUMBER:
                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                     ----TLSTVIATVASSPAGYKTASPPGPPPYGKRAPS
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Patent No. 6150081
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VAN RIJN, ALEXIS C.
BOUNSTRA, JAN B.
DE WOLF, FREDERIK A.
MOOBROEK, ANDREAS
WERTEN, MARC W.T.
WIND, RICHELE D.
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TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE TITLE OF INVENTION: PREPARATION THEREOF FILE REPERENCE: 2728-2 CURRENT APPLICATION NUMBER: US/09/219,849 CURRENT FILING DATE: 1998-12-23 NUMBER OF SEQ ID NOS: 50 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 5 LENGTH: 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     881 EAAEATAEGALKAEKKEGGSGRATTAKSSGAPQDSDSSATCSADEVDEAEGGDKNRLLSP 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 -PGAHGPAG-PKGAHGPAGP-----KGAHGPAGPKGAHGPAGPKGAPGAPGPAGPFGSR 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 726 ASGNEVPRGECSGPATVNNSSD--TESIPSPHTEAAKDTGQNGPKPPATLGADGPP---- 779
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                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Illustrative ; OTHER INFORMATION: amino acid sequence US-09-219-849-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.8%; Score 365; DB 4; Length 960;
Best Local Similarity 21.3%; Pred. No. 4e-13;
Matches 337; Conservative 33; Mismatches 490; Indels 720;
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ORGANISM: Artificial Sequence
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                                                                                    1526 APVIVPELGKPRQSPLTYEDHGAPFAGHLPRGSPVTMREPTPRLQEGSLSSSKASQDRKL 1585
                                                                                                                                                                                                                                                                     1646 AAAYYLPRHLAPNPTYPHLYPPYLIRGYPDTAALENRQTIINDYITSQQMHHNTATAMAQ 1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1763 TAPQPFSSRHSSSPLSPGGPTHLTKPTTTSSSERERDRDRERDRDREREKSILTSTTTVE 1822
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1466 TGSKKHDVRSLIGSPGRTFPPVHPLDVMADARALERACYEESLKSRPGTASSSGGSIARG 1525
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                                                                                                                   1586 TSTPREIAKSPHSTVPEHHPHPISPYEHLLRGVSGVDLYRSHIPLAFDPTSIPRGIPLDA
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APPLICANT: Lendahl, Urban
APPLICANT: Lendahl, Urban
TITLE OF INVENTION: Nestin Expression As An Indicator of
TITLE OF INVENTION: Neuroepithelial Tumors
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                            ----GAPGPAGPP---
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                                                                                                 PatentIn Release #1.0, Version #1.25
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Local Similarity 21.1%; Pred. No. 1.9e-12;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/853,913
FILING DATE: 19920319
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/60,412
FILING DATE: 22-FEB-1991
PRIOR APPLICATION NUMBER: US 07/603,803
FILING DATE: 25-OCT-1990
PRIOR APPLICATION NUMBER: US 07/201,762
FILING DATE: 02-UNH-1988
PRIOR APPLICATION NUMBER: US 07/201,762
FILING DATE: 02-UNH-1988
PRIOR APPLICATION NUMBER: US 07/201,762
FILING DATE: 02-UNH-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Granaha, Patricia
REGIZTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                            A Method for Assaying Collagen Fragments in Body Fluids, A Teek Kit and Means for Carrying Out the Method and Use of the Method to Diagnose the Presence of Disorders Associated with the Metabolism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | : | || || || || || ETKNCPGAEVPEGECC-PVCPDGSESPTDQETTGYEGPKGDTGPRGPRGPAGPPGRDGIP 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EALHASGNEVPRGECSGPATVNNSSDTESIPSPHTEAAK-DTGQNGPKPPA-TLGADGPP 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 GOPGLPGPPGPP------GPPGPPGLGGNFAPQLYGYDEKSTGGISVPG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 812 PPSPSAP-----PPVVPKEEKEEETAAAPPVEEGE------EOKPPAAEELAVDTGKA 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEPVKSECTEEAEEGPAKGKDAEAAEATAEGALKAEKKEGGSGRATTAKSSGAPQDSDSS 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKPGR-----PGZRGPPGPZGARGLPGTA--GLPGMKGHRGFSGLBGAKGBAGPAG---- 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            919 ATCSADEVDEAEGGDKNRLLSPRPSLLTPTGDPRANASPQKPLDLKQLKQRAAAIPPIQV 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 PMGPSGPRGLPGPPGAPGPZGFZ----GPPGZPGZPGASGPMGPRGPPGPPGKBGBBGZA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atch 2.7%; Score 351; DB 3; Length 1341; cal Similarity 20.1%; Pred. No. 3.8e-12; 350; Conservative 106; Mismatches 573; Indels 714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----PGPPTPPRRTSRAPIEPTPASEATGAPTPP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/187,319
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/963,825
                              Sequence 18, Application US/08963825
Patent No. 6110689
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                              \Sigma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RECIETRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 43
FELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELDE AN. 236687
TELEX: 236687
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
TENGTH: 1341 amino acids
                                                                                                                                                                                                                                                                                            ADDRESSEE: Darby & Darby STREET: 805 Third Avenue
                                                                        GENERAL INFORMATION:
APPLICANT: Qvist, Per
APPLICANT: Bonde, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                            TITLE OF INVENTION: A METITLE OF INVENTION: In FITLE OF INVENTION: Metititle OF INVENTION: Discussinum of Secular Correspondence address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Gogoris, Adda C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U
ZIP: 10022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
-08-963-825-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-963-825-18
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : | : | : | 137 KDRHVWFGESMTDGFQFEYGGQGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQ 1256
                                                                            ---AGPRGPPGSAGAPGKDGLNGLPGPI-----GPPGPRGRTG 1048
                                                                                                                    2052 GVEPVSPYSSPSLTHDKGLPKHLEELDKSHLEGELRPKQPGPVKLGGEAAHLPHLRPLPE 2111
                                                                                                                                                                                                    2112 SQPSSSPLLQTAPGVKGHQ----------RVVTLAQHISEVITQDYTR 2149
                                                                                                                                                                                                                                                                                2150 HHPQQLSAPLPAPLYSFPGASCPVLDLRRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEP 2209
                                                                                                                                                                                                                                                                                                                        --KSGEYWIDP 1154
                                                                                                                                                                                                                                                                                                                                                                 2210 NKTSVLGGGEDGIEPVSPPEGMTEPGHSRSAVYPLLYRDGEQTEPSRMG-----SKSPGN 2264
                                                                                                                                                                                                                                                                                                                                                                                                       1155 NQ----GCNLDAIKVFCNME-----TGETCVYP-----TQPSVAQKNWYISKNPKD 1196
                                   1992 ATIARTPAKNLAPHHASPDPPAPPASASDPHREKTQSKPFSIQELELRSLGYHGSSYSPE 2051
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---NSAMVKSKKQEINKKLNTHNRNEPEYNIS 2307
                                                                                                                                             APPLICANT: KINZLER, KENNETH
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: THILYERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
TOWERSPONDENCES: 94
CORRESPONDENCE ADDRESS:
GPQGPRGDKGETGEQGDRGIKGHRGFSGLQGPPGPPGSPGEQGPSGASGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, NW
                                                                                                                                                                                                                                                                                                                        --TC--RDLKMCHSDW--
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FILING DATE: 19920109
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/07741940 Patent No. 5352775
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IBM PC compatible
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NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANAND, RAKESH
CARLSON, MARY
GRODEN, JOANNA
HEDGE, PHILIP J.
JOSLYN, GEOFF
KRNELEH
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                                                                                                                                                          1049 DAGPVGPPGPPG------
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                             2265 TSQPPAFFSKLTES---
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APPLICANT:
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964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1033 -------EQLNSGRQ------SPSQNERWARPKHIIEDEIKQSEQRQSR 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1236 QSRSGQ----PQKAATCKVSSINQETIQTYCVEDIP-----ICFSRCSSLSSLS 1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---TP 1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RLQGSSLSSESARHKAVEFSSGAKSPSKSGAQTPKSPPEHYVQETPLMFSRCTSVSSLDS 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      370 HEVSEIIDGLSEQENLEKQMRQLAVIPPMLYDADQQRIKFINMNGLMADPMKVYKDRQVM 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 488 RRRGKSQQQQQQQQQQQQQQQQQPMPRSSQEEKDEKEKE-----AEKEEEKPEVEND 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       542 KEDLLKEKTD------DTSGEDN-DEKEAVASKGRKTANSQGRRKGRITRSMA 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEAAKPPEPEKPVSPPPIESKHRSLVQIIYDENR--KKAEAAHRILEGLGPQVELPLYNQ 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVSAIHTSQEDRSSGSTTE-----LHCVTDERNALRRSSAAH-----THSNTYN- 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 PSDTRQYHENIKINQAMRKKLILYFKRRNHARKQWKQKFCQRYDQLMEALEKKVERIENN 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----DSL-----B72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320 PRRRAKESKVREYYEK------OFP-EIRKQRELQERMQSRVGQRGSGLSMSAARSE 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      588 NEANSEEAITPOQSAELASMELNESSRWIEEEMETAKKGLLEHGRNWSAIARMVGSKTVS 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            648 QCKNFYFNYKKRQNLD--EILQQHKLKMEK--ERNARRKKKKAPAAASEEAAFPPVVEDE 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              704 EMEASGVSGNEE-----EMVEEAEALHASGNEVPRGE-----CSGPATVNNSSDTESIPS 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 LPELGKSEMEFIESKRPRLELLPDPLLRPSPLLATGQPAGSEDLT---KDRSL----- 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  799 VFDTNRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSSSSRGSLDSSRSEKDRSLERERGIG 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 TGKLEPVSPPSPPHTDPELELVPPRLSKEELIQNMDRVDREITMVEQQISKLKKKQQQLE 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    859 LGNYHPATEN------PGTSSKRGL-----QISTTAAQIAKV-----ME 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHTEAAKDTGQNGPKPPATLGADGP-----PPGPPTPPRRTSRAPIEPTPASEATGAPTP 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            430 NMWSEQE--KETFREKFMQHPKNFGLIASFLERKTVAECVLYYYLTKKNENYKSLVRRSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 821;
                                                                                                                                                                                                                                                                                                                                                                                         Length 2842;
                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.7%; Score 350.5; DB 1; Best Local Similarity 17.8%; Pred. No. 1.1e-11; Matches 473; Conservative 357; Mismatches 1007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1395 FESRSIASSVQSEPCSGMVSGIISPSDLPDSPGQTMPPSRSK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 ASHLSPGSIIQP--QRRRPSLLSEFQ---
SEQUENCE CHARACTERISTICS:
LENGTH: 2842 amino acids
                                                                                                                                           MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: APC
                                                                                         single
                                                       TYPE: AMINO ACID
STRANDEDNESS: Sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                               US-07-741-940-7
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2236R	QY 1821VEHAPIWRPGTEQSSGSSGSSGGGGGSS   : :          :  :  Db 2273 AKPSVKSELSPVARQ-TSQIGGSSKAPSRSGSRD	Oy 1875 PSVLHNTGMKGIITAVEPSKPTVLRSTSTSVRR :	QY 1931TLMEPVLLPKEAPRVARPERPRADTGHAFLA	Qy 1981PRPLVPPVSGHATIARTPA-KNLAPHHASP 	QY 2036 LELRSLGYHGSSYSPEGVEPVSPVSSPSLTHDKG 	OY 2096 LGGEAAHLPHLRPLPESQPSSSPLLQTABGVK  1	Oy 2154 QLSAPLPAPLYSFPGASCPVLDLRRPPSDLYLPP  1	Qy 2214VLGGGEDGIEPVSPPEGMTEPGHSRS	2266	Qy 2326 TYRSQAVQEHASTNMGLEAIIRKALMGKYDQWEE  Db 2711 PMRTVGLENRLNSFIQVDAPDQKGTEIKPGQNNP	2386 ADGRSDHTLITSPGGGGRAP :             2764 SSS-SKHSSPSGTVAAN	OY 2443 TPLINRVWEDRPSSAGST 2460   :   :        Db 2806 TPVNNNT-KKRDSKTDST 2822	RESULT 10 US-08-289-548A-7 ; Sequence 7, Application US/08289548A	; Patent No. 5648212 ; GENERAL INFORMATION: ; APPLICANT: ALBERTSEN, HANS ; APPLICANT: ANAND, RAKESH	: CARLSON, : GRODEN, C : HEDGE, PI : JOSLYN, C	; APPLICANT: KINZLER, KENNETH ; APPLICANT: MARKHAM, ALEXANDER F. ; APPLICANT: NAKAMURA, YUSUKE ; APPLICANT: THLIVERIS, ANDREW	; TITLE OF INVENTION: INHERITED AND SOMA; ; TITLE OF INVENTION: GENE IN COLORECTAL; ; NUMBER OF SEQUENCES: 102 ; CORRESPONDENCE ADDRESS:	ADDRESSEE: Banner & Allegretti, LTD ; STREET: 1001 G Street, NW
OY 809 PPAPPSPSAPPPVVPKEEKEETAAAPPVEGGEEQKPPAAEELAVDTGKAEEPVKSE 865	QY 866 CTEEAEEGPAKGKDAEAARAEGALKAEKKEGGSGRATTAKSSGAPQDS 915	KNRLLSPRPSLLTPTGDPRANASPOKPLDLKQLKQR :::  ::   ::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   ::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   ::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   ::   ::   :::   ::   :::   :::   ::   :::   :::   ::   :::   :	INLOPESDAPQOPGSS-PRGKSRSPAP 102	SGLPFPVPPREVIKASPHAPDPSAFSYAPPGHPLPLGL	1089 HDTARPVLPRPPTISNPPPLISSAKHPSVLERQIGAISQGMSVQLHVPYSEHAKAPVGFV   1   1   1   1   1   1   1   1   1	1149 TMGLPLPMDPKKLAPFSGVKQEQLSPRGQAGPPESLGVPTAQEASVLRGTALGSV 1161 :	1204 PGGSITKGIPSTRVPSDSAITYRGSITHGTPADVLKKGIIRRI	IGEDSPSRLDRGREDSLPKGHVIYEGKKGHVLSYEGGMSVTQCSKEDGRSSSGPPHE     :		OY 1356 TQGIPRSYVEAQEDYLRREAKLLKREGTPPPPPPSRDLTEAYKTO 1400  1894 TSHTELTSNQQSANKTQALAKQPINRGQPKPILQKQSTFPQSSKDIPDRGAATDEKLQNF 1953	QY 1401 ALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGSIT 1452	QY 1453 QGTPLKYDTGASTTGSKHDVRSLIGSPGR 1482	QY 1483 TFPPVHPLDVWADARALERACYEESLKSRPGTASSSGGSIARGAPVIVPELGKPRQSPLT 1542	Qy 1543 YEDHGAPFAGHLPRGSPVTMREPTPRLQEGSLSSKASQDRK 1584	Qy 1585 LTSTPREIAKSPHSTVPEHHPPISPYEHLLRGV-SGVDLYRSHIPLAFDPTSIPRGIPL 1643	Qy         1644         DAAAAYYLPRHLAPNPTYPHLYPPYLIRGYPDTAALENRQTIINDYITSQOMHHNTATAM         1703           Db         2197	QY         1704         AQRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAMDRLAYLPT         1763           Db         2213	Qy 1764 APQPFSSRHSSSPLSPGGPTHLTKPTTTSSSERERDRDRERDRDREREKSILTSTTT 1820
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LNOMNNGNGANKKVELSRMSSTKSSGSE 2427 NSTPSRPAQQPLSRPIQSPGRNSI--- 2328 /RPAATFPPATHCPLGGTLDGVYP---- 1930 | : : | : : | | : | : | SFESLSPSSRPASPTRSQAQT-PVLSPS 2486 GLPKHLEELDKSHLEGELRPKQPGPVK 2095 | | :::|| | |: OGRPAKRHDIARSHSESPSRL----PIN 2541 GSSSSILSASSESSEKAKSEDEKH--- 2590 RIEDCPI-----NNPRSGRSPTGNT 2678 |: : |: | DNQAKQNV-----GNGSV 2710 ESPPLSANAFNPLNASASLPAAMPITA 2385 : |:||: 5Q-----TATTSPRG 2272 SSSRPASHSHAHQHSPISPRTQDALQQR 1874 SPDPPAPPASASDPHREKTQSKPFSIQE 2035 KGHQRVVTLAQHISEVITQDYTRHHPQ 2153 PPDHGAPARGSPHSEGGKRSPEPNKTS 2213 :: |:|: SKENQVSAKGTWRKIKENEFSPTNSTS 2626 SAVYPLLYRDGEQTEPSRMGSKSPGNT 2265 RNEPEYNISQPGTEIFNMPAITGTGLM 2325 I :: I :: 1 STORMED I :: 1 STORMED I SPAPGLASGDRPPSVSSVHSEGDCNRR 2442 MATIC MUTATIONS OF APC AL CANCER IN HUMANS

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                                                                                                   CUMPUTEK KEALABLE FORM.

MEDIUM TYPE: Floppy disk,
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 12-AUG-1994
CLASSIFICATION NUMBER: US/08/289,548A
FILING DATE: 12-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kagan: Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.46943
TELEPHONICATION INFORMATION:
TELEPHONE: 202-508-919
INFORMATION FOR SEQ. 1D NO: 7:
SEGUIENCE CHARACTERISTICS:
TEMBERATION FOR SEQ. 1D NO: 7:
SEGUIENCE CHARACTERISTICS:
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                                           COUNTRY: USA
ZIP: 20001-4598
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
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Washington
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                                      1176 IDYSLKYATDIPSSOKOSFSFSKSSSGOSSKTEHMSSSSENTSTPSSNAKRONOLHPSSA 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1491 ATESTPDGFSCSSSLSALSLDEPFIQKDVELRIMPPVQENDNGNETESEQPKESNENQEK 1550
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                                                                                                                                                                                                                                                                                                                                                                                                                                     PPAPPSPSAPPPVVPKEEKEEETAAAPPVEEGEEQKPPAAEELAVDTGKA----EEPVKSE 865
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                                                                                                                                                                      648 OCKNFYFNYKKRONLD--EILOOHKLKMEK--ERNARRKKKKAPAAASEEAAFPPVVEDE
                                                                                                                                                                                                 SAEDEIGCNQTTQEADSANTLQIAEIK-EKIGTRSAEDPVSEVPAVSQH-----PRTKSS
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542 KEDLLKEKTD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 LPELGKSEMEFIESKRPRLELLPDPLLRPSPLLATGQPAGSEDLT---KDRSL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2842;
                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.7%; Score 350.5; DB 1; Local Similarity 17.8%; Pred. No. 1.1e-11; les 473; Conservative 357; Mismatches 1007;
                                                                                                                                                                                                                                                                                                                                                                                    Banner, Birch, McKie & Beckett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 ASHLSPGSIIQP--QRRRPSLLSEFQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAPLICATION NUMBER: US/08/452,654
FILING DATE: 25-MAY-1995
CLASSIPRICATION S18
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AGG-1991
ATTORNEY AGENT INFORMATION:
NAME: Ragan, Sarah A.
REGISTRATION NUMBER: 33,141
REGISTRATION NUMBER: 31,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/452,654
Sequence 7, Application US/08452654 Patent No. 5691454
                                                                                                                                                                                                                              4ARKHAM, ALEXANDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                 NAKAMURA, YUSUKE
THLIVERIS, ANDREW
                                                                                                                                                                                                  APPLICANT: KINZLER, KENNETH
APPLICANT: MARKHAM, ALEXANDI
APPLICANT: NAKAMURA, YUSUKE
                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1001 G Street, NW CITY: Washington
                                                                                                           APPLICANT: CARLSON, MARY
APPLICANT: GRODEN, JOANNA
APPLICANT: HEDGE, PHILIP J.
APPLICANT: JOSLYN, GEOFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20001-4598
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 473;
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λ	260	PSDTRQYHENIKINQAMRKKLILYFKRRNHARKQWKQKFCQRYDQLMEALEKKVERIENN 31	
ą	936		
χ̈	320	PRRRAKESKVREYYEKQFP-EIRKQRELQERMQSRVGQRGSGLSMSAARSE 369	
ą	973	GKRGQMKPSIESYSEDDESKFCSYGQYPADLAHKIHSANHMDDNDGELDTPINYSLKYS	
<u></u>	370	HEVSEIIDGLSEGENLEKQMRQLAVIPPMLYDADQORIKFINMNGLMADPMKVYKDRQVM 429	
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<u>&amp;</u> &	430	NMWSEQEKETFREKEMQHPKNFGLIASFLERKTVAECVLYYYLTKKNENYKSLVRRSY 487   :	
λ	488		
ą	1119	GINONVSQSLCQEDDYEDDKPINYSERYSEEEQHEEEERPINYSIKYNEEKRHVDQP 1175	
<u>ک</u> ۾	542	KEDLLKEKTDDTSGEDN-DEKEAVASKGRKTANSOGRRKGRITRSMA 587 :	
⋩	588		
æ	1236	SERGQPQKAATCKVSSINQETIQTYCVEDTPICFSRCSSLSSLS 1280	
λ	648	QCKNFYFNYKKRQNLDBILQQHKLKMEKERNARRKKKAPAAASBEAAFPPVVEDE 7 ::	
ą	1281	SAEDEIGCNQTTQEADSANTLQIAEIK-EKIGTRSAEDPVSEVPAVSQHPRTKSS 1334	
λ	70		
ą	1335	RLQGSSLSSESARHKAVEFSSGAKSPSKSGAQTPKSPPEHYVQETPLMFSRCTSVSSLDS 1394	
۲	754	PHTEAAKDIGQNGPKPPATLGADGPPPGPPTPRRTSRAPIEPTPASEATGAPTP 808 :: : :  :	
ð	1395	FESRSIASSVQSEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTP 1438	
λ	808	PPAPPSPSAPPPVVPKEEKEEETAAAPPVEEGEEQKPPAAEELAVDIGKAEEPVKSE	
ą	1439		
≿ £	966	CTEEAEEGPAKGKDAEAAEATAEGALKAEKKEGGSGRATTAKSSGAPQDS	
<b>a</b> .	1431		
<u>≽</u> 4	916	DSSATCSADEVDEREGGDKNRLLSPRPSLLTPTGDPRANASPQKPLDLKQLKQR 969   :-   :-   :-   :-   :-   :-	
<b>~</b>	970		
ą	1597	: :     :    :    :    :      :	
λ	1029	PADKEAFAAEAOKLPGDPPCWTSGLPFPVPPREVIKASPHAPDPSAFSYAPPGHPLPLGL 1088	
á	1640	VXCVEGTSL 1656	
λ	1089	HDTARPVLPRPPTISNPPPLISSAKHPSVLERQIGAISQGMSVQLHVPYSEHAKAPVGPV 1148	
ą	1657	SDLTIESPPNELAAGEGVRGGAQSGEFEKRDTIPT 1691	
Δ.	1149		
ð	1692	EGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAM 1731	

ð í	0 (	GGSITKGIPSTRVPSDSAITYRGSITHGTPADVLYKGFITRI 124
අු	1732	- 179
OY Dp	1247	IGEDSPSRLDRGREDSLPKGHVIYEGKKGHVLSYEGGMSVTQCSKEDGRSSGPPHE 1303
yo da	1304	TAAPKRIYDMMEGRVGRAISSASIECLMCRAIPPERHSPHHLKEQHHIRGSI 1355
oy.	35	-PPPSRDLTEAYKTQ 140
QQ	1894	: : :     : :     : :     : :     : : :     : : :     : : : :   :
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<u>a</u> ;	1954	SSLSDIDQENNNKENEPIKETEPPDSQGEPSKPQASGYAPKSFHV
g 5	2014	EDTPVCFSRNSSLSSLSSLSBDDLQECISSAMPKKKKPSRLKGDNEKHSPRNMGGILGE 2073
Οy	1483	TFPPVHPLDVMADARALERACYEESLKSRPGTASSSGGSIARGAPVIVPELGKPRQSPLT 1542
QQ	2074	DLTLDLKDIQRPDSEHGLSPDSENFDWKAIQEGANSIVSSL 2114
Qy	1543	REPTPRLQEGSLSSSKASQDRK 1
qq	2115	PFHLTPDQEEKPFTS
δ δ	1585	STPREIAKSPHSTVPEHHPHPISPYEHLLRGV-SGVDLYRSHIPLAFDPTSIPRGIPL 
a à	1644	PKILKPGERSIL
3 8	2197	
ò	1704	MDRLAYLPT
2 8	2213	
Qy	1764	APQPPSSRHSSSPLSPGGPTHLTKPTTTSSSERERDRDRERDRDREREKSILTSTTT 1820
qq	2236	
δλ	1821	PIWRPGTEQSSGSSGSGGGGSSSRPASHSHAHQHSPISPRTQDA
qq	2273	AKPSVKSELSPVARQ-TSQIGGSSRAPSRSGSRDSTPSRPAQQPLSRPIQSPGRNSI 2328
ΟŅ	1875	PSVLHNTGWKGIITAVEPSKPTVLRSTSTSSPVRPAATFPPATHCPLGGTLDGVP 1930
qq	2329	SPGRNGISPPNKLSQLPRTSSPSTASTKSSGSGKMSYTSPGRQM 2372
Qy	1931	ARPE
qq	2373	SOONLTKOTGLSKNASSIPRSESASKGLNOMNNGNGANKKVELSRMSSTKSSGSE 2427
Qy	1981	PRPLVPPVSGHATIARTPA-KNLAPHHASPDPPAPPASASDPHREKTQSKPFSIQE 2035
qq	2428	SDRSERPVLVRQSTFIKEAPSPTLRRKLEESASFESLSPSSRPASPTRSQAQT-PVLSPS 2486
Qy	2036	LELRSLGYHGSSYSPEGVEPVSPSLTHDKGLPKHLEELDKSHLEGELRPKQPGPVK 2095
qq	2487	LPDMSLSTH-SSVQAGGWRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPSRLPIN 2541
Óγ	2096	LGGEAAHLPHLRPLPESQPSSSPLLQTAPGVKGHQRVVTLAQHISEVITQDYTRHHPQ 2153
qq	2542	RSGTWKREHSKHSSSLPRVSTWRRTGSSSSILSASSESSEKAKSEDEKH 2590
'n	2154	OLSAPLPAPLYSPDGASCPVLDLRRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEPNKTS 2213

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LENGTH: 2843 amino acids
       TYPE: am....
TOPOLOGY: linear
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                             ; TOPOLOGY:
; MOLECULE TYI
US-08-452-655B-2
                                                                                                     Query Match
                                                                                                                    Best Local
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   2678
                                                                                                  2266 SQPPAFFSKLTESNSAMYKSKKQEINKKLNTHNRNEPEYNISQPGTEIFNMPAITGTGLM 2325
                                                                                                                                 --PP-------VIDSVSEKANPNIKDSKDNQAKQNV--------GNGSV 2710
                                                                                                                                                              2326 TYRSQAVQEHASTNMGLEAIIRKALMGKYDQWEESPPLSANAFNPLNASASLPAAMPITA 2385
                                                                                                                                                                             2386 ADGRSDHTLTSPGGGGKAKVSG---RPSSRKAKSPAPGLASGDRPPSVSSVHSEGDCNRR 2442
                                                                     2627 QTVSSGATNGAESKTLIYOMAPAVSKTEDVWVRIEDCPI------NNPRSGRSPTGNT
                                                                                                                                                                                                                                        2764 SSS-SKH--SSPSGTVAARVTPFNYNPSPRKSSAD----STSARPSQIP-----
                                           --VLGGGEDGIE-----PVSPPEGMTEPGHSRSAVYPLLYRDGEQTEPSRMGSKSPGNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DAFF:
FILLCATION UNMER: US/08/452,655B
FILING DATE: 25-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/289,548
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, NW
CITY: Washington
STATE: D.C.
COUNTRY: USA
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ANADI, RAKESH
CARLSON, MARY
GRODEN, JOANNA
HEDGE, PHILIP J.
JOSLYN, GEOFF
KINZLER, KENNETH
MARKHAM, ALEXANDER F.
NAKAMURA, YUSUKE
NAKAMURA, YUSUKE
THLIVERIS, ANDREW
                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08452655B Patent No. 578366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DC
SOFTWARE: PatentIn Release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                   2806 TPVNNNT-KKRDSKTDST 2822
                                                                                                                                                                                                                                                                              2443 TPLTNRVWEDRPSSAGST 2460
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & W
                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          974 GKRGOMKPSIESYSEDDESKFCSYGOYPADLAHKIHSANHMDDNDGELDTPINYSLKYSD 1033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 370 HEVSEIIDGLSEQENLEKQMRQLAVIPPMLYDADQQRIKFINMNGLMADPMKVYKDRQVM 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   754 PHTEAAKDTGQNGPKPPATLGADGP-----PPGPPTPPRRTSRAPIEPTPASEATGAPTP 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPAPPSPSAPPPVVPKEEKEEETAAAPPVEEGEEQKPPAAEELAVDTGKA---EEPVKSE 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               866 CTEEAEEG-----PAKGKDAEAAEATAEGALKAEKKEGGSGRATTA---KSSGAPQDS 915
                                                                                                                                                                                          202 EEAAKPPEPEFEKPVSPPPIESKHRSLVQIIYDENR--KKAEAAHRILEGLGPQVELPLYNQ 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  893 EVSAIHTSQEDRSSGSTTE-----LHCVTDERNALRRSSAAH-----THSNTYN- 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 PSDTRQYHENIKINQAMRKKLILYFKRRNHARKQWKQKFCQRYDQLMEALEKKVERIENN 319
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     142 TGKLEPVSPPSPPHTDPELELVPPRLSKEELIQNMDRVDREITMVEQQISKLKKKQQQLE 201
                                                                                                                                                 -----PGNERSQELHLRPESHSY 91
                                                                                                                                                                                                                                                                                                                                        800 VFDTNRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSSSSRGSLDSSRSEKDRSLERERGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 PRRRAKESKVREYYEK------QFP-EIRKQRELQERMQSRVGQRGSGLSMSAARSE
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                                                                                                                                                                                                                                                                                       92 LPELGKSEMEFIESKRPRLELLPDPLLRPSPLLATGQPAGSEDLT---KDRSL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        860 LGNYHPATEN-----PGTSSKRGL------QISTTAAQIAKV-----ME
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                                                                          Indels 821;
2.7%; Score 350.5; DB 1; Length 2843; 17.8%; Pred. No. 1.1e-11;
                                                                          Matches 473; Conservative 357; Mismatches 1007;
                                                                                                                                                 50 ASHLSPGSIIQP -- QRRRPSLLSEFQ------
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qq	1492	ATESTPDGFSCSSSLSALSLDEPFIQKDVELRIMPPVQENDNGNETESEQPKESNENQEK 1551	
oy og	916	DSSATCSADEVDEAEGGDKNRLLSPRPSLLTPTGDPRANASPQKPLDLKQLKQR 969 ::	
ογ	970	AAAIPPIQVTKVHEPPREDAAPTKPAPPAPPPPQNLQPESDAPQQPGSS-PRGKSRSPAP	
Q D	1598	ASKLPPPVARKPSQLPVYKLLPSQNRLQPQKHVSFTPGDDMPR	
Qy Dp	1029	PADKEAFAAEAQKLPGDPPCWTSGLPFPVPPREVIKASPHAPDPSAFSYAPPGHPLPLGL 1088 VYCNEGTEL 1657	
QΫ	1089	HDTARPVLPRPPTISNPPLISSAKHPSVLERQIGAISQGMSVQLHVPYSEHAKAPVGPV	
Op	1658	SDLTIESPPNBLAAGEGVRGAQSGEFEKRDIIPT	
Οy	1149	TMGLPLPMDPKKLAPFSG	
qq	1693	EGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAM 1732	
O.Y DB	1204	PGGSITKGIPSTRVPSDSAITYRGSITHGTPADVLYKGTITRI 1246	
οy	1247	IGEDSPSRLDRGREDSLPKGHVIYEGKKGHVLSYEGGMSVTQCSKEDGRSSSGPPHE 1303	
qq	1792	- NADSKNNINAERVFSDNKDSKKQNLKNNSKDFNDKLPNNEDRVRGSFAFDSPHH 1845	
οy	1304	TAAPKRTYDMMEGRVGRAISSASIEGLMGRAIPPERHSPHHLKEQHHIRGSI 1355	
g	1846	YTPIEGTPYCFSRNDSLSSLDFDDDDVDLSREKAELRKAKENKESEAKV 1894	
δ	1356	TQGIPRSYVEAQEDYLRREAKLLKREGTPPPPPPSRDLTEAYKTQ	
g	1895	TSHTELTSNQQSANKTQAIAKQPINRGQPKPILQKQSTFPQSSKDIPDRGAATDEKLQNF 1954	
Q Dp	1401	ALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGSIT 1452	
ογ	1453	OGTPLKYDTGASTTGSKKHDVRSLIGSPGR 1482	
Dp	2015	EDTPVCFSRNSSLSSLSIDSEDDLLQECISSAMPKKKKPSRLKGDNEKHSPRNMGGILGE 2074	
Qy Db	1483	TFPPVHPLDVMADARALERACYEESLKSRPGTASSSGGSIARGAPVIVPELGKPRQSPLT 1542	
<b>^</b> 0	1543	SSKASODRK 158	
· 8	2116	ASSDSDSILSLKSGISLGSPFHLTPDQEERPFTSNKG	
δy	1585	LTSTPREIAKSPHSTVPEHHPHPISPYEHLLRGV-SGVDLYRSHIPLAFDPTSIPRGIPL 1643	
q	2165	PRILKPGEKSTLETKKIESESKGIKGGKKVYKS 2197	
δý	1644	DAAAAYYLPRHLAPNPTYPHLYPPYLIRGYPDTAALENRQTIINDYITSQQMHHNTATAM 1703	
qq	2198		
οy	1704	AQRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAMDRLAYLPT 1763	
QQ	2214		
٥y	1764	APQPFSSRHSSSPLSPGGPTHLTKPTTTSSSERERDRDRERERSILTSTTT 1820	
QQ	2237	RNSSSSTSPVSKKGPP-LKTPASKSPSEGQTATTSPRG 2273	
δ	1821	VEHAPIWRPGTEQSSGSSGSGGGGSSSRPASHSHAHQHSPISPRTQDALQQR	
면 연	2274	AKPSVKSELSPVARQ-TSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPIQSPGRNSI 2329	

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2330 ----SPGRNGI---SPPNKLSQLPRTSSPSTA-----STKSSGSGKMSYTSPGRQM 2373
                                                                                                                                                  2374 SQQNLTKQTGLSKNASSI-----PRSESASKGLNQMNNGNGANKKVELSRMSSTKSSGSE 2428
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1875 PSVLHNTGMKGIITAVEPSKPTVLRSTSTSSPVRPAATFPPATHCPLGGTLDGVYP---- 1930
                                                                                                                                                                                                                      ----PRPLVPPVSGHATIARTPA-KNLAPHHASPDPPAPPASASDPHREKTQSKPFSIQE 2035
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                                                                                                                                                                                                                                                                                                                                                                   2628 QTVSSGATNGAESKTLIYQMAPAVSKTEDVWVRIEDCPI------NNPRSGRSPTGNT 2679
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                                                                                                                                                                                                                                                                                                                                                                                                                                          2096 LGG--EAAHLPHLRPLPESQPSSSPLLQTAPGVKGHQRVVTLAQHISEVITQDYTRHHPQ 2153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2543 RSGTWKREHSKH-----SSSLPRVSTWRRTGSSSSILSASSESSEKAKSEDEKH--- 2591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2154 QLSAPLPAPLYSFPGASCPVLDLRRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEPNKTS 2213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2214 --VLGGGEDGIE-----PVSPPEGMTEPGHSRSAVYPLLYRDGEQTEPSRMGSKSPGNT 2265
                                                                                                                                                                                                                                                                             SDRSERPVLVRQSTFIKEAPSPTLRRKLEESASFESLSPSSRPASPTRSQAQT-PVLSPS
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APPLICANT: GRODEN, JOANNA,
APPLICANT: HEDGE, PHILIP J.
APPLICANT: HEDGE, PHILIP J.
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: THLIVERIS, ANDREW
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: INHERITED AND SOMATIC MUTATIONS OF APPLICE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APPLICE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---TLMEPVLLPKEAPRVARPERPRADTGHAFLAKPPARSGLEP--
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; Patent No. 578366
; GENERAL INFORMATION:
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ADDRESSEE: Banner & Witcon
STREET: 1001 G Street, NW
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COUNTRY: USA
ZIP: 20001-4598
COMPOTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ALBERTSEN, HANS APPLICANT: ANAND, RAKESH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          370 HEVSEIIDGLSEQENLEKQMRQLAVIPPMLYDADQQRIKFINMNGLMADPMKVYKDRQVM 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RRRGKSQQQQQQQQQQQQQQQQQPMPRSSQEEKDEKEKE-----AEKEEEKPEVEND 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPELGKSEMEFIESKRPRLELLPDPLLRPSPLLATGQPAGSEDLT---KDRSL----- 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGKLEPVSPPSPPHTDPELELVPPRLSKEELIQNMDRVDREITMVEQQISKLKKKQQQLE 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  860 LGNYHPATEN-------METSSKRGL------QISTTAAQIAKV----ME 892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.7%; Score 350.5; DB 1; Length 2843; Best Local Similarity 17.8%; Pred. No. 1.1e-11; Matches 473; Conservative 357; Mismatches 1007; Indels 821;
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,655B
FILING DATE: 25-MAY-1995
                                                                                                                                        CLASSIFICATION: 530
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILLING DATE: 12-A0G-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILLING DATE: 08-A0G-1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.49964
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELEPHONE: 202-508-9190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 ASHLSPGSIIQP--QRRRPSLLSEFQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2843 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ANTI-SENSE:
US-08-452-655B-7
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1439 1089 HDTARPVLPRPPTISNPPPLISSAKHPSVLERQIGAISQGMSVQLHVPYSEHAKAPVGPV 1148 PGG------SITKGIPSTRVPSDSAITYR----GSITHGTPADVLYKGTITRI 1246 1894 1400 AAAIPPIQVTKVHEPPREDAAPTKPAPPAPPPPQNLQPESDAPQQPGSS-PRGKSRSPAP 1028 1029 PADKEAFAAEAQKLPGDPPCWTSGLPFPVPPREVIKASPHAPDPSAFSYAPPGHPLPLGL 1088 PKGKSHKPFRVKKIMDQVQQASASSAPNKNQLDGKKKKPTSPVKPIPQNTEYRTRVRK- 1791 1792 -NADSKNNINAERVFSDNK-----DSKKONLKNNSKDFNDKLPNNEDRVRGSFAFDSPHH 1845 1304 TAAPKRIYDMMEGRVGRAISSASIEGL-----MGRAIPPERHSPHHLKEQHHIRGSI 1355 1336 RLQGSSLSSESARHKAVEFSSGAKSPSKSGAQTPKSPPEHYVQETPLMFSRCTSVSSLDS 1395 1440 PP-PPQTAQTKREVPKNK-----APTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHF 1491 ALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHT------PELPLAPRPLKEGSIT 1452 QGTPLKYDTGASTTG------SKKHDVRSLIGSPGR 1482 1483 TFPPVHPLDVMADARALERACYEESLKSRPGTASSSGGSIARGAPVIVPELGKPRQSPLT 1542 1895 TSHTELTSNQQSANKTQAIAKQPINRGQPKPILQKQSTFPQSSKDIPDRGAATDEKLQNF 1954 1237 QSRSGQ----PQKAATCKVSSINQETIQTYCVEDTP------ICFSRCSSLSSLS 648 QCKNFYFNYKKRQNLD--EILQQHKLKMEK--ERNARRKKKRAPAAASEEAAFPPVVEDE SAEDEIGCNQTTQEADSANTLQIAEIK-EKIGTRSAEDPVSEVPAVSQH-----PRTKSS 588 NEANSEEAITPQQSAELASMELNESSRWTEEEMETAKKGLLEHGRNWSAIARMVGSKTVS 704 EMEASGVSGNEE-----EMVEEAEALHASGNEVPRGE-----CSGPATVNNSSDTESIPS 1396 FESRSIASSVQSEPCSGMVSGIISPSDLPDSPGQTMPPSRSK------TP PPAPPSPSAPPPVVPKEEKEEETAAAPPVEEGEEQKPPAAEELAVDTGKA---EEPVKSE DSSATCSA--DEVDEAEGGD----KNRLLSPRPSLLTPTGDPRANASPQKPLDLKQLKQR 1552 EAEKTIDSEKDLLDDSDDDIEILEECIISAMPT-----KSSRKAKKP----AQT 1598 ASKLPPPVARKPSQLPVYKLLPSQ-----NRLQPQKHVSFTPGDDMPR-----SDL-----TIESPP-----TIESPP-TIESPP-----NELAAGEGVRGGAQSGEFEKRDTIPT 1149 IMGLPLPMDPKKLAPFSGVKQEQLSPRGQAGPPESLGVP----TAQEASVLRGTALGSV 1247 IGEDSPSRLDRGREDSLPKGHVIYEGKKGHVLSYEGGMSVTQCSKED----GRSSSGPPHE 1846 -----YTPIEGTPYCFSRNDSLSSLDFDDDDVDLSR----EKAELRKAKENKESEAKV 1356 TQGIPRSYVEAQEDYLRREAKLLKREGTPPP-----PPPSRDL-----TEAYKTQ 1955 AIENTPVCFSHNSSLSSLSDIDQENNNKENEPIKETEPPDSQGEPSKPQASGYAPKSFHV 754 PHTEAAKDTGQNGPKPPATLGADGP-----PPGPPTPPRRTSRAPIEPTPASEATGAPTP 866 CTEEAEEG-----PAKGKDAEAAEATAEGALKAEKKEGGSGRATTA---KSSGAPQDS ------TPINFSTA-----TSL -----VYCVEG-----1641 1733 970 1693 1204 1401 1453 916 ò 셤 셤 ò g 셤 g g g g ŏ δ D δ g g 셤 qq 염 ŏ ð ò ŏ ò ă ò δ g à ŏ ò á

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----PRPLVPPVSGHATIARTPA-KNLAPHHASPDPPAPPASASDPHREKTQSKPFSIQE 2035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2214 --VLGGGEDGIE-----PVSPPEGMTEPGHSRSAVYPLLYRDGEQTEPSRMGSKSPGNT 2265
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                                                   --GSPVTMREPTPRLQEGSLSSSKASQDRK 1584
                                                                                                                                              LISTPREIAKSPHSTVPEHHPHPISPYEHLLRGV-SGVDLYRSHIPLAFDPTSIPRGIPL 1643
                                                                                                                                                                                                                                               DAAAAYYLPRHLAPNPTYPHLYPPYLIRGYPDTAALENRQTIINDYITSQQMHHNTATAM 1703
                                                                                                                                                                                                                                                                                                                                           1704 AQRADMIRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAMDRLAYLPT 1763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----VEHAPIWRPGTEQSSGSSGSGGGGSSSRPASHAHQHSPISPRTQDALQQR 1874
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                                                                                           2116 ---HQAAAAACLSRQASSDSDSILSLKSGISLGSPFHL---TPDQEEKPFTSNKG--
----DLTLDLKDIQRPDSEHGLS--PDSENFDWKAIQEGANSIVSSL-
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                                                                                                                                                                                            2165 ----PRILKPGEKSTL-----ETKKIESESKGIKGGKKVYKS-----
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RESULT 14 US-08-450-582-2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 TGKLEPVSPPSPPHTDPELELVPPRLSKEELIQNMDRVDREITMVEQQISKLKKKQQQLE 201
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                                                                                                APPLICANT: CARLSON, MAN.
APPLICANT: GRODEN, JOANNA
APPLICANT: GRODEN, JOANNA
APPLICANT: HEDGE, PHILIP J.
APPLICANT: NIZLEN, GENFF
APPLICANT: KINZLER, KENNETH
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: THILFERS, ANDREW
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
TITLE OF SEQUENCES: 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ed. No. 1.1e-11;
Mismatches 1007;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/452,655
FILING DATE: 25-MAY-1995
APPLICATION NUMBER: US 08/289,548
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATTORNEY,AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1107.49964
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                                                                                                                                                                                                                                                                                                                                                                                     Banner & Witcoff, Ltd
1001 G Street, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: D.C.
COUNTRY: USA
ZIP: 20001-459
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBN PC COMPAtible
COMPUTER: IBN PC COMPATIBLE
Application US/08450582
6114124
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Best Local Similarity 17.8%; Pro
Matches 473; Conservative 357;
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TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32,141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2843 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington
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                                                                    APPLICANT:
APPLICANT:
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936	319	969	1033	429	1069	487	541	587	1236	647	1281	703	1335	753 1395	808	1439	865	1491	915	696	1597	1028	1640	1088	1657	1148	1692	1203	1732	1246
:	PSDTRQYHENIKINQAMRKKLILYFKRRNHARKQWKQKFCQRYDQLMEAL	33.0 PRRRAKESKVREVYEKOFP-ETRKORFLOFFMOSRVGORGRGISMAARSE	GKRGQMKPSIESYSEDDESKFCSY	0 HEVSEIIDGLSEQENLEKQMRQLAVIPPMLYDADQQRIKFINMNGLMADPMKVYKDRQVM	4EQLNSGRQSPSQNERWARPKHITEDEIKQSEQRQSR	0 NAMSEQEKETFREKFMQHPKNFGLIASFLERKTVAECVLYYYLTKKNENYKSLVRRSY	RRRGKSQQQQQQQQQQQQQQQQPMPRSSQEEKDEKEFKEAEKEEEKPEVEND   :         : :       : :	×	:       :  :  :  :		QSRSGQPQKAATCKVSS	8 QCKNFYFNYKRQNLDEILQQHKLKMEKERNARRKKKAPAAASEEAAFPFVVEDE	SAEDEIGCNOTTOEADSANTLOIAEIK-EKIGTR	4 EMEASGVSGNEEEMVEEAEALHASGNEVPRGECSGPATVNNSSDTESIPS ::   :       :     :   :   :   :   :	4 PHTEAAKDIGQNGPKPPATLGADGPPPGPPTPPRKTSRAPIEPTPASEATGAPTP	FESRSIASSVQSEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTP	9 PPAPPSPSAPPPVVPKEEKEEETAAAPPVEEGEEGKPPAAEELAVDTGKAEEPVKSE	0 PP-PPQTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHF	6 CTEEAEEGPAKGKDAEAAEATAEGALKAEKKEGGSGRATTAKSSGAPQDS				: :		1VYCVEGTSL	9 HDTARPVLPRPPTISNPPPLISSAKHPSVLERQIGAISQGMSVQLHVPYSEHAKAPVGPV	SDLTIE	TMGLPLPMDPKKLAPFSGV		4 PGGSITKGIPSTRVPSDSAITYRGSITHGTPADVLYKGTITRI : :     :  :  : ::
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1482 1247 IGEDSPSRLDRGREDSLPKGHVIYEGKKGHVLSYEGGMSVTQCSKED---GRSSSGPPHE 1303 1304 TAAPKRIYDMMEGRVGRAISSASIEGL-----MGRAIPPERHSPHHLKEQHHIRGSI 1355 1356 TQGIPRSYVEAQEDYLRREAKLLKREGTPPP------PPPSRDL-----TEAYKTQ 1400 1895 TSHTELTSNQQSANKTQAIAKQPINRGQPKPILQKQSTFPQSSKDIPDRGAATDEKLQNF 1954 ALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHT------PELPLAPRPLKEGSIT 1452 2014 : | | : : | | EDTPVCFSRNSSLSSLSIDSEDDLLQECISSAMPKKKRPSRLKGDNEKHSPRNMGGILGE 2074 1483 TFPPVHPLDVMADARALERACYEESLKSRPGTASSSGGSIARGAPVIVPELGKPRQSPLT 1542 2164 2197 2236 2273 2274 AKPSVKSELSPVARQ-TSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPIQSPGRNSI--- 2329 1930 2373 2213 -----YIPIEGIPYCFSRNDSLSSLDFDDDVDLSR----EKAELRKAKENKESEAKV 1894 1585 LTSTPREIAKSPHSTVPEHHPHPISPYEHLLRGV-SGVDLYRSHIPLAFDPTSIPRGIPL 1643 ------LITG------KVRSNSEISGOM----- 2213 1704 AQRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAMDRLAYLPT 1763 1764 APQPFSSRHSSSPLSPGGPTHLTKPTTTSSSERERDRDRERERSILTSTTT--- 1820 1931 ---TLMEPVLLPKEAPRVARPERPRADTGHAFLAKPPARSGLEP-----ASSPSKGSE 1980 2374 SQQNLTKQTGLSKNASSI----PRSESASKGLNQMNNGNGANKKVELSRMSSTKSSGSE 2428 ----PRPLVPPVSGHATIARTPA-KNLAPHHASPDPPAPPASASDPHREKTQSKPFSIQE 2035 2429 SDRSERPVLVRQSTFIKEAPSPTIRRKLEESASFESLSPSSRPASPTRSQAQT-PVLSPS 2487 1543 YEDHGAPFAGHLPR------GSPVTMREPTPRLQEGSLSSSKASQDRK 1584 1644 DAAAAYYLPRHLAPNPTYPHLYPPYLIRGYPDTAALENRQTIINDYITSQQMHHNTATAM 1703 -----VEHAPIWRPGTEQSSGSSGSGGGGSSSRPASHAHQHSPISPRTQDALQQR 1874 LELRSLGYHGSSYSPEGVEPVSPVSSPSLTHDKGLPKHLEELDKSHLEGELRPKQPGPVK 2095 1733 PKGKSHKPFRVKKIMDQVQQASASSAPNKNQLDGKKKKPTSPVKPIPQNTEYRTRVRK- 1791 2543 RSGTWKREHSKH-----SSSLPRVSTWRRTGSSSSILSASSESSEKAKSEDEKH--- 2591 2592 -----VNSISGTK-----QSKENQVSAKGTWRKIKENEFSPTNSTS 2627 1792 -NADSKNNLNAERVFSDNK----DSKKQNLKNNSKDFNDKLPNNEDRVRGSFAFDSPHH 1955 AIENTPVCFSHNSSLSSLSDIDQENNNKENEPIKETEPPDSQGEPSKPQASGYAPKSFHV 1875 PSVLHNTGMKGIITAVEPSKPTVLRSTSTSSPVRPAATFPPATHCPLGGTLDGVYP----: | | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : LGG--EAAHLPHLRPLPESQPSSSPLLQTAPGVKGHQRVVTLAQHISEVITQDYTRHHPQ QGTPLKYDTGASTTG-----SKKHDVRSLIGSPGR ---HQAAAAACLSRQASSDSDSILSLKSGISLGSPFHL---TPDQEEKPFTSNKG----2214 --------KOPLQANMPSISRG----RTMIHIPGV------2154 QLSAPLPAPLYSFPGASCPVLDLRRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEPNKTS 1453 2015 2075 2116 1846 1401 2165 2198 2237 1821 2330 1981 2036 2096 g ò q ò g δ q ò a ò 셤 òγ a ŏ q ÓΥ g δ QQ δ q δ QQ à g ŏ qq δ g á g à g ò q ŏ g

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                                                                         2266 SQPPAFFSKLTESNSAMVKSKKQEINKKLNTHNRNEPEYNISQPGTEIFNMPAITGTGLM 2325
                                                                                                                                                                                                                        2386 ADGRSDHTLTSPGGGGKAKVSG---RPSSRKAKSPAPGLASGDRPPSVSSVHSEGDCNRR 2442
                                                                                                                                                                                     2712 PMRTVGLENKLNSFIQVDAPDQKGTEIKPGQNNPVPVSETN-----ESSIVERTPFSS
                                    2628 OTVSSGATNGAESKTLIYQMAPAVSKTEDVWVRIEDCPI------NNPRSGRSPTGNT
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APPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
TITLE OF GENERAL SERVER OF THE OF THE OF THE OF T
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                                                                                                              2680 -- PP------VIDSVSEKANPNIKDSKDNQAKQNV---
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APPLICATION NUMBER: US 08/452,655
FILING DATE: 25-MAY-1995
APPLICATION NUMBER: US 08/289,548
FILING DATE: 12-MG-1994
PRIOR APPLICATION DATA: US 07/741,940
APPLICATION NUMBER: US 07/741,940
APPLICATION NUMBER: US ATOWNAYAGENT INFORMATION:
NAMME: Kagan, Sarah A.
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REFERENCE/DOCKET NUMBER: 1107.49964
TELECOMMUNICATION INFORMATION:
TELEDHONE: 202-508-9100
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IBM PC compatible
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                                                                                                                                                                                                                                                                                                    2443 TPLTNRVWEDRPSSAGST 2460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202-508-9299
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ZIP: 20001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: D
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                            Query Match 2.7%; Score 350.5; DB 3; Best Local Similarity 17.8%; Pred. No. 1.1e-11; Matches 473; Conservative 357; Mismatches 1007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 ASHLSPGSIIQP--QRRRPSLLSEFQ----
2843 amino acids
                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                    MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                       ; ANTI-SENSE:
US-08-450-582-7
   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       893
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>	9		915
Д	1492	ATESTPDGFSCSSSLSALSLDEPFIQKDVELRIMPPVQENDNGNETESEQPKESNENQEK	1551
>- A	on 1	DSSATCSADEVDEAEGGDKNRLLSPRPSLLTPTGDPRANASPQKPLDLKQL	696
ο :	7007		1597
~ t	1500	ACT DODGE TO THE TOTAL TOT	1028
a >	1029	DANKERRARARANKT DCHODOWINGCT DEDVIDODENTRA COURDIDGA EGYA DOGUDT DT.	1040
, α	1641		1657
>-	1089	HDTARPVLPRPPTISNPPPLISSAKHPSVLERQIGAISQGMSVQLHVPYSEHAKAPVGPV	1148
Ω	1658		1692
>-	1149	TMGLPLPMDPKKLAPFSGVKQEQLSPRGQAGPPESLGVPTAQEASVLRGTALGSV	1203
Ω	1693	GRSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAM	1732
>-	1204		1246
۵	1733	PKGKSHKPFRVKKIMDQVQQASASSAPNKNQLDGKKKKPTSPVKPIPQNTEYRYRK-	1791
>-	1247	IGEDSPSRLDRGREDSLPKGHVIYEGKKGHVLSYEGGMSVTQCSKEDGRSSSGPPHE	1303
۵	1792	-NADSKNNLNAERVFSDNKDSKKQNLKNNSKDFNDKLPNNEDRVRGSFAFDSPHH	1845
>.	1304	TAAPKRTYDMMEGRVGRAISSASIEGLMGRAIPPERHSPHHLKEQHHIRGSI	1355
۵	1846	YTPIEGTPYCFSRNDSLSSLDFDDDDVDLSREKAELRKAKENKESEAKV	1894
>-	1356	TQGIPRSYVEAQEDYLRREAKLLKREGTPPPPPPSRDLTEAYKTQ	1400
Ω	1895	TSHTELTSNQQSANKTQAIAKQPINRGQPKPILQKQSTFPQSSKDIPDRGAATDEKLQNF	1954
>-	1401		1452
۵	1955	AIENTPVCFSHNSSLSSLSDIDQENNNKENEPIKETEPPDSQGEPSKPQASGYAPKSFHV	2014
>-	1453	QGTPLKYDTGASTTGSKKHDVRSLIGSPGR	1482
Q	2015	EDTPVCFSRNSSLSSLSIDSEDDLLQECISSAMPKKKKPSRLKGDNEKHSPRNMGGILGE	2074
>-	1483	TFPPVHPLDVMADARALERACYEESLKSRPGTASSSGGSIARGAPVIVPELGKPRQSPLT	1542
Q	2075	DLTLDLKDIQRPDSEHGLSPDSENFDWKAIQEGANSIVSSL	2115
>-	1543	YEDHGAPFAGHLPRGSPVTWREPTPRLQEGSLSSSKASQDRK	1584
۵	2116	HQAAAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQEERPFTSNKG	2164
>-	1585	VPEHHPHPISPYEHLLRGV-SGVD	1643
۵	2165	PRILKPGEKSTLETKKIESESKGIKGGKKVYKS	2197
>-	1644	DAAAAYYLPRHLAPNPTYPHLYPPYLIRGYPDTAALENRGTIINDYITSQQMHHNTATAM	1703
۵	2198	TITE TO THE TOTAL TO	2213
>-	1704	AQRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTFGTPATAMDRLAYLPT	1763
۵	2214	KQPLQANMPSISRGRTWIHIPGV	2236
<b>5.</b>	1764	APQPESSRHSSSPLSPGGPTHLTKPTTTSSSERBRDRDRERDRDREREKSILTSTTT	1820
۰	2237	RNSSSTSPVSKKGPP-LKTPASKSPSEGOTATTSPRG	2273

λ d	2274	VEHMATURKPGTEQESGESGESGEGGESSERPAKHAHAHQHESTESPRYQDALQQR 18/4   : :	
Qy	1875	PSVLHNTGMKGIITAVEPSKPTVLRSTSTSSPVRPAATFPPATHCPLGGTLDGVYP 1930	
qq	2330	SPGRNGISPPNKLSQLPRTSSPSTASTKSSGSGKMSYTSPGRQM 2373	
Qy	1931	TLMEPVLLPKEAPRVARPERPRADIGHAFLAKPPARSGLEPASSPSKGSE 1980	
qq	2374	SQQNLTKQTGLSKNASSIPRSESASKGLNQMNNGNGANKKVELSRMSSTKSSGSE 2428	
٥y	1981	PRPLVPPVSGHATIARTPA-KNLAPHHASPDPPAPPASASDPHREKTQSKPFSIQE 2035	
qq	2429	SDRSERPVLVRQSTFIKEAPSPILRRKLEESASFESLSPSSRPASPTRSQAQT-PVLSPS 2487	
Οy	2036	LELRSLGYHGSSYSPEGVEPVSPVSSPSLTHDKGLPKHLEELDKSHLEGELRPKQPGPVK 2095	
qq	2488	LPDMSLSTH-SSVQAGGWRKLPPNLSPFIEYNDGRPAKRHDIARSHSESPSRLPIN 2542	
οy	2096	LGGEAAHLPHLRPLPESQPSSSPLLQTAPGVKGHQRVVTLAQHISEVITQDYTRHHPQ 2153	
qa	2543	RSGTWKREHSKHSSSLPRVSTWRRTGSSSSILSASSESSEKAKSEDEKH 2591	
Óλ	2154	QLSAPLPAPLYSFPGASCPVLDLRRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEPNKTS 2213	
qq	2592	VNSISGTKQSKENQVSAKGTWRKIKENEFSPTNSTS 2627	
ΟŸ	2214	VLGGGEDGIEPVSPPEGMTEPGHSRSAVYPLL/RDGEQTEPSRMGSKSPGNT 2265	
qq	2628	QTVSSGATNGAESKTLIYQMAPAVSKTEDVWVRIEDCPINNPRSGRSPTGNT 2679	
Qy	2266	S	
QQ	2680	PPVIDSVSEKANPNIKDSKDNQAKQNVGNGSV 2711	
δλ	2326	TYRSOAVOEHASTNMGLEAIIRKALMGKYDQWEESPPLSANAFNPLNASASLPAAMPITA 2385	
qq	2712	PMRTVGLENRLNSFIQVDAPDQKGTEIKPGQNNPVPSETNESSIVERTPFSS 2764	
QY	2386	ADGRSDHTLTSPGGGGKAKVSGRPSSRKAKSPAPGLASGDRPPSVSSVHSEGDCNRR 2442	
qq	2765	SSS-SKHSSPSGIVAARVIPFNYNPSPRKSSADSTSARPSQIP 2806	
δy	2443	TPLINKVWEDRPSSAGST 2460	
qq	2807	TPVNNNT-KKRDSKIDSI 2823	

Search completed: September 8, 2001, 14:35:09 Job time: 17211 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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8, 2001, 09:57:13 ; Search time 70.16 Seconds (without alignments) 2732.773 Million cell updates/sec September Run on:

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BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

٠,	transcription cornuclear receptor c hypothetical prote microtubule-associ hypothetical prote maccent polypeptid proline-rich peptid proline-rich peptid proline-rich peptid proline-rich peptid passon protein - elastic titin - hu MHC class III hist Basson protein - elastic titin - hu MHC class III hist eyelid - fruit fly Basson protein - microtubule-associ hypothetical prote high molecular mas microtubule-associ hypothetical prote
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å Query Match Length	1495 2453 2453 2649 20142 21142 21187 20187 3948 1870 1870 2282 4957 2282 1151 1252 1151 1264 11791 1274 11791 1270 11791 1270
å Query Match	8.40 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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Result No.	222 222 223 223 224 225 225 226 226 227 228 238

hypothetical prote	alpha-fetoprotein	ankyrin 2, neurona	extensin-like prot	All-1 protein +GTE	TCOF1 protein - mo	trithorax homolog	collagen alpha 1(V	collagen alpha 5(I	atrophin-1 related	hypothetical prote	atrophin-1 - human	protein-tyrosine-p	cell proliferation	collagen alpha 2(I	C-terminal domain-
T00273	A41948	537431	S49915	A48205	JC5630	A44265	A54849	S22917	T42731	T20532	S50832	T14355	T30249	S16366	T31421
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1520	2783	3924	1188	3869	1320	3968	2944	1691	1006	2722	1184	1494	2938	1763	1173
3.0	3.0	3.0	5.9	2.9	5.9	6.2	5.9	2.9	2.8	2.8	2.8	2.8	2.8	7.8	2.8
395	394	391	389,5	389.5	389	383.5	383	377	375	374.5	373.5	373.5	373.5	373	372.5

## ALIGNMENTS

hormone receptors

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RESULT 1 S60255 S60255 C.Date: lo-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 05-Nov-1999 C.Date: lo-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 05-Nov-1999 C.Date: D.D.; Evans, R.M. Nature 377, 454-457, 1995 A.Title: A transcriptional co-repressor that interacts with nuclear hormone 34, Reference number: S60255, MUD:96008552	A.Accession: S60255 A.Status: preliminary; nucleic acid sequence not shown A.Molecule type: mRNA A.Residues: 1-1495 <che> A.Cross-references: EMBL:U37146; NID:g1045654; PIDN:AAC50236.1; PID:g1045655</che>	Query Match 59.6%; Score 7871; DB 2; Length 1495; Best Local Similarity 100.0%; Pred. No. 3.1e-269; Matches 1487; Conservative 0; Mismatches 0; Indels 0; Gaps	1031 DKEAFAAEAQKLPGDPPCWTSGLPFPVPPREVIKASPHAPDPSAFSYAPPGHPLPLGLHD 1090	9 DKEAFAAEAQKLPGDPPCWTSGLPFPVPPREVIKASPHAPDPSAFSYAPPGHPLPLGLHD 68	1091 TARPVLPRPPTISNPPPLISSAKHDSVLERQIGAISQGMSVQLHVPYSEHAKAPVGPVTM 1150 		129 GLPLPMDPKKLAPFSGVKQEQLSPRGQAGPPESLGVPTAQEASVLRGTALGSVPGGSITK 188	11 GIPSTRVPSDSAITYRGSITHGTPADVLYKGTITRIIGEDSPSRLDRGREDSLPKGHVIY 1270	m	71 EGKKGHVLSYEGGMSVTQCSKEDGRSSSGPPHETAAPKRTYDMMEGRVGRAISSASIEGL 1330	249 EGKKGHVLSYEGGMSVTQCSKEDGRSSSGPPHETAAPKRTYDMMEGRVGRAISSASIEGL 308	31 MGRAIPPERHSPHHLKEQHHIRGSITQGIPRSYVEAQEDYLRREAKLLKREGTPPPPPPS 1390	309 MGRAIPPERHSPHHLIKEQHHIRGSITQGIPRSYVEAQEDYLRREAKLLKREGTPPPPPPS 368	31 RDLTEAYKTQALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGS 1450	369 RDLTEAYKTQALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGS 428	51 ITQGTPLKYDTGASTTGSKKHDVRSLIGSPGRIFPPVHPLDVMADARALERACYEESLKS 1510	429 ITQGTPLKYDTGASTTGSKKHDVRSLIGSPGRTFPPVHPLDVMADARALERACYEESLKS 488
S60255 S60255 C5Decies: Ho C5Date: 10-Ap C3Accession: R;Chen, J.D.; Nature 377, 4 A;Title: A tr A;Reference n tr	Acces Statu Molec Resid Cross	Query Best Match		•		1151		1211	18	1271		, 1331		, 1391		, 1451	
成の亡ひひひま <b>以本々</b>	<b>4444</b>		οy	q	Qy Db	Qy	a	οy	qq	οy	qa	QY	qq	οy	qq	Qy	ΩD

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       AFDPTSIPRGIPLDAAAAYYLPRHLAPNPTYPHLYPPYLIRGYPDTAALENRQTIINDYI
                                                                                                         RPGTASSSGGSIARGAPVIVPELGKPRQSPLTYEDHGAPFAGHLPRGSPVTMREPTPRLQ
                                                            TSQQMHHNTATAMAQRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGT
                                                                                       LOORPSVLHNTGMKGIITAVEPSKPTVLRSTSTSSPVRPAATFPPATHCPLGGTLDGVYP
                                                                                                                                                                      TLMEPVLLPKEAPRVARPERPRADTGHAFLAKPPARSGLEPASSPSKGSEPRPLVPPVSG
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                                                                                                                                    EKSILTSTTTVEHAPIWRPGTEQSSGSSGGGGGSSSRPASHSHAHQHSPISPRTQDA
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RESULT 2
S60254
nuclear receptor co-repressor N-CoR
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mediated 106; C; Species: Mus musculus (house mouse)
C;Date: 10.Apr-1996 #sequence\_revision 19.Apr-1996 #text\_change 08-Oct-1999
C;Accession: S60254
R;Hoerlein, A.J.; Naeaer, A.M.; Heinzel, T.; Torchia, J.; Gloss, B.; Kurokawa A;Tile: Ligand-independent repression by the thyroid hormone receptor mediat A;Reforence number: S60254; MuID:96008539
A;Accession: S60254
A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: mRMA
A;Molecule type: mRMA
A;Molecule type: mRMA
A;Residues: 1-2453 <a href="https://doi.org/10.2017/7">https://doi.org/10.2017/7</a>; PID:91022718 253 304 313 364 432 484 492 541 598 652 712 768 424 544 604 664 Gaps 73 EPRYPPHSLSYPVQIARTHTDVGLLEYQ - - HHSRDYASHLSPGSIIQPQRRRPSLLSEFQ PGNERSQELHLRPESHSYLPELGKSEMEFIESKRPRLELLPDPLLR-----PSPLLATGO PAG---SEDLTKDRSLTGKLE-PVSPPSPPHTDPELELVPPRLSKEELIQNMDRVDREIT LMEALEKKVERIENNPRRAKESKVREYYEKQFPEIRKQRELQERMQSRVGQRGSGLSMS DRQVMNMWSEQEKETFREKFMQHPKNFGLIASFLERKTVAECVLYYYLTKKNENYKSLVR RSY-RRGKSQQQQQQQQQQQQQQQQQQQQQPRSSQEEKDEKEKEKEAEK--EEEKPEVEND ||||| |::| |NEEENPEDSEG------AENSSDIESAPSPSPVEAAKSSEDSSENA--MVEQQISKLKKKQQQLEEEAAKPPEPEKPVSPPPIESKHRSLVQIIYDENRKKAEAAHRI LEGLGPQVELPLYNQPSDTRQYHENIKINQAMRKKLILYFKRRNHARKQWKQKFCQRYDQ **AARSEHEVSEIIDGLSEQENLEKQMRQLAVIPPMLYDADQQRIKFINMNGLMADPMKVYK** KEDLLKEKTDDTSGEDNDEKEAVASKGRKTANSQGRRKGRITRSMANE---ANSEEAITP QQSAEL-----ASMELNESSRWTEEEMETAKKGLLEHGRNWSAIARMYGSKTVSQCKNF EPPPPLPPPPEPISTEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAKWVGTKSEAQCKNF YFNYKKRQNLDEILQQHKLKMEKERNARRKKKKAPAAASEEAAFPPVVEDEEMEASGVSG NEEEMVEEAEALHASGNEVPRGECSGPATVNNSSDTESIPSPH-TEAAK---DTGQNGPK PPATLGADGPPPGPPTPPRRTSRAP1EPTPASEATGAPTPPPAPPSPSAPPPVVPKEEKE --- ASRGNTEPVAELEATTDPAPCASP--SSAVPTTKPAERES Indels 444; Length 2453 Query Match 31.7%; Score 4187; DB 2; Best Local Similarity 41.0%; Pred. No. 1e-139; Matches 1103; Conservative 348; Mismatches 796; 373 134 185 194 16 74 17 129 245 314 365 425 485 542 545 605 305 433 493 599 999 713 717 691 757 ö g ŏ g ò 셤 δ g ò g δ Db ò qq QY qq δ g δ g οχ Op g g g ŏ δ ò

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AE 871 KG 851	)E 928 : 7D 902	97	01 5		113	KG 1197 	IG 1248   IE 1204	ж 1308    -   1255	or 1361   or 1313	A 1421 M 1358	it 1476  -  t 1417	IV 1530 : -L 1472	K 1584     1525	G 1640 H 1582	T 1699 L 1633	A 1759 T 1685	T 1818 R 1742
KSECTEE     -PENTAS	DSSATCSADEVD	AIPPI    : VIPPMVSCTPC	PPQNLQPESDAPQQPGSSPRGK	PDPSAFSYAPP	WSVQLHVPY KSVQLHVPY	GVPTAQEASVLRG	FRI- : : SRMP	SSSGPPHETAAPK       :   RSPRTAHEMSL-K	HHIRGSITQGI) :       FVLSGSIMQGT	LKLKPAHEGLVATVKEA      ::  :   TKGKP-YDG-ITTIKEM	STIGSKKHDVR:   :   : : GGOSAIKHNVK:	SGGSIARGAPV	DEGSLSSSK-ASQDRK :        :   :TSDVSSSKSASHERK	[PLAFDPTSIP] :	ALEN-RQTIINDYITSQQMHNT  :                	IPGTPATAMDRI 	OREREKSILTS: :    ; RERERERERE
PAAEELAVDTGKAEEPV    :  :   PAPTKADSVDPEMQV	AEKKEGGSGRATTAKSSGAPODSDSSATCSADEVDE :	ASPOKPLDLKQLKQRAAA1PPI 	QVTKVHEPPREDAAPTKPAPPAPPPQNLQPESDAPQQPGSSPRGK	PREVIKASPHA	SVLERQIGAISQG-	KAPVGPVTWGLPLPMDFKKLAPFSGVKOEQLSPRGQAGPPESLGVPTAQEASVLRG	PAD       PALPQAGIPTE	SPSRLDRGREDSLPRGHVIYEGKKGHVLSYEGGMSVTQCSKEDGRSS:    ::    ::                : :     SPEKVREEAASKGHVIYEGKSGHILSYDNIKNAREGTRS:	DWMEGRVGRAISSASIEGLMGRAIPPERHSPH-HLKEQHHIRGSITQGIPR ::   ::	KTQALGP	QGTPLKYDTGA     : :  QGTPIKFDNN-	PPVHPLDVMAD-ARALERACYEESLKSRPGTASSSGGSIARGAPVIV 	MREPTPRLOEG    -   NRTS	IAKSPHSTVPEHHPHPISPYEHLLRGVSGVDLYRSHIPLAFDPTSIPRG 	AC I	RADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTBGTPATAMDRLA    :	KPTTJSSSERERDRDRERDRDREREKSILTST      :  :  :
KP   EGSSVLDP	KEGGSGRATTAI   TEARDEDVVVAI	PRANASPQKP:  -      ILI-SSPIKPN	EDAAPTKPAPPA	PCWTSGLPFPVI	APPLISSAKHPSVL	APFSGVKQEQLS	AITYRGSITHGI :          ISSLRGSITQGI	KKGHVLSYEGGN     :  :  KSGHILSYDNIF	IEGLMGRAIPPE     :   :  LEGLICRALP	PPPPSRDLTEAY        PPIRAFEGAI	LAPRPLKEGSIT :     :	DVKA	FAGHLPRGSPVT: :     : YONTISRGSPMN	ЭНРІ SРУЕНЦІЯ     ::   SHSPFDРИНЯ	PPYLIRGYPDT.	/AAGPRGIIDLS             /PA-TRGIIDLT	CHLTKPTTTSSS     : :   AAAASA
TAAAPPVEEGEEQ-    ::  : AETAEPMDVDHEEC	ATAEGALKAEK :	KNRLLSPRPSLLTPTGDPRANASPQKP : 1: : :         RQRVFPMDAKPSLLTPPGSILI-SPIKP	-QVTKVHEPPR : :   RHTKAMHESAL	AAEAQKLPGDP	DTARPVLPRPPTISNPP	GLPLPMDPKKL	GIPSTRVPSDS.	SLPKGHVIYEG :          AASKGHVIYEG	ISSAS::   SAS::  	<u> </u>	RHTPELPI      : TQESRKTPEVV(	LDVMAD-ARALI  ::::::: LEIVPENIKVVI	EDHGAPI :    DDSSARRTPVS	PREIAKSPHSTVPEHHPHP   :        PTQRESIPAKSPVPGVDPIVSH-	HLAPNPTYPHLN  :          LSPTPGYPSQN	LSPRESSLALN)               SPREQPLGLP)	HSSSPLSPGGPT ::::        /NAASLSPGHPT
E   EAQVTDSAS	BGPAKGKDAEAAEATAEGALKAEKKEGGSGRATTAKS.       :	GGDKNRL- ::  :	- AL	SRSPAPPADKEAFAAEAQKLPGDPPCWTSGLPFPVPRREVIKASPHAPDPSAFSYAPPGH	PLPLGLHDTARPVLPRPPTISNPPPLI PLPLGLHDTARPVLPRPPTISNPPLI STD	<. O-	ფ — ფ	SPSRLDRGRED    ::   : SSPEKVREE	RTYDMMEGRVGRAIS  : ::  ::  RSYEAVEGSIKQGMSI	SYVEAQEDYLRREAKLLKREGTP :  :      :   :    ATAESFEDGL-KYPKQIKRES	GRSIHEIPREELRHTPELPLAPRPLKEGSITQGTPLKYDTGASTTGSKKHDVRSL 	IGSPGRTFPPVHPLDVMAD-ARALERACYE 	PELGKPRQSPLTYEDHGAPFAGHLPRGSPVTMREPTPRLQEGSLS 	STPRE    : LTPTQRESI	IPLDAAAAYYLPRHIAPNPTYPHLYPPY 	ATAMAQRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAMDRLA	YLPTAPQPFSSR-HSSSPLSPGGPTHLTKPTTTSSSERERDRDRERDRDREREKSILIT  :
829 El	872 E       852 E	929 AEG   903 GE	7	23	n m 10	138	1198 TAI     146 TA	1249 ED:	1309 RT 	1362 S) : 1314 A1	1422 GI 	1477 IC    -   1418 IJ	1531 PE 1473 HE	1585 LT 1 1526 ST	1641 IE 1583 RA	1700 AT 1634	1760 YI  : 1686 YI
Oy Db	Qy Dp	Qy Dp	6 G	Ş Ş	3 & 4	6 0y	9 6	oy op	O.y Db	O.y Dp	Qy Dp	Oy Op	Oy Dp	oy Og	oy Dp	oy Og	Oy Dp

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---PGRPGSHGYVRSPSP-SVRTQETILQQR 1787
                                                                                                                             1875 PSVLHNTGMKGIITAVEPSKPTVLRSTSSPV----RPAATFPPATHCPLGGTLDGVYP 1930
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Cipate: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
Cipate: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
Ribersterhoeft, A.: Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, January 2000
A;Reference number: 223035
A;Reference number: 223035
A;Reference number: 223035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2021 ESTRQYEGP------LHHYRSQOESPSPQQQPPLPPSSQSEGMGQVPRTHRLITLAD 2071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HISEVITODYTRHH-PQQLSAPL----PAPLYSFPGASCPVLDLRRPPSDLYLPPPD--- 2189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2190 --HGAPA-RGSPH----SEGGKRSPEPNKTSVLGGGEDGIEPVSPPEGMTEPG-HSRSA 2240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2124 VLHPRPGPRVSPENLYDKSRGSRPGKSPERSHI---PSEPYEPISPPQG---PAVHEKQD 2177
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1819 TIVEHAP---IWRPGTEQSSGSSGGGGSSSRPASHSHAHQHSPISPRTQDA-LQQR 1874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2414 AKSPAPGLA--SGDRPPSVSSVHSEGDCNRRTPLTNRVWEDRPSSAGSTPFPYNPLIMRL 2471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2241 VYPLLYRDGEQTEPSRMGSKSPGNTSQPPAFFSKLTESNSAMVKSKKOEINKKLNTHNRN
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hypothetical protein DKFZp434M075.1 - human (fragment)
                                                                  1743 ERIAAAPADLYLRPGSEQ------
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54; 1752 ATAMORLAYLPTAPQPFSSR-HSSSPLSPGGPTHLTKPTTTSSSERERDRDRERDRDRER 1810 2125 2177 2286 2400 EKSILTSTTTVEHAPIWRPGTEQSSGSSGSSGGGGSSSRPASHAHQHSPISPRTQDA 1870 1871 -LQQRPSVLHNTGMKGIITAVEPSKPTVLRSTSSPV----RPAATFPPATHCPLGGTL 1925 1958 AFLAKPPARSGLEPASS---PSKGSEPRPLVPPVSGHATIARTPAKN--LAPHHASPDPP 2012 2013 APPASASDPHREKTQSKPFSIQELELRSLGYHGSSYSPEGVEPVSPVSSPSLTHDKGLPK 2072 1524 RGAPVIVPELGKPRQSPLTYEDHGA-----PFAGHLPRGSPVTMREPTPRLQEGSLSSSK 1578 1579 A-SQDRKLTSTPRE----IAKSPHSTVPEHHPHPISPYEHLLRGVSGVDLYRSHIPLAFD 1633 SQQMHHNTATAMAQRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGTP 1751 -----TGH 1957 2178 RPPSDLYLPPPD-----HGAP-ARGSPH----SEGGKRSPEPNKTSVLGGGEDGIEPVS 2226 2287 KQEINKKLNTHNRNEPEYNISQPGTEIFNMPAITGTGLMTYRSQAVQEHASTNMGLEAII 2346 2401 G--KAKVSGRPSSRKAKSPAP--GLASGDRPPSVSSVHSEGDCNRRTPLINRVWEDRPSS 2456 1470 KHDVRSLIGSPGRTFPPVHPLDVMAD-ARALERACYE----ESLKSRPGTASSSGGSIA 1523 PTSIPRGIPLD-AAAAYYLPRHLAPNPTYPHLYPPYLIRGYPDTAALEN-RQTIINDYIT 1691 RST---LHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSPM-----MNRTSDVTISSNK 118 STNHERKSTLTPTQRESIPAKSPVPGVDPVVSH--SPFDPHHRGSTAGEVYRSHLPTHLD 176 227 SQQMQVNL-----RPDVARGLSPREQPLGLPYPA-TRGIIDLTNMPP-TILVPHPGGTS 278 -----PGRPGSHGYVRSPSP-SVRIQET 373 DAAASAPQMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSS 492 600 QPEVVKANQAENDPTRQYEGP-----LHHYRP---QQESPSPQQQLPPSSQAEGMG 647 Gaps 2073 HLEELDKSHLEGELRPKOPGPVKLGGEAAHLPHLRPLPESQPSSSPLLQTAPG-----2126 -VKGHQRVVTLAQHISEVITQDYTRHH-----PQQLSAPLPAPLYSFPGA--SCPVLDLR 2347 RKALMGKYDQWEE----SPPLSANAFNPLNASASLPAAMPITAADGRSDHTLTSPGGG 546 RQIASDKDARERGSQSSDSS-----SSLSSHRYETPSDAIEVISPASSPAPPQEKLQTY PPEGMTEPGHSRSAVYPLLYRDGEQTEPSRMGSKSPGNTSQPPAFFSKLTESNSAMVKSK Best Local Similarity 35.0%; Pred. No. 8.1e-38; Matches 401; Conservative 149; Mismatches 393; Indels 202; DGVYPTLMEPVLLPK----EAPRVARPERPRAD-----IAAASSDL----YLRPGSEQ-----119 1634 177 1692 1811 1926 493 336 2227 875 67 433 ò 셤 ŏ a Óγ g οý g ò q ò a ογ g ò g δy g ά qq δ g Qγ g Qγ g ò g ŏ g δ g à

105; microtubule-associated protein homolog - fruit fly (Drosophila melanogaster)
N;Alternate names: hypothetical protein EG:49E4.1
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #text\_change 17-Nov-2000
C;Accession: T13564
R;Spanos, L; Papagiannakis, G.; Siden-Kiamos, I.; Louis, C.
R;Spanos, L; Papagiannakis, G.; Siden-Kiamos, I.; Louis, C.
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: 217689
A;Reference number: 217689
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Redidues: 15237
A;Molecule type: DNA
A;Redidues: 15237
A;Molecule type: DNA
A;Redidues: 15237
A;Molecule type: DNA RESIAESLKAESTKDEKSAPPSKEASRPGSVVESVKDETEKSKE----PSRRESIAESAK 1571 RPASVAESVKDEAEKSKEESRRESVAEK-----SPLPSKEASRPASVAESIKDEA 1807 EKSKEESRRESVAEKSPL-----PSKEASRPASVAESIKDEAEKSKEESRRESVAEKS 1860 -----EKSPLASEEAS 1757 A;Introns: 24/2; 52/3; 104/3; 179/1; 232/1; 1669/3; 2566/1; 4798/3; 5272/1 A;Note: EG:49E4.1 C;Superfamily: Drosophila 576K microtubule-associated protein homolog SEMEFIESKRPR--LELLPDPLLRP----SPLLA--TGQPAGSEDLTKDRSL--TGKLE 146 PVSPPSPPHTDPELELVPPRLSK-----EELIQN-MDRVDREITMVEQQISKLKKKQQQL 200 Gaps SDTRQYHENIKINQAMRKKLILYFKRRNHARKQWKQKFCQRYDQLMEALEKKVERIENNP 320 RRRAKESKVREYYEKQFPEIRKQRELQERMQSRVGQRGSGLSMSAARSEHEVSEIIDGLS 380 EQENLEKQMRQLAVIPPMLYDADQQRIKFINMNGLMADPMK--VYKDRQVMNMWSEQEKE 438 TFREKFMQHPKNFGLIASFLERKTVAECVLYYYLTKKNENYKSLVRRSYRRGKSQQQQQ 498 GVCKPKLISKSNSRKSKSPIPGQGYLGTERPSSVSSVHSEGDYHRQTP--GWAWEDRPSS 984 R-----RP-SILSEFQPGNERSQELHLRPESHSYLPELGK 97 2457 AGSTPFPYNPLIMRLQAGVMASPPPPGLPAGSG-PLAGPH---HAWDEEPKPLLCSQYET **EEEAAKPPEPEKPVSPPPIESKHRSLVQIIYDENRKKAEAAHRILEGLGPQVELPLYNQP** Indels 752; Length 5327; Query Match 4.3%; Score 574; DB 2; L Best Local Similarity 19.4%; Pred. No. 1.5e-12; Matches 531; Conservative 332; Mismatches 1123; ESTTQSKEAGSIKD-----A;Cross-references: EMBL:AL031128; PIDN:CAA20006.1 C;Genetics: IARTHTDVGLL----EYQHHSRDYASHLSPGSII---A; Cross-references: FlyBase: FBgn0025392 LSDSE 2517 1042 LSDSD 1046 985 2513 30 1516 86 147 1632 1686 1733 1758 927 64 261 321 201 381 439 δ g q g ŏ δy δy gg Q οy Q g QQ δ QΥ g νδ. ŏ g ò a δ

1861 PLPSKEASRP-----KASVAESI------KDEAEKS------K 1885

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čo č	1547	GAPFAGHLPRGSPVTMREPT-PRLQEGSLSSSKASQDRKLISTPREIAKSPHSTVP 1601
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q	2962	SKEHSRPESVLGSLKDEGDKTTSRRVSVADSIKDEKSLLVSQEASRPESEAESLK-DAAA 3023
ΟŅ	1648	AYXLPRHLAPNPTYPHLYPPYLIRGYPDTAALENRGTIINDYITSQQMHHNTATAMAQRA 1707
QΩ	3024	PSQETSRPESVTESVKDGKSPVASKEASRPASVAENAKDSADESKEQRP 3072
ΟŸ	1708	RGLSPRESSLALNYAAGPRGIID
q	3073	ESLPQSKAGSIKDEKSPLASKDEAEKSKEESRRESVAEQFPLVSKEVSRPAS 3124
Qy	1754	AMDRLAYLPTAPQPFSSRHSSSPLSPGGPTHLTKPTTTSSSERERDRDRERDRDRER 1810
qq	3125	VAESVKDEAEKSKEESPLMSKEASRPASVAGSVKDEAEKSKEESR-RESVA 3174
δλ	1811	EKSILTSTTTVEHAPIWRPGTEQSSGSSGGGGSSSRPASHSHAHQHSPISPRTQDA 1870
qq	3175	EKSPLPSKEASRPASVAESVKDEADKSKEESRRESGAEKSPLASKEASRPASVAESIKDE 3234
Οy	1871	LQQRPSVLHNTGMKGIITAVEPSKPTVLRSTSTSSPVRPAATFPPATHC 1919
qq	3235	AEKSKEESRRESVAEKSPLPSKEASRPTSVAKSVKDEAEKSKEESSRDSVAEKSP 3289
Qy	1920	PLGGTLDGVYPTLMEPVLLPKEAPRVARPERPRADTGHAFLAKPPARSGLEPASSPS 1976
qa	3290	
Οy	1977	KGSEPRPLVPPVSGHATIARTPAKNLAPHHASPDPPAPPASASDPHREKTQSKPFSIQEL 2036
QQ	3331	EASPPASVAESIKDEAEKSKEESRRESVAEKSPLASKEASRPTSVAES 3378
οy	2037	ELRSLGYHGSSYSPEGVEPVSPVSPSLTHDKGLPKHL-EELDKSHLEGELRPKQPG 2092
q	3379	VKDEAEKSKEESSRDSVAEKSPLASKEASRPASVAESVQDEAEKSKEESRRESVAEKSPL 3438
δy	2093	PVKLGGEAAHLPHLRPLPESQPSSSPLLQTAPGVKGHQRVVTLAQHISEV 2142
qq	3439	ASKEASRPASVAESVKDDAEKSKEESRRESVAEKSPLASKEASRPASVAESVKDE 3493
οy	2143	ITQDYTRHHPQQLSAPLPAPLYSFPGASCPVLDLRRPPSDLYLPPPDHGAPARGSPHS 2200
qq	3494	AEKSKEESRRESVAEKSPLPSKEASRPTSVAESVKD 3529
ΟŊ	2201	PGHSR
qq	3530	EAEKSKEESRRESVAEKSSLASKEASRPASVAESVKDEAEKSKEESRRESVAEK 3583
Qy	2261	SPGNTSQPPAFFSKLTESNSAMVKSKKQEINKKLNTHNRNEPEYNISQPGTEI 2313
qq	3584	SPLASKEASRPASVAESVKDEAEKSKEVSRRESVAEKSPLPSKEASRP 3631
ΟŅ	2314	FNMPAITGIGLMTYRSQAVQEHASTNMGLEAIIRKALMGKYDQWEESPPLSANAFNPLNA 2373
qq	3632	TSVAESVKDEADKSKEESRRESGAEKSPL 3660
Οy	2374	SASLPAAMPITAADGRSDHTLISPGGGGKAKVSGRPSSRKAKSPAPGLASGDRPPSVS-S 2432
QQ	3661	-ASMEASRPTSVAESVKDETEKSKEESRRESVTEKSPLPS-KEASRPTSVAES 3711
οy	2433	VHSEGDCNRRTPLTNRVWEDRPSSAGST 2460

Op	: :: :: ::   :  ::   :  :: 3712 WDEAEKSKEESRRESVAEKE-SSRPASVAES 3748	Qy	583TRSMANEANSEEAITPQQSAE
RESULT T51023 hypoth C; Spec C; Date C; Acce R; Schu	RESULT 5 T51023 hypothetical protein B7F21.40 [imported] - Neurospora crassa C;Species: Neurospora crassa C;Species: Neurospora crassa C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000 C;Accession: T51023 R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,	oy do oy	604
A; A	Submitted to the Protein Sequence Database, July 2000 A;Reference number: 225286 A;Accession: T51023 A;Status: preliminary	Qy	668 OHKLKMEKERNARRKKKAPAAASEEAAFPPVVEDEEMEASGVSGNEEEMVEEAEALHAS 727 11 :
2 4 4 4 C	A;Rockcute Cype: Unc. A):Residues: 1.2649 <sch> A):Residues: 1.2649 <sch> A):Cross-references: EMBL:AL389901; GSPDB:GN00116; NCSP:B7F21.40 A):Experimental source: BAC clone B7F21; strain OR74A</sch></sch>	Oy Dp	728 GNEVPRGECSGPATVNNSSDIESIPSPHTEAAKD-TGQNGPKPPATLGAD-GPPPG 781
A A S	V.Yeurellos: 40 A;Gene: NCSP:B7F21.40 A;Map position: 6 A;Introns: 1619/3; 2584/1	Qy	782 PPTPPRRTSRAPIEPTPASEATGAPTPPPAPPSPSAPPPVVPKEEKEEETAAAPPVEEGE 841
OME	Ouery Match 4.2%; Score 552; DB 2; Length 2649; best Local Similarity 19.3%; Pred. No. 4.1e-12. Matches 406; Conservative 268: Mismatches 771; Indels 658: Gans 92.	ΟΥ Db	842 EOKPPAAEELAVDTGKAEEPVKSECTEEAEEGPAKGKDAEAARATAEGALKAEKKEGGSG 901 1785 SQPPAQTQHQPVRISQKTAAPVPSSSMPSASEAMPRSA-GMIPEANRPTPLLSQQHE 1839
, y	QPQRRRPSLLSEFQPGNERSQELHLRPESHSYLPELGKSEMEFIESKRPRLELLPD 115   :	Qy	902 RATTAKSSGAPQDSDSSATCSADEVDEAEGDKNRLLSPRPSLLTPTGDPRA 953
6 G		Qy Dp	954 NASPQKPLDLKQLKQRAAAIPPIQVTKVHEPPREDAAPTKPAPPAPP 1000   1:1
Oy Dp		Oy Dp	1001 -PPQNLQPESDAPQQPGSSPRGKSRSPAPPADKEAFAAEAQKLPGDPPCWTS 1051
Qy Dp	EDS	Oy Dp	1052 GLPPPUPPREVIKASPHAPDPSAFSYAPPGHPLPLGLHUTARPVLPRPPTI 1102
Oy Dp		Qy Dp	SNPPPLISSAKHPSVLERQIGAISQGMSVQLHVPYSEHAKAPVGPVTMGLPLPMDPKKLA           STPPP
oy Og	284 FKRRNHARKQWKQKFCQRYDQLMEALEKKVERIENNPRRAKESKVRE 331	Qy	PFSGVKQEQLSPRGQAGPPESLGVPTAQEASVLRGT-ALGSVPGGSITKGIPS
Qy Dp	332 YYEKQFPEIRKQRELQERMOSRVGQRGSGLSMSAARSEHEVSEII-DGLSE-QENLE 386	Qy	TRVPSDSAITY-RGSITHGTPADVLYKGTITRIIGEDSPSRLDRGREDSLPKGHVIY- 
oy do	387 KQMRQLAVIPPMLY-DADQQRIKFINMNGLMADPMKVYKDRQVMNMW 432 ::   ::   ::     ::     :	Qy Dp	
දු දු		Qy	ISSASIEGLMGRAIPPERHSPHHIKEQHHIRGSITQGIPRSYVEAQEDYLRREAKLLKRE   : :   :   :   : :   : :   : :   :
Qy	488 RRRCKSQQQQQQQQQQQQQQQQQDMPRSSQEEKDEKERAEKEEEKPEV 538             : :   : :   : :   : :           1 1344 RRRKGRGKOKYNALVSELGNPENTTEDNOENCENSORPRAAAPSWGHEATPNA 1403	Oy Dp	1382 GTPPP-PPPSRDLTEAYKTQALGP-LKLKPAHEGLVATVKEAGRSIHEIPREELR 1434  [
QY Db		Oy Dp	1435 HTPELPLAPRPLKEGSITQGTPLKYDTGASTTGSKKHDVRSLIGSPGRTFPPVHPLDVWA 1494  1431PHALGLREPAPRGQAVFSAHEAQSPTGSVVSHQHHRSLDGRSQFPPMP 2358
		δλ	1495 DARALERACYEESLKSRPGTASSSGGSIARGAPVIVPELGKPRQSPLTYEDH-GAPFAGH 1553

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QY         758 AAKDTGQNGPKPPATLGADGPPGPPTPP	545 STPTPGVAAAPTLVSGGGSTSSTSSGSFEASPVEPOLDSKEGPEPPEE  938 LSPRPSLLTPTGDPRANASPQKPLDLKOLKQRAAAIPPIQVTKVH	Db 693 PGALGRPPMPPMNFDPRWMMIPPYVDPRLLQGRPPLE 730  Qy 1103 SNPPPLISSAKHPSVLERQIGAISQGMSVQLHVPYSEHAKAPVGPVTMGLPLPMDPKKLA 1162	Db 858SGAG 898  Qy 1335 IPPERHSPHHLKEQHHIRGSITGIPRSYVEAQEDYLRREAKLIKREGTPPP 1386	QY         1502ACYEESL
Db 2359 DPRDRQ		RESULT 6 B35098 MHC class III histocompatibility antigen HLA-B-associated protein 2 [imported] - human c; Species: Homo sapiens (man) C; Date: 10-Aug-1990 #sequence_revision 06-Nov-1992 #text_change 15-Sep-2000 C; Accession: B35098 R; Banerji, J.; Sands, J.; Strominger, J.L.; Spies, T. Proc. Natl. Acad. Sci. U.S.A. 87, 2374-2378, 1990 A; Title: A gene pair from the human major histocompatibility complex encodes large prolif A; Reference number: A35098; MUID:90192810 A; Status: preliminary A; Molecule type: mRNA A; Residues: 12142 *RBAP	A;Note: the authors translated the codon AGT for residue 97 as Gly  Query Match  Query Match  Best Local Similarity 20.4%; Score 526; DB 2; Length 2142;  Best Local Similarity 20.4%; Pred. No. 2.7e-11;  Matches 511; Conservative 214; Mismatches 863; Indels 912; Gaps 115;  Qy 474 KKNBNYSLVRRSYRRRGKSQDQQQQQQQQQQQQQPMPRSSQBEKDEKEKEAE 530	Db 120 NOPKRPPAAPENTPLVPSGVKSWAQASVTHGAHGDGGRASSLLSRFSREEF 170  Qy 590ANSEBAITPOQSAELASMELNESSRWTEEEMETAKKGLEHGR 632    11

Mon Sep 10 08:14:34 2001

οy	1685	IINDYITSQQMHHNTATAMAQRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLP 1741	
qq	1214	GSNVGMEDGERPRRRRHGRAQQQDKPPRFRRLKQERENAARGSEG 1258	
δŏ	1742	VLVPPTPGTPATAMDRLAYLPTAPQPFSSRHSSSPLSPGGPTHLTKPTTTSS 1793	
g G	1259	KPSLTLPASAPGPEEALTTVTVAPAPPRAAAKSPDLSNQNSDQANEEWETASESSDF 1315	
0y	1794		
2	1316	TSERRGDKEAPPPVLLTPKAVGTPGGGGGAVPGISAMSRGDLSQRAKDLSKRSFSSQRP 1375	
δý	1821	VEHAPIWRPGTEQSSGSSGSSGGGGGSSSRPASHSHAHQ 1859	
q	1376	GMERQNRRPGPGGKAGSSGSSSGGGGGGPGGRTGPGRGDKRSWPSPKNRSRPPEERPPGL 1435	
οy	1860	HSPISPRIQDALQQRPSVLHNTGMKGIITAVEPSKPTVLRSTSTSSPVRPAATFPPATHC 1919	
qq	1436	PLPPPPSSSAVFRLDQVIHSNPAGIQQALAQLSSRQGSVTAPGGH- 1481	
Οy	1920	PLGGTLDGVYPTLMEPVLLPKEAPRVARPERPRADTGHAFLAKPPARSGLEPA 1972	
g	1482		
Qγ	1973	SSPSKGSEPRPLVPPVSGHATIARTPAKNLAPHHAS 2008	
g	1513	SSDPHFEERGPWYRGVGGTPRDSAGVSPFPPRRRERPPRRPELLQEESLPPPHSSGFLGS 1572	
οy	2009	-PDPPAPPASASDPHREKTQSKPFSIQ	
qq	1573	KPEGPGPQAESRDIGIEALIPHINNRLHTATSRKSYRPISMEPUMEPLSPFEDVAGTEMS 1632	
ογ	2038	LRSLGYHGSSYSPEGVEPVSPVSSPSLTHDKGLPKHLEELDKSHLEG 2084	
qq	1633	QSDSGVDLSGDSQVSSGPCSQRSSPDGGLKGAAEGPPKRPGGSSPLNAVPCEGPPG 1688	
ΟŊ	2085	SQPSSSPLLQT	
qq	1689	SEPPRRPPARHDGDRKELPREQPLP	
٥y	2145	QDYTRHHPQQLSAPLPAPLYSFPGASCPVLDLRRPPS-DL 2183	
qq	1727	DRGTEPGPIRPS-HRPGPPVQF-GTSDKDSDLRLVVGDSLKAEKELFASVTEAIPVSRDW 1784	
οy	2184	YLPPPDHGAPARGSPHSBGGKRSPBPN	
qq	1785	ELLPSAAASAEPQSKNLDSGHCVPEPSSSGQRLYPEVFYGSAGPSSSQISGGSHGLS 1841	
δý	2223		
qq	1842	ITSKQWRLRPGTPSLHPYRSQPLYLPPGPAPPSALLSGVALKGQFLDFSTWQATELGKLP 1901	
δy	2262	PGNTSQPPAFFSKLTESNSAMVKSKKQEINKKLNTHNRNEPEYNISQPGTEI 2313	
qq	1902	AGGVLYPPPSFLYSPAFCPSPLPDTSLLQVRQDLPSP-SDF 1941	
οy	2314	HASTNMGLEAIIRKALMGKYDQWEESPPI	
qq	1942	YSTPLQPGGQSGFLPSGAPAQQMLLPMVDSQLPVVNFGSLPPAPPPAPPPL 1992	
ΟŊ	2372	NASASLPAAMPITAADGRSDHTLTSPGGGGKAKVSGRPSSRKAKSPAPGLASGDRPPSVS 2431	
qq	1993	SLLPVGPALQPPSLAVRPPPAPATRVLPSPARPFPAS 2029	
οy	2432	SVHSE	
Dp	2030	LGRAELHPVELKPFQDYQKLSSNLGGPGSSRTPPTGRSFSGLNSRLKATPSTYSGVFRTQ 2089	
οy	2470		
QQ	2090	RVDLYQQASPPDALRWIPKPWERTGPPPREGPSRR-AEEP 2128	

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NAIdernate names: alpha-NAC proteins angular control of the Species was musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 12-oct-1999 #sequence_revision 22-oct-1999 #text_change 24-Nov-1999
C;Accession: T30826
R;Yotov, W.V.; St-Arnaud, R.
Genes Dev. 10, 1763-1772, 1996
A;Title: Differential splicing-in of a proline-rich exon converts alphaNAC into a mus A;Reference number: 220889; MUID:96312450
A;Accession: T30826
                                                                                                                                                                                                                                                                                                      A, Molecule type: DNA
A, Residues: 1-2187 < YOT>
A, Cross-references: EMBL: U48363; NID: 91666688; PID: 91666689; PIDN: AAB18732.1
C, Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Throw: 10
A, Map position: 10
A; Introns: 24/1; 1996/1; 2024/3; 2050/3; 2099/3; 2142/3; 2183/3
A; Introns: 24/1; 1996/1; 2024/3; 2050/3; 2099/3; 2142/3; 2183/3
A; Note: differential splicing converts alphaNAC into a tissue-specific DNA-binding ac C; Keywords: alternative splicing; DNA binding; transcription factor
     - monse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93;
nascent polypeptide-associated complex alpha chain, muscle splice form gp220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1042 LPGDPPCWTSGLPF-PVPPREVIKASPHAPDPSAFSYAPPGHPLPLGL----HDTARPVL 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----RPPTISNPPPLISSAKHPSVLERQIGAISQGMSVQL 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HVPYSE-HAKAPVGPVTMGLPL------PMDPKKLAPFSGVKQEQLSPRGQAGPPE 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---STRVPSDSALTYRGSI 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----REDAAPTKPAPPAPPPQONLQPESDAPQQPGSSPRGKSRSPAPPADKEAFAAEAQK 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 QKGARSSSAPLSLVALAPHSVQKSSVCPPHPLTSPPSAAGAELGALTASIPPLEPKTSTS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : | : | : | 13 QVPSQGTLNLKGTAPCPPDVVRAFPSHLENPLASVQPGLMSCPQTLSNTSPVKGVPISSA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                410 HALDNPSAISVAPATHVPPPT------SSGLVSSKDPASPVTSLVVPAAHKQ 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIALKESPSSQSASSLEVLSEDTVTKKTTGGPAPVVRPA-----IAGVATTTSLRA 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----APPSPSAPPVVPKEEKEETAAAPPVE----- 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | : | | | : | | | 243 IITQSRLSLNLKGPVSPPARNTAAPSIPLAPSTSLGCHLPLLHHSSVDSPIQPPGQSGLAV 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPATVNNSSDTESIPSPHTEAA-------KDTGQNGPKPPATLGADGPP---PGPPT 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 PLPSSVSSTPFEVPFAQPITAETALPSGTAPPTFTLPHLIGPPISPAALALASPMIGLA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        905 T-----AKSSGAPQDSDSSATCSADEVDEAEGGDK- 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNPTSVGHSGIAASCPPERCVVPALPSRLLAVDSGAAPSDDKGSSAVTNELCSPPGSSNV 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 AGTSLSPKASLV-----PKGSNVALQPL------VTQVPASQKTGLKEIPVSCIGATH 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GEATETVPATEQELPQPQAETAVLPMSSALKVAAVGQPGPTPPSSLGPQQSPIVTAHQPS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.9%; Score 520; DB 2; Length 2187; Best Local Similarity 19.7%; Pred. No. 4.4e-11; Matches 448; Conservative 219; Mismatches 782; Indels 830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               935 -NRLLSPRPSLLTPTGDPRANASPQKPLDLKQLKQRAAAIPPIQVTKVHEPP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                785 P-PRRTSRAPIE-----PTPASEA----TGAPTP-----PP--
                                                                                                                                                                                                                                                       A;Accession: T30826
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    866 CTEEAEEGPAKGKDAEAAEATAEGALKAE-----
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q d	621	: : : :	
6 Q	1230	THGTP-ADVLYKGTITRIIGEDSPSRLDRGREDS	
Qy Dp	1270	YEGKKGHVLSYEGGMSVTQCSKEDGRSSSGPPHETAA	
oy Ob	1307	PKRTYDWMEGRVGRAISSASIEGLMGRAIPPERHSPHHLKEQHHI 1351  ::  ::  :  :  :  : ::    PQKTPEVTASRLISAVGSPKVDPIMSDVTPTSPKKTSATAVPKDTSATLSLKSVPAVTSL 850	
δ	1352	RGSITQGIPR1361	
g	851	SPPKAPVAPSNEATIVPTEIPTSLKNALAAATPKETLATSIPKVTSPSPQKTPKSVSLKG 910	
Oy Op	1362	SYVEAQEDYLRREAKLLKRE	
oy op	1389 971	PSRDLTEAYKTQALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPEL 1439 :	
٥ م	1440	PLAPRPLKEGSITQ GTPLKYDTGASTTGSKKHDVRSLIGSPGRT 1483 	
3	1001	ASSPAKSPKTAGP	
Oy Dp	1484	FPPVHPLDVMADARALERACYEESLKSRPGTASSSGGSIAR 1524 	
ç q	1525	GAPVIVPELGKPRQSPLTYEDHGAPFAGHLPRGSPVTMREPTPRLQEGSLSSSKASQD 1582     -  -  -  -  -  -  -  -  -  -  -  -	
0y	1583	RKLTSTPREIAKSPHSTVPBHPHPIPISPYBHLLRGVSGV 1 :: :	
Q D	1188	KEAPATPSVGVIAVSGEISPSPKKTSKTAAPKENSATLPPKRSPKTAAPKETPATSSEGV 1247	
Qy Dp	1622	DLYRSHIPLAFDPTSIPRGIPLDAAAAYYLPRHIAPNPTYPHLYPPYLIRGYPDTAALEN 1681	
δ	1682	NYAAGPRGIIDLSQVPHLP	
q	1298	-	
ογ	1742		
qq	1318	-ATPPSKKTPKTAVPKETSAPSEGVTAVPLEIPPSPRKAPKTAAPKETPA 1366	
Oy Dp	1792 1367	SSSERERDRDRERERSILTSTTTVEHAPIWRPGTEQSSGSSGSSGGGGGSSSRP 1851	
οy	1852	ASHSHAHQHSPISPRTQDALQQRPSVLHNTGMKGIITAVEPSKPTVLRSTSTSSP 1906	
q	1397	TTPSPEGVTAAPLEIPISSKKTSKMASPKETLVTPSSKKLSQTVGPKETSLEGATAVPLE 1456	
ολ	6	AFLAK 1	
g O	1457	IPPSHKKAPKTVDPKQVPLTPSPKDAPTTLAESPSSPKKAPKTAAPPSERVTTV 1510	
oy G	1963	PPARSGLEPASSPSKGSEPRPLVPPVSGHATIARTPAKNLAPHHASPDPPAPPASASD 2020 	
δý	2021	208	

qq	1557	PSSHKKTSKTIELKE1594
οy	2081	HLEGELRPKQPGPVKLGGEAAHLPHLRPLPES-QPSSSPLLQTAPGVKGHQRVVTLAQHI 2139
! 1	1	
QC C	1595	TSAPKEFPASPSIKPVTTSLAQTAPPSLQKAPS
δλ	2140	SEVITQDYTRHHPQQLSAPLPAPLYS-FPGASCP 2172
ΩD	1628	TIIPKENLAAPAVLPVSSKSPAAPARASASLSPATAAPQTAPKEATTIPSCK 1679
. 0y	2173	VLDLRRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEPNK 2211
qq	1680	:
οy	2212	TSVLGGGEDGIEPVSPPEGMTEPCHSRSAVYPLLYRDGEQTEPSRMGSKSPG 2263
qa	1740	
Qy	2264	VKSKKQEINKKL
ga .	1782	PTAFTEMLAAPAPESALAITAPIQKSPGANSNSASSPKCPDPSSKKDTKGLPS 1834
ογ	2322	TGLMTYRSQAVQEHASTNMGLEAIIRKALMGKYDQWEESPPLSANAFNPLNA 2373
qa	1835	AVALAPQTVPVEKDTSKAIETLLVSPAKGSDCLHSPKGPVGSQVATPLAAFTSDKVPP 1892
Qy	2374	SASLPAAMPITAADGRSDHTLTSPGGGGKAKVSGRPSSRKAKSPAPGLASGDRP 2427
qq	1893	EAVSASV-APKPAPAASLTLAPSPVAPLPPKQPLLESAPGSVLES 1936
Οy	2428	PLIMRLQAGVMA
qq	1937	PSKLPVPAEEDELPPLIPPEAVSGEPFQPILVNMPAPKPAGTPA 1981
RESULT A41819	ULT 8 819	ALCO ACCOUNTS ACCOUNTS ACCOUNTS
2 2 2 2 2 2 2 2 2 2 2 2 3 2 3 3 3 3 3 3	pecies: ate: 13	proine firm peptides 03/n predisor, prosente - mar C.Species: Rattus norvegicus (Norway rat) C.Date: 13-May-1992 #sequence revision 13-May-1992 #text change 05-Noy-1999
C;A R;D	ccessic e Clerc	
J. A; T	Biol. C itle: I	s of the rat
le . A:R	exon.	
A;A	ccessic	A.A.Cession: A42663
. A.	A; Residues:	motecure Lype: DNA, MINA Residues 1706, 17306, 183768-4077, F',4079-4155,'S',4157-5761 <de2> Crose-references GR.M87614</de2>
Α, Ε.	xperime	intal source: ventral prostate
A; N A; N	A;Note: se A;Note: se	it with the nucleotide translation irom NCBI backbone (NCBIN:100347, NCBIP:
R; D subi	e Clerc mitted	R; De Clercq, N.; Hemschoote, K.; Devos, A.; Peeters, B.; Heyns, W.; Rombauts, W. submitted to the Protein Sequence Database, April 1992
A; R	eferenc	e number: A41819 n: A41819
A; S	tatus:	Status: not compared with conceptual translation
A;R	olecule esidues	Molecule type: DNA Residues: 1-5762 <de1></de1>
R; H	Hemschoote,	Hemschoote, K.; Peeters, B.; Dirckx, L.; Claessens, F.; De Clercq, N.; Heyns, W.; W Biol. Chem. 263, 19159-19165, 1988
A; T	itle: A	single 12.5-kilobase, androgen-regulated mRNA encoding multiple proline-ric
A;R	ererenc ccessic	A;Kererence number: A3196b; MUID:8906b721 A;Accession: A31966
A; W	olecule	: type: mrNA :: 3372-3540 <hem></hem>
A;C	ross-re	ferences: GB:M20721; GB:J04188; NID:9206397; PIDN:AAA41950.1; PID:9554494 B . Houng W . Bossung D . Bombants W
, D	Biol. C	;
A; E	itle: F eferenc	A;Title: Proline-rich polypeptides bound to rat prostatic binding protein. The primar A;Reference number: A94675; MUID:84061859
A; A	ccessio	n: B20593

Db 2037 AEPPTGPFUETKTTKSKPVEWTLTRTDKSRKEWVSGSPKYEEBAVLP 2088  Qy 698 PVVEDEEMEASGVSGNEEEAVEEAEALHASGNEVPRGECSGPATVNNSSDTESIPSPHTE 757	817APPPVVPKEKEEEETAAAPPVEKGEEGKPPAAEELAVDTGKAEEPVKSECT 2232 IXLHYAEPPTGPFVEPPDLFLRTTKSKPVGGTTTEBAAKSPKENSGOTSGR 1	QY 1463 ASTIGSKKHDVRSLIGSPGRTFPPVHPLDVMADARALERACYEESLKSRPGTASSS 1518 
A; Molecule type: protein A; Residues: 2020-2057 <pee> A; Note: this peptide, designated proline-rich polypeptide V, can be found at several loc A; Accession: A20593 A; Molecule type: protein A; Residues: 2822-2859 <pee> A; Note: this peptide, designated proline-rich polypeptide IV, can be found at several loc C; Genetics: A; Introns: #status absent A; Note: single copy gene with no introns C; Superfamily: rat prostatic proline-rich peptides 637K precursor C; Reywords: prostate; tandem repeat C; Reywords: prostatic proline-rich peptides 637K proprotein #status predicted <mb #status="" 27-5761="" 637k="" <mb<="" f;="" peptides="" predicted="" product:="" proline-rich="" proprotein="" prostatic="" td=""><td>Gaps 155; SE 99 QT 1355 LL 146 LL 146 LL 146 LL 1474 PE 211 PH 1533 EN 269 ST 1583 VF 1474 VT 1638 MN 430 OP 1744 FK 461 L H 64 EN 478 LH 1864 EN 478 LH 1864 EN 478 LH 1864 EN 478 HN 430 AN 588 N' 588 HN 588 HN 5983 AI 637</td><td>Qy 638 ARMVGSKTVSQCKNFYFNYKKRQNLDEILQQHKLKMEKERNARRKKKRAPAAASEEAAFP 697</td></mb></pee></pee>	Gaps 155; SE 99 QT 1355 LL 146 LL 146 LL 146 LL 1474 PE 211 PH 1533 EN 269 ST 1583 VF 1474 VT 1638 MN 430 OP 1744 FK 461 L H 64 EN 478 LH 1864 EN 478 LH 1864 EN 478 LH 1864 EN 478 HN 430 AN 588 N' 588 HN 588 HN 5983 AI 637	Qy 638 ARMVGSKTVSQCKNFYFNYKKRQNLDEILQQHKLKMEKERNARRKKKRAPAAASEEAAFP 697

7	0		
Q Q	2989	LSAPGENRDESPSSPNMSLHPLDQELSLSSQPHGWIPHPPNT	3030
ò	1519	GGSIARGAPVIVPELGKPRQSPLTYEDHGAPFAGHLPRGSPVTMRE	1564
g	3031	HGKIYLHYAEPPTGPFVEPPDLFFLKTTKSKPVQGSPSQIDKSPKEVFS	3079
οy	1565	PTPRLOEGSLSSSKASQDRKLTSTPREIAKSPHSTVPEHHPH-PIS	1609
qq	3080	QSPESEESVLPAQAEGQEESRAPPHMSLQLLDQKLTLSSHPHGWIP-HHPNTPGK	3133
ογ	1610	PYEHLLRGVSGVDLYRSHIPLAFDPTSIPRGIPLDA	1645
qq	3134	I : : : : : : : : : : : : : : : : : : :	3193
ογ	1646	AAAYYLPRHLAPNPTYPHLYPPYLIRGYPDTAALENRQTII	1686
g	3194	ECQEESRAPPHWSLQPLDQDLTLSSHPHGWITHHPNTPDKIYLHYAEPPTGPFVEPPDLF	3253
ογ	1687	NDY ITSQQMHHNTATAMAQRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPP	1746
qq	3254	FLRTTKSKPAQWTPTQMAKSPEEMVSLSPENKETVFPAQGKGQEESISPPHMSLQPLD	3311
ογ	1747	TPGTPATAMDRLAXLPTAPQPFSSRHSSSPLSPGGPTHLTKPTTTSS     :   :	1793
2	3312	QDLTPSSHPHGWIPHHPNTHGKIYLHYAEPPTGPFVEPPDLFFLKTTKSKPVQVSP	3367
δ	1794	SERERDRDRERDRDREREKSILTSTTTVEHAPIWRPGTEQSSGSSGSGGGGSSSRPAS	1853
Op	3368	RQIDKSPKEVFTQSPEYEESVLPAQAEGQEE	3398
οy	1854	HSHAHQHSPISPRTQD-ALQQRPSVLHNTGMKGIITAVEPSKPTVLRS	1900
qq	3399		3457
δy	1901	TSATFPPA	1916
QQ	3458	:     :     TKSKPVHGSPRQIDKSHKEMFTQSPEXEESVLPAQAEGQEESRAPPHMSLQPLDQDLTLS	3517
ογ	1917	THCPLGGTLDGVYPTLMEPVLLPKEAPRVARPERPRADTGH	1957
οg	3518	SH-PHGWIPHHPNTPDKIYLHYAEPPTGPFVEPPDLFFLKTTKSKPVQGSPRQIDKSPKE	3576
οy	1958	AFLAKPPARSGLEPASSPSKGSEPRPLVPPVSGHATIARTPAKNLAPHHA-SPD	2010
g	3577	:     :     :	3635
οy	2011	PPAPPASASDPHREKTQSKPFSIQELELRSLGYHGSSYSP	2050
q	3636	:  :    :  :       :	3682
οy	2051	EGVEPVSSPVSSPSLTHDKGLPKHLEELDKSHLEGELRPKQPGPVKLGGEAA	2101
q	3683		3736
οy	2102	HLPHLRPLPESQPSSSPLLQTAPGVKGHQRVVTLAQHISEVITQDYTRHHPQQLSAPLPA	2161
QQ	3737	:   :   :   :   :	3791
á	2162	PLYSFPGASCPVLDLRRPPSDLYLPPPD	2189
q	3792	AAEDQEESRAPPHMSLQPLDQDLTLSSHPHGWITHHPNTHGKIYLHYAEPPTGFFVEPPD	3851
γ̈́ο	2190	HGAPARGSPGIEPV-	2225
g	3852	LFFLRTTKSKPVQWTPTQIDKSREEMVSQSPENEEADIPRHGDGQDELRNPPIISLQPLD	3911
٥y	2226	SPPEG-MTEPGHSRSAVYPLLYRDGEQTEPSRMGSKSPGNTSQPPAFFSKL	2275
g	3912	QELTLSSQPHGWVPHPPSTPDKIY-LHYAEPPTGPFVEPPDLFFLRT	3957
δ	2276	TESNSAMVKSKKQEINKKLNTHNRNEPEYNISQPGTEIFNMPAITGTGLMT	2326
qq	3958	TKSKPVQGTPTQLAKSPKEMVFQTPEYKEAVLSAPGEDQDETP	4000

QQ Dp	QY 2327 YRSQAVQEHASTNMGLEAIIRKALMGKYDQ-WEESPPLSANAFNP :          : : :   : : : :   : : : : :	NP 2370 :   DPPTGPFVEPPD 4051
Qy Db	QY 2371LNASASLPAAMPITAADGRSDHTLTSPGGGGKAKVSGRPSSRKAKSPAPGLASGDRP	AKSPAPGLASGDRP 2427           -KSPKQGLL 4079
Q Q	HL	-PYNPLIMRLQAGVMASPP 2480 
Qy Db	OY 2481PPGLPAGSGPLAGPHHAWDEEPKPLCSOYETLSDSE 25	
SS WH	ociated	in 2
002	5 #text_ch rina, D.;	.change 15-Sep-2000 ; Primas, G.; Perrot, V.; Ju
A A A	member of	f'the NFkappaB family withi
444	Afteression: Stails Afterus: preliminary Affecule type: DNA Afresidues: 1-1872 <iri></iri>	
AAA	A, Cross-references: EMBL: 215025 A; Note: in the authors' translation residues 32-34 are shown a A; Note: the authors translated the codon AAT for residue 1000	wn after residue 4 and, con 000 as His
0 4 0	; 279/2;	327/1; 357/2; 429/3; 588/1;
	Query Match 3.8%; Score 508.5; DB 2; Length Best Local Similarity 20.9%; Pred. No. 9.4e-11; Matches 428; Conservative 173; Mismatches 695; Indels	gth 1872; els 749; Gaps 94;
Qy	663	715
qq	Db 331 EEVDYTEKLKFSDEEDGRDSDEEGAEGHRDSQSASGEERPP	
y g	716 EMVEEAEALHASGNEVPRGECSGPATVNNSSDTE	SIPSPHTEAAKDTGQNGP 767
ò	768 KPPATLGADG	
d d		48
Qy	796PTPASEATGAPTPPPAPSPS/	TAAAPPVEEGEE 842
q	485 ACAEKLKRLDEKFGAPDKRLKAEPAAPPAAPSTPAPPPAVPKE	-LPAPPA 533
δ <sub>0</sub>	843 QKPPAAEELAVDTGKAEEPVKSECTEEAEEGPAKGKDAEAAEATAEGAL	
a a	534PPF:PASAPTPEKEPEEPAQAPPAQSTPTF	GVAA 565
OY D	QY 903 ATTAKSSGAPQDSDSSATCSADEVDEAEGGDKNRLLSPRPSLLTPTGDPRANA DD 566 APTLVSGGGSTSSTSSGSFRASPVEPQLESKEGPEPPEEVPPPTTPPVPKVEPKGDGIGP	PTGDPRANA 955   : : : PKVEPKGDGIGP 625
Qy	926	
qq	DD 626 TRQPPSQGLGYPKYQKSLPPRFQRQQQQQLLKQQQQHQWQQHQWQQHQWGQHQWGQHQWGAAPPTPVPPSPPQPV	:     eTPVPPSPPQPV 685
ò	Ov 1004 NLOPESDAPOOPGSSPRGKSRSPAPPADKEAFAAEAOKLPGDPPCWTSGLPFPVPPREVT	T.PFPVPPREVI 1063

719	1123 758	1176 811	1236 849	1295	1355	4 6	1453	1500	1548 1098	1601	1658 1193	1710	1764	1803	1846 1413	1885	1945	1998
	KASPHAPDPSAFSYAPPGHPLPLGLHDTARPVLPRPPTISNPPPLISSAKHPSVLERQIG	AISQGMSVQLHVEYSEHAKAPVGPVTMGLPLPMDPKKLAPFSGVKQEQLSPRG 	QAGPPESLGVPTAQEASVLRGTALGSVPGGSITKGIPSTRVPSDSAITYRGSITHGTPAD 	VLYKGTITRI-IGEDSPSRLDRGREDSLPKGHVIYEGKKGHVLSYEGGMSVTQCSKEDGR  :  :	SSSGPPHETAAPKRTYDMMEGRVGRAISSASIEGLMGRAIPPERHSPHHLKEOHHIRGSI 	TOGIPRSYVEAQEDYLRREAKLLKREGTPPPPPPSRDLTEAYKTQALGPLKL 	KPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGSITQ 	GTPLKYDTGASTTGSKKHDVRSLIGSPGRTFPPVHPLDVMADARALE 	RACYEESLKSRPGTASSSGGSIARGAPVIVPELGKPRQSPLTYEDHGA 	PFAGHLØRGSPVTMREPTPRLQEGSLSSSKASQDRKLISTPREIAKSPHSTVP  :	EHHPHPISPYEHLLRGVSGVDLYRSHIPL-AFDPTSIPRGIPLDAAAAYYLP-RHLAPN- 	-PTYPHLYPPYLIRGYPDTAALENRQTIINDYITSQQMHNTATAMAQRADML 	RGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPDTPGTPATAMDRLAYLPTA 	POPFSSRHSSSPLSPGGPTHLTKPTTTSSSERERDRDRE		SSSRPASHSHAHOHSPISPRTQDALQQRPSVLHNTGMKG	EAPR'	RPERPRADTGHAFLAKPPARSGLEPASSPSKGSEPRPLVPPVSGHATI
989	1064	1124	1177	1237.	1296	1356 932	1408 965	1454	1501	1549	1602	1659	1711	1765 1294	1804	1847	886	
qq	Qy Db	Qy Db	QY Db	Qy GD	oy Op	Qy Db	Oy Op	Qy Db	Qy Db	Qy Dp	Qy	Oy Dp	Qy Dp	0y 0p	Qy	00 ع	3 & 5	δ <sub>λ</sub>

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Bassoon protein - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C;Accession: T42730
R;Dicck, S; Sammarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; W
J;Cell Biol. 142, 499:509, 1998
A;Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively locali
A;Reference number: 222249; MUID:98345363
A;Accession: T42730
A;Accession: T42730
A;Accession: T42730
A;Accession: T42730
A;Accession: Tanslated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Description: may be involved in cytomatrix organization at the site of neurotransmi A; Note: component of the presynaptic cytoskeleton C; Reywords: coiled coil; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-3942 CDIE>
A; Cross-references: EMBL:Y17034; NID:g3413809; PIDN:CAA76598.1; PID:g3413810
A; Experimental source: strain 129 SVJ
C; Genetics:
A; Map position: 9F1
A; Introns: 72/2; 208/3; 505/3; 675/3; 2889/3; 3582/1; 3851/3; 3886/1; 3930/1
C; Function:
                                             1999 AKNLAPHHASPDPPAPPASASDPHREKTQSKPFSIQELEL---RSLGYHGSSYSPEGVEP 2055
                                                                                                                                                                       2158
                                                                                                                                                                                                                                                             2397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2457
                                                                                                                                                                                                                                                                                                                                                        1781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|:: | | :
-----ITSKQWRLRPGTP 1866
1496 HKPGPPQAPQGPS--PRPPTRYEPQRVNSGL---SSDPHFEEPGPMVRGVGG-----TP 1544
                                                                                                                                                                                                                                                                                                                           LPA-PLYSFPGASCPVLDLRRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEPNKTSVLGG 2217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2278 SNSAMVKSKKQEINKKLNTHNRNEPEYNISQPGTEIFNMPAITGTGLMTYRSQAVQEHAS 2337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 PGSIIQPQRRRPSLLSEFQPGNERSQELHLRPESHSYLPELGKSEMEFIESKRPRLELLP 114
                                                                              2056 VSPVSSPSLTHDKGLPKHL------EELDKSHLEGELRPKQPGPVKLGGEAAHLPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                2398 GGGGKAKVSGRPSSRKAKSPAPGLASGDRPPSVSSVHSEGDCNRRTPLTNRVWEDRPSSA
                                                                                                                                                                                                                                2106 LRPLP-ESQPSSSPLLQ-TAP--GVKGHQRVVTLAQHISEVITQDYTRHHPQQL---SAP
                                                                                                                                                                                                                                                                                                                                                                                                                 2218 GEDGIEPVSPPEGMTEPGHSRSAVYPLLYRDGEQTEPSRMGSKSPGNTSQPPAFFSKLTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----GTSDKDS-----BLRLVVGDSL-----KAEKE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2338 THMGLEAIIRKALMGKYDQWEESPPLSANAFNPLNASASLPAAMPITAADGRSDHTLTSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 1052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.8%; Score 504; DB 2; Length 3942; Best Local Similarity 19.1%; Pred. No. 3e-10; Matches 590; Conservative 324; Mismatches 1122; Indels 105:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1836 GSAG------PSSSQISGGSHGLS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2458 GSTPF: 2462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1867 SLHPY 1871
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<u> </u>	115	DPLLRPSPLLATGQPAGSEDLTKDRSLT-GKLEPVSPPSPPHTDPELELVPPRLSKEELIAKPLEPARPERT	173
: *	174	QNMDRVDREITWVEQQISKLKKKQQQLEEEAAKPPEPEKPVSPPPIESKHRSLVQIIYDE	233
ą	650	SGVKRTDPATPVVKPVPEAPKGGBAEBPVPKPYSQDLSRS	689
λ.	234	NRKKAEAAHRILEGLGPQVELPLYNQPSDTRQYHENIKINQAMRKKLILYFKRRNHARKQ	293
ð	069	PQSLSDTGYSSDGVSSSQS	708
<u>~</u> 4	294	WKQKFCQRYDQLMEALEKKVERIENNPRRRAKESKVREYYEKQFPEIRKQRELQERM	350
Ω.	60/	EITGVVQQEVEQLDSAGVTGPRPPSPSELHKVGSSLRPSLEAQAVAPSAE	758
<u>≽</u> a	351 759	QSRVQQRGSGLSMSAARSEHEYSEIIDGLSEQENLEKQMRQLAVIPPMLYDADQQRIKFI     :       :	410 797
≿	411	NMNGLMADPMKVYKDRQVMNNWSEQEKETFREKFWQHPKNFGLIASFLERKTVAECVLYY	470
ð	798	::	816
⋩	471	YLTKKNENYKSLVRRSY RRRGKS QQQQQQQQQQQQQQQQQQPMPRSSQEEKDE	522
ą	817	SDDFGSQLRHDYVEDSSEGGLSPLPPQPPARADMTDEEFWRRQILEMSAEEDNLE	872
<u>~</u>	523	KEKEKEAEKEEEKPEVENDKEDLLKEKTDDTSGEDNDEKEAVASKG-RKTA	572
ą	873	EDDTAVSGRGLAKHSAQKASARPRPESSQEPKRRLPHNATTGYEELLSEAGPAEPT	928
<b>≿</b>	573	NSQGRRKGRITRSMANEANSEAITPQQSAELASMELNESSRWTEEEMETAKK	625
ð	929	DSSGALGGGLRRFKTIELNSTGSYGHELDLGQGPDPNLDREPELEMESLTGSP	981
<u>&gt;</u>	626		029
ð	982	EDRSRGEHSSTLPASTPSYTSGTSPTSLSSLEEDSDSSPSRRQRLEEAKQQRKARHRSHG	1041
<b>≿</b>	671	KAPAAASEEAAF	969
ą	1042	PLLPTIEDSSEEBELREBEBLLREQEKMREVEQORIRSTARKTRRDKEELRAQRRRERSK	1101
۲	697	EEMEASGVSGNEEEMVEEABALHASGNEVPRGECSGPATVNNSSDTESI	751
g	1102	TPPSNLSPIEDASPTEELRQAAEMEELHRSSCSEYS	1137
<b>≿</b>	752	PSPHTEAAKDTGQNGPKPPATLGADGPPPGPPTPPRRTSRAPIEPTP	798
ą	1138	PSPSLDSEAETLDGGPTRLYKSGSEYNLPAFMSLYSPTETPSGSSTTPSSGRPLKSAE	1195
<b>≿</b>	799	ASEATGAPTPPPAPPSPSAPPVVPKEEKEEETAAAPPVEEGEE	842
ą	1196	EAYEDMMRKAEMLQRQQQQVAGARGPHGGPSQPTGPRSQGSFEYQDTQDHDYGGR	1250
<u>≻</u>	843		893
ð	1251	ASQPVAESTPAGLGAAVYEEILQTSQSIARMRQASSRDLGFTEDKKKEKQFLNAESAYMD	1310
Ā	894		915
ą	1311		1370
<u>≯</u>	916	AAA	972
ą	1371	PVSSTLTSKEVGMTFSQGPGSPATTASPTRGYMTPTSPAGSERSPSTSSTIHSYGQ	1426
<u>≯</u> ,	973	IPPIQVTKVHEPPREDAAPTKPAPPAPP-PPQNIQPESDAPQQPGSSPRGKSRSPAPPAD	1031
٩	1427		1474
۶,	1032	KEAFAAEAQKLPGDPPCWTSGLPFPVPPREVIKASPHAPDPSAFSYAPPGHPLP	1085

qa	t   ;   ;   ;   ;   ;   ;   ;   ;   ;	::  :   :
Οy	y 1086 LGLHDTARPVLPRPPTI	
qq	b 1532 MVAQGTQTPHRPSTPRLVWQQSSQEAPIM-	SSQEAPIMHILASDASSQTRWVH 1576
oy .	1141 AKAPVGPV	QLSPRGQAGPPESLGVPTAQEASVLRG
g è	1198 TAL	SYSQTTPPSASOMPSEPAGPPGFPRAPSAGIDGP 1629 GSVPGGSTTKGTPGTRVDGDGATTVRGGI1229
7 A	1630 LALYGWGALPAENISLCRI	PGPRPPGTAVVDLRTAVKPTPIILTDQGM 1
QY	үү 1230	GTPADVLYKGIITR 1245
qq	1688 DLT	SLAVEARKYGLALDPVSGRQSTAVQPLVINLNAQEQTHTFLATATTVSITMASSVLM 1747
Qy	1246	EDSLPKGHVIYEGKKGHVLSYEGGMSVTQCSKEDGRS 1296
qq	1748	AQQKQPVYYGDPFQSRLDFGQGSGSPVCLAQVKQVEQAVQTAPYRGG 1794
Qy	1297	AAPKRIYDMMEGRVGRAISSASIEGLMGRAIPPE- 1338
qq	1795	PRĞRPREAKFARYNLPNQVTPLARRDILITQMGTAQGVGLKPGPVPEPGAEPHRATPAEL 1854
δλ	1339	-RGSITQGIPRSYVEAQE-DYLRREAKLL 1378
qq	1855	RSHAPPGTRKPHTVVVQMGEGTAGTVTTLLPEEPAGALDLTGMRPESQLACCDMVYKFPF 1914
οy	1379	-AYKTQALGPLKLKPAHEGLVATVKEAGRSIHEIPREEL 1433
Ω	b 1915 GSSCTGTFHPAPSAPDKSVTDTALPGQSSGPF-	
οy	1434 RH	KEGSITQGTPLKYDTGASTTGSKKHDVR 1474
QQ	1947 -Y	SPRDPEPPEPLTFRTQGVVGPGPHEEGRPYPQGLPGRLYSSMSDTNLAEAGLNYHAQR 2005
Qy	1475	SLIGSPGRTFPPVHPLDVMADARALERACYEESLKSRPGTASSSGGSIARGA 1526
đ	2006 LGQLFQGPGR	DSAVDLSSIKHSYSLGFADGRYLGQGLQYGSFTDLRHPT 2054
٥y	1527 PVIVPELGKPRQSPLT-	GAPE
qa	2055 DLLSHPLPLRRYSSVSN	HRYGPRGDAVGFQEASLAQYSA 2097
ογ	1585 LISTPREIAK	PYEHLLR
οQΩ	2098TTAREISRM	GGRHGSGSGGPDLVQ-YQPQHGPGLSAPQGLA 2147
Oy	1642	PLDAAAAYYLPRHLAPNPTYPHLYPPYLIRGYPDTAALENRQTIINDYITSQQMHHNTAT 1701
QO	2148	EGOPSPGNLAQYGPAASQATAVRQLLPSTAT 2191
Οý	у 1702 АМА	QRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHL 1740
qq	b 2192 VRAADGMIYSTINTPIAATLPITTQPASVLRPMV-	
δλ	1741	PVLVPPTPGTPATAMDRLAYLPTAPQPFSSRHSSSPLSPGGPTHLTKPTTTSSSERERDR 1800
qq	2250	
δλ	1801 DRERDRDREREKSI-LT	STITYEHAPIWRPGTEQSSGSSGSSGGGGSSSRPA 1852
q	2302 RPELPAGVAREEPF	STTAPAVIKEAPVAPAPGPAPAPPGQKPAGEAAAGSGSGVLSRPA 2361
δλ	y 1853 SH	1854
QQ	2362	SEKEEASQEDRQRKQQEQLLQLERERVELEKLRQLRLQEELERERVELQRHREEEQLLVQ 2421
δ	N 1855SHAHQHSPISPRTQDALQORP	RTQDALQQRPSVLHNTGMKGIITAVEPSK 1894

PTVLRSTSSPVRPAAT RAPFPATCEAFSRGPPPAATELAQNG LIPKEAPRVARPERPRADTGHAFLAK	THE COURT IN COURT IN CO. LECT.	1937
KAPFPATCEAPSRGPP -LPKEAPRVARPERPR	TLMEPVL	1001
1	REPVLHR	2537
		1979 2597
1980EPRPLV	-PPVSGHATIARTPAKNLAPHHASPDP	2011
11 2598 EEGEGRYLVTRRRTRRSADCSVQTDDEDNADWEQPV		2650
2012 PAPPASASDPHREKTQSKPFSIQELELRSLGYHGSSYSPEGVEPVSP		2058
2651 SKHDATASSSTTAAATARAMSSVGIQTISDCSVQ1	SVGIQTISDCSVQTEPEQLPRVSPAIHITAATDPKVE	2708
2059VSSPSLTE	-VSSPSLTHDKGLPKHLE-·ELDKSHLEGELR	2087
2709 IVRYISAPEKTGRGESLACQTEPDGQAQGVAGPQLIGPTAISPYLPGIQIVTPGALGRFE		2768
2088 PKQPGPVKLGGEAAHLPHLRPLPESQPSSSPLLQTAPGVKGHQRVVTLAQH	1	2138
2769 KKKPDPLEIGYQ-AHLPPESLSQLVSRQPPKSPQVLYSP	VSPLSPHRLLDTSF	2820
2139 -ISEVITQDYTRHHPQQLSAPLPAPLYSFPC	-APLPAPLYSFPGASCPVLDLRRPPSDLYLPPP	2188
2821 ASSERLNKAHVSPQKQFIADSTLRQQTLPRPMKT		2867
2189 DHGAPARGSPHS-EGGKRSPEPNKTSVLGGGEDGIE-	PVSPPEGMTEPGH	2236
2868 TAEESAKERFSLYQHQGGLGSQVSVLPPNGI	- QVSVLPPNGLVRKVKRTLPSPPPEEAHLPLAGQ	2921
2237 SRSAVY PLLYRDGEQTEPSRMGSKSPGNTSQPPAFFSKLTESNSAMVKSKKQEINKKL		2294
2922 VPSQLYAASLLQRGLAGPTTVPATKAS		2971
2295 NTHNRNEPEYNISQPGTEIFW	-FNMPAITGIGLMTYRSQAVQEHAS	2337
2972 AELDEEEKEIDAKLKYLELGITQRKESLAKDRGGRDYPPLRGLG	  EHRDYL	3021
2338TNMGLEAIIRKALMGKYDQWEESPPLSANAFNPLNASASLPAAMPITAADGR	Ø	2390
3022 SDSELNÇLKLQGCTTPAGQYVDYPASAAVPATPSGPTAFQQPRFPPAAPQYTAGS	!	3076
2391 DHTLTSPGGGGKAKVSGRPSSRKAKSPAPGLA	KAKVSGRPSSRKAKSPAPGLASGDRPPSVSSVHSEGDCNRRTP	2444
3077SGPTQNGFPAHQAPTYTGPSTYPAPTYPPGTGYPAEPGLPSQPAFHPTGHYAAPTY		3132
2445 LSTPFPY	SPPPPGLPAGS	2488
:  :           3133 MPTTQSAPFPVQADSRAAHQKPRQTSLADLEQKVPTNYEVIGSPAVTMSSAPPETGY	— თ	3190
2489 GPLAGPHHAWDEEPKPLLCSQYETLSDS 2516		
3191 GPAVSGSYEQGKAPEHPRGSDRSSVSQS 3218		
RESULT 11		
138340 elastic titin - human (fragment)		
cies: now apteus (man) e: 29-May-1998 #sequence_revision 29-May-1 ession: 138346	xt_change 21-Jul	-2000
eit, S.; Kolmerer, B.		
A;Title: 111ins: glant proteins in charge of muscle ul A;Reference number: A57430; MUID:96026330	trastructure and	elasticity.
ession: 138346 cus: preliminary; translated from GB/EMBL	/DDBJ	
scule type: mRNA		

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Gaps 124;
Cross-references: EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g1017427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : : | : | : | : | 5556 TIHNVIPDDDEGVYSVIARLEPRGEARSTAELYLTITKEIKLEKPPDIPDSRVPIPTMPIR 5615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5616 AVPPEEIPPVVAPPVPLLLPTPEEKKPPPKRIEVTKKAVKKDAKKVAKPKEMTPREEIV 5675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5814 VIQVQKEVYEESHERKV-PAKVPEKKAPPPPKVIKKPVIEK-------IEKTSRR 5860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:| : :: | | | : :| | | 5498 PIQFTKRIQNIVVSE--HQSATFECEVSFDDAIVTWYKGPTELTESQKYNPRNDGRCHYM 5555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5949 -----PPPKVPELPEKPAPEEVAPVPIPKKVEPPAPKVPEVPKKPVPEKKPVPVFKKEP 6003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6064 VPEIPKKKVPEERKPVPRKEEEVPPPRVPALPKKPVPEEKVAVPVPVAKKAPPPRAEVS 6123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6178 --EREBEBERAUT--EYEVMEEPEBYVVEEKLHIISKRV---------EAEP 6216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5721 ------YEKK-----QAVHKEKRVFIESFEEPYDELEVEPYTEPFEQPYYEEPDE 5764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            486 SYRRRGKSQQQQQQQQQQQQQQQQQQPMPRSSQEEKDE-KEKEKEAEKEEEKPEVENDKED 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 ELH-LRPESHSYLPELGKSEME------115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 -----LTKDRSLTGKLEPV 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 SPPSPPHTDPELELVPPRLSKEELIQNMDRVDREITMVEQQISKL-KKKQQQLEEEAAKP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 PEPEKPVSPPPIESKHRSLVQIIYDENRKKAEAAHRILEGLGPQ-----VELPLYNQPSD 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 ALEKKVERIENNPRRRAKESKVREYYEKQFPEIRKQRELQERMGSRVGQRGSGLSMSAAR 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEHEVSEI--IDGLSEQENLEKOMROLAVIPPMLYDADQORIKFINMNGLMADPMKVYKD 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROVMNMWSEQEKETFREKFMQHPKNFGLIASFLERKTVAECVLYYYLTKKNENYKSLVRR 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        545 LLKEKTODTSGEDNDEKEAVASKGRKTANSQGR----RKGRITRSMANEANSEEAITPQQ 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           601 SAELASMELNESSR---WIEEEM-----ETAKKGLLEH-----GRNWSAIARMVG 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          643 SKTVSQCKNFY----FNYKKRQNLDEILQQHKLKMEKERNARRKKKKAPAAASEEAAFPP 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  699 VVEDEEMEASGVSGNEEEMVEE-----AEALHASGNEVPRGECSGPATVNNSSDTESIP 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     753 SPHTEAAKDIGQNGPKPPATLGADGPPPGPPTPPRRTSRAPIEPTPASEAIGAPTPPPAP 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        813 PSPSAPPPVVPKEEKE--EETAAAPPVEEGEEQKPPAA------EELAVDTGKAEE 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 TRQYHENIKINQAMRKKLI------LYFKRR---NHARKQWKQKFCQRYDQIME 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5911 KMFFASHTEEE------VSVTVPEVQKEIVTEEKIHVAVSKRVE-----
                                                                                                                                                                                                                                                                                                    Indels 913;
                                                                                                                                                                                                                               Query Match 3.8%; Score 503.5; DB 2; Length 7962; Best Local Similarity 18.4%; Pred. No. 6.8e-10; Matches 522; Conservative 349; Mismatches 1047; Indels 913;
                                                                                                                                                                                                                                                                                                                                                                     27 PVQIARTHTDVGLLEYQHHSRDYASHLSPGSIIQPQRRRPSLLSEFQPGNERS--
                                                                                         Cross-references: GDB:127867; OMIM:188840; Map position: 2q31-2q31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ==
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                                                                    Gene: GDB:TIN
                                     :Genetics:
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3	0204	KKEKVPPPKVPEEPKKPVPEKKVPPKVIKMEEPLPAKVTEKHMQITQEEKVLVAVTKKEA 635	23
٥y	861	KAEKKEGGSGR 90	2
qq	6324	PPKARVPEEPKRAVPEEKVLKLKPKREEEPPAKVTEFRKRVVKEEKVSIEAPKREPQPIK 638:	13
Oy	903	₩.	
QQ	6384	EVTIMEEKERAYTLEEERAVSVQREEEYEEYEEYEKEFEEVEPTEEYDQYEEYEERE 6440	0,
λŏ	955	ASPQKPLDLKQLKQRAAAIPPIQVTKVHEPP 985	
qq	6441	YERYEEHEEYITEPEKPIPVKPVPEEPVPTKPKAPPAKVLKKAVPEEKVPVPIPKKLKPP 6500	00
ογ	986		
QQ	6501	PPKVPEEPKKVFEEKIHISITKREKEGVTEPAAKVPMKPKRVVAEEKVPVPRKEVAPPVR 6560	0:
δλ	966	APPPPQNLQPESDAPQQPG 1016	9.
Q D	6561	VPEVPKELEPEEVAFFEEVVTHVEEYLVEEEEEVIHEEEEFITEEEVVPVIPVKVPEVP- 6619	6.
λο d	1017	SSPRGKSRSPAP-PADKEAFAAEAQKLPGDPPCWT	
2	0700		D
oy B	1051 6680	SGLPFPVPPREVIKASPHAPDPSAFSYAPPGHPLPLGLHDTA 1092	2 9
οy	1093	RPVLPRPPTISNPPLISSAKHPSVLERQIGAISQGMSVQLHVPYSEHAKAPVGPVTM 1150	0
q	6737		<u>ε</u>
ογ	1151	GLPLPMDPKKLAPFSGVKQEQLSPRGQAGPPESLGVPTAQEASVLRGTALGSV 1203	33
අ	6784		33
οχ	1204	PGGSIIKGI-PSTRVPSDSAIIYRGSITHGTPADVLYKGTIITRIIGEDSPS 12:	53
QQ	6834	PEEEVLPEVKPVPVPAPVPEIKKKVTEKKVVIPKKEEAPPAKVPEVPK 688:	22
λ̈́o	1254	RLDRGREDSLPKGHVIYEGKKGHVLSYEGGMSVTQCSKEDGRSSSGPPHETAAPKRTYDM 131:	er
qq	6883	69	29
o,	1314	HHLKEQHHIRGSITQGIPRSYVEAQEDYL	٤,
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ογ	1374	EAKLLKREGTPPPPPPSRDLTEAYKTQALGPLKLKPAHEGLVA····-TVKE···- 1420	0;
QQ	6977	EAPPAKVPEVPKKVPEKKVLVPKKEAVPPAKGRTVLEEKVSVAFRQEVVVKERLELEV 7034	7
ογ	1421	AGRSIHEIPREELRHTPELPLAPRPLKEGSITQGTPLKYDTGASTTGSKKHDVRSLIGSP 1480	0
QQ	7035	VEAEVEEIPEEEEFHEVEBYFEEGEF	0.
οχ	1481	GRIFPPVHPLDVMADARALERACYEESLKSRPGTASSSGGSIARGAPVIVPELG 153	4
qq	7071	QHRVEBEHRVEKVHRVIEVFEABEVEVFEKP-KAPPKGPEISEKIIPPKKPPTKVVPRKE 7129	6
0y	1535	KPRQSPLTYEDHGAPFAGHLPRGSPVTWREPTPRLQEGSLSSSKASQDRKLTST 1588	82
qq	7130	PPAKVPEVPKKIVVEEKVRVPEEPRVPPTKVPEVLPPKEVVPEKKVPVPPAKKPEAP 7186	9
οy	1589	LLRGVSGVDI	<b>6</b> 0
qq	7187	PPKVPEAPKEVVPEKKV-PVPPPKKPEVPPTKVPE-VPKAAVPE 7228	80
ò	1649	YYLPRHLAPNPTYPHLYPPYLIRGYPDTAALENRQTIINDYITSQQMHHNTATAMAQRAD 1708	ω .

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RESULT 12
MHC class III histocompatibility antigen HLA-B-associated protein 2 [similarity] - hu c.; Species: Homo sapiens (man)
C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 15-Sep-2000
C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 15-Sep-2000
C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 15-Sep-2000
R; Bougueleret, L.
Submitted to the EMBL Data Library, August 1992
A; Reference number: S37671
A; Reference number: S37671
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1870 < A; Cross references: EMBL: Z15025; NID: 929374; PID: 929375
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2042
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---LPVLVP---- 1745
                                      ----EPEESPSAPPKKPEVPPVRVPEVPKEVVPEKKVPAAPPKKPEVTPVKVPEAPKEV 7303
                                                                                -----PTPGTPATAMDRLAYLPTAPQPFSSRHSSSPLSPGGPTHLTKPTTTSSSERE 1797
                                                                                                                                                                   1798 RDRDRERDRDREREKSILTSTTTVEHAPIWRPGTEQSSGSSGSGGGGSSSRPASHSHA 1857
                                                                                                                                                                                                             ---PEKKAPAVVAKK 7400
                                                                                                                                                                                                                                                        HQHSPISPRTQDALQQRPSVLHNTGMKGIITAVEPSKP------TVLRSTSTSS 1905
                                                                                                                                                                                                                                                                                              7401 PELPPV------KVPEVPKEVVPEKKVPLVVPKKPEAPPAKVPEVPKEVVPEKKVAV 7451
                                                                                                                                                                                                                                                                                                                                          PVRPAATFPPATHCPLGGTLDGVYPTLMEPVLLPKEAPRVARPERPRADTGHAFLAKPPA 1965
                                                                                                                                                                                                                                                                                                                                                                 7552 ЕРЕРЕКVІЕКРКІКРЯРРРРРРРРРРРРРЯНІКТІРОТКАІРККУРЕNPOVPEKVELTPLK 7611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2043 YHGS-----SYSPEGVEPVSPVS----SPSLTHDKGLPKHLEELDKSHLEGELRPK 2089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2090 OPGPVK-----LGGEAAHLPHLRPLPESOPSSSPLLQTAPGVKGHORVVTLAQHISEVI 2143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2144 TQDYTRHHPQQLSAPLPAPLYSFPG-ASCPVLDLRRPPSDLYLPPPDHGAPARGSPHSEG 2202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7720 KPPPVEPETPIAAPVTVPVVGKKAEAKAPKEEAAKPK-------GPIKGVP---- 7764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7824 IFECLVSPSTAITTWMKDGSNIRESPKHRFIADGKDRKLHIIDVQLSDAGEYTCVLRLGN 7883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSGLEPASSPSK-----GSEPRPLVPPVSGHATIARTPAKNL------APHHA 2007
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                                                                                                                          7304 VPEKKVPVPPPKKPEVPPTKVPEVPKVAVPEKKVPEAIPPKPESP----PPEVFEEPEEV
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--LNYAAGPRGIIDLSQVPH---
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7944 RIV---PGVIG 7951
1709 MLRGLSPRESSLA-
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A; H C; S	A.Map position: 6p2l.3 A.Introns: 38/2; 97/2; 129/3; 154/1; 202/1; 252/3; 279/2; 327/1; 357/2; 429/3; 588/1; 65 C.Superfamily: collagen alpha 1(IV) chain	Qy 1 Db 1
Õι	3.88;	Qy 1
mΣ	<pre>Best Local Similarity 21.2%; Pred. No. 1.5e-10; Matches 431; Conservative 175; Mismatches 700; Indels 728; Gaps 97;</pre>	Dp 7
& g	9 663 DEILQOHKLKMEKERNARRKKKAPAAASEEAAFPPVVEDEEMEASGUSGUEE 715 11	QY 1
Qy	716 EMVEEARALHASGNEVPRGECSGPATVNNSSDTESIPSPHTEAAKDTGQNGP	Qy 1
qq		Dp 1
ογ	768 KPPAT 	o da
යි ර	428 YPDRGGPPCKPPAPEDEDEAWRQRRKQSSSEISLAVERARRREEEERRMQEERRA	0y 1
g d	790	Dp 1
ογ	943 QKPPAAEELAVDTGKAEEPVKSECTEEAEEGPAKGKDAEAAEATAEGALKAEKKEGGSGR 902	ογ 1
qq		Dp 1
δλ	903 ATTAKSSGAPQDSDSSATCSADEVDEAEGGDKNRLLSPRPSLLTPTGDPRANA 955	Oy 1
qq	565 APTLVSGGGSTSSTSSGSFBASPVEPQLPSKEGPEPPEEVPPPTTPPVPKVEPKGDGIGP 624	Db 1
δλ	956SPOKPLDLKQLKQRAAAIPPIQVTKVHEPPREDAAPTKPAPP	0y 1
q		do .
δλ	1004 NLQPESDAPQQPGSSPRGKSRSPAPPADKEAFAAEAQKLPGDPPCWTSGLPFP	λο i
qq	685 TLGAVPAPKAPPPPPKALYPGALGRPPPMNF- 718	
οχ	1064	7 Z
qq	719DPRWMMIPPYVDPRLLQGRPPLDFYPPGVHPSGLVPRER 757	
ογ	1124	5 E
Q Q	758	
oy S	1177 QAGPPESLGVPTAQEASVLRGTALGSVPGGSITKGIPSTRVPSDSAITYRGSITHGTPAD	
a d	811 UAADEBDKGM	Qy 2
e e	123/ VLYKGTITKI-1GEDSPSRLDRGREDSLPRGHVIXEGKRGHVLSYEGGMSVTQCSKEDGR 1295       :       :   :         :	Db 16
ογ	1296 SSSGPPHETAAPKRTYDMMEGRVGRAISSASIEGLMGRAIPPERHSPHHLKEQHHIRGSI	0y 2:
QQ	875	
Qy	1356 TQGIPRSYVEAQEDYLRRE	
QΩ	931 RRGIPPEEPGAPPRRAGPIKKPPPPTVVEELPP 963	
δ ά	1408 KPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKBGSITQ	D 69
3 8	304 AFLEGG	0y 24
<b>3</b> 8	1003	Db 18
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δλ	1501 RACYEESLKSRPGTASSS	KPRQSPLTYEDHGA 1548
Op	1053 TESFEEMMGVEVGGGDQTT	9S
δŏ	1549 PFAGHLPRGSPV	TMREPTPRIQEGSLSSKASQDRKLTSTPREIAKSPHSTVP 1601
QQ	Db 1098 GSGAQKQAARPWRVIWLLQTRRLPHPRREHSPRSS-	:     :     :     :     :       :
οy	OY 1602 EHHPHPISPYEHLLRGVSGVDLYRSHIPL-AFDPTSIPRGIPLDAAAAYYLP	PRGIPLDAAAAYYLP-RHLAPN- 1658
Op	1141 TLHRAPARFTCPGVG	- ESSLPEGAISPGPRRREAPPQVCPGWSPPAKSLAPKK 1192
δy	1659 -PTYPHLYPP	YLIRGYPDTAALENROTIINDYITSQOMHHNTATAMAQRADML 1710
QΩ	Db 1193 PPTGPLPPSKEPLKEKLIPGPLSPVARGGSNGGSNVGMEDGERPRRRRHGRAQQQDK	: : 11: 1 WGMEDGERPRRRHGRAQQQDK- 1249
Οŷ	1711 RGLSPRESSLALNYAAGPRGIIDLSQVPHLPVU	PPTPGTPATAMDRLAYLPTA 1764
qq	1250PPRFRRLKQERENAARGSEG	:     :     :
δy	1765 POPFSSRHSSSPLSPGGPIHLTKPTTTSS	SERENDRDRE 1803
qq	1293 PAPRRAAAKSPDLSNQNSDQANEEWETASESSDFTS	RRGDKEAPPPVLLTPKAVGTPGG 1352
Qy	1804	IAPIWRPGTEQSSGSSG-SSGGGG 1845
qq	1353 GGGAVPGISAMSRGDL	RONRRPGPGGKAGSSGSSGGAG 1412
Qy	Qy 1846 GSSSRPASHSHAHQHSPISPRTQD-ALQQRPSVLHNTGMKGIITAVEPSKPTVLRSTST	GMKGIITAVEPSKPTVLRSTST- 1903
qq	Db 1413 GGPGGRTGPGRGDKRSWPSPKNRSRPPEERP	PGLPLPPPPSSSVFRLDQVI 1464
QY	QY 1904 -SSPVRPAATFPPATHCPLGGTLDGVYPTLME	PVLLPKEAPRVARPERPRADIG 1956
QQ	1465 HSNPA	GIQQALAQLSSRQGSVTAPGGHPR-HKPGPPQAPQG 1504
δ	1957 HAFLAKPPAR	HATIARTPAKNLAPH
qq	1505 PSPRPPTRYEPQRVNSGLSSDPHFEEPGP	GVGGTPRDSAGVSP 1550
Qy	2010 DPPAPPASASDPHREKTQSKPFSIQELEL	RSLGYHGSSYSPEGVEPVSPVSSPSLTH 2066
Dp	Db 1551 FPPKRRERPPRKPELLQEESLPPPHSSGFLGS	LGSKPEGPGPQAESRDTG 1597
δy	2067	VKLGGEAAHLPHLRPLP-ESQPS 2115
Q	DD 1598 TEALTPHIWNRLHTATSRKSYRPSSMEDWMEPLSPFEDVAGTEMSQSDSGVDLSGDSQVS	DVAGTEMSQSDSGVDLSGDSQVS 1657
δ	2116	HHPQQLSAPLPA-PLYSFPG 2168
QQ	1658 SGPCSQRSSPDGGLKG	AAEGPPKRPGGSSPLNAVPCEGPPG 1698
δy	QY 2169 ASCPVLDLRRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEPNKTSVLGGGEDGIEPVSPP	SPEPNKTSVLGGGEDGIEPVSPP 2228
οp	1699 SEPPR	I.PREQPLPPGPIGTERSQRT 1736
Οy	2229	SQPPAFFSKLTESNSAMVKSKKQ 2288
qq	1737 DRATEPGPIR	SHRPGPPVQF1757
Qγ	QY 2289 EINKKLNTHNRNEPEYNISQPGTEIFNMPAITGTGLMTYRSQAVQEHASTNMGLEAIIRK	TYRSQAVQEHASTNMGLEAIIRK 2348
Ωp	Db 1758GISDKDSDLRLVVGDSL-	KAEKELTASVTE 1786
δλ	2349 ALMGKYDQWEESPPLSANA	ADGRSDHTLTSPGGGGKAKVSGR 2408
q	1787 AIPVSRD-WELLPSAAA	SSGQRLYPEVFYGSAG 1837
δy	2409 PSSRKAKSPAPGLASGDRPPSVSSVHSEGDCNRRT	TNRVWEDRPSSAGSTPF 2462
qq	1838 PSSSQISGGSHGLS	- ITSKOWRLRPGTPSLHPY 1869

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1713 LSPRESSLALNYAAGPRGI-----
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     C:Species: Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Accession: 13049
R:Treisman, J.E.; Luk, A.; Rubin, G.M.; Heberlein, U.
Submitted to the EMBL Data Library, March 1998
A:Retaus: prediminary; translated from GB/EMBL/DDBJ
A:Retaus: prediminary; translated from GB/EMBL/DDBJ
A:Residues: 1-2715 <TRE>
A:Residues: 1-2715 <TRE>
A:Cross-references: EMBL:AF053091; NID:q2981220; PID:q2981221; PIDN:AAC06254.1
C:Genetics:
A:Gene: eld
A:Cross-references: FlyBase:FBgn0003013
C:Function:
C:Runction:
A:Description: could act as a transcription factor antagonistic to the Wg pathway
C:Keywords: DNA binding
                                                                                                                                                                                                                                                                                                 pathway
                                                                                                                                                                                                                                                                                                                                                                                                         111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 302 PPPTNTSRGQSPYPPAHGQNSGSYPSSPQQQQQQQQQQQQQQQQQQGPGGPPPGTGQ 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --QPPQQNTPPTSQXSPYPQRYPTPPGLPAGGSNHRTAYSTHQYPEPNRPWPGGSSPSPG 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 NRPPQQRYIPGQPPQGPTPTLNSLLQSSNPPPPPPQHRYANTYDPQQAAASAAAAAQQQ 253
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                                                                                                                                                                                                                                                                                                                                                                                                      763;
                                                                                                                                                                                                                                                                                                                                                                   Length 2715;
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                                                                                                                                                                                                                                                                                                                                                                   3.8%; Score 502.5; DB 2; ilarity 20.9%; Pred. No. 2.3e-10; Conservative 189; Mismatches 752;
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Matches 450; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1666 PPYLIRGYPD--TAALENRQTIINDYITSQQMHHNTA--TAMAQRADMLR-----G 1712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --IDLSQVPHLPVLVPPTP 1748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1046 FVEVTKSKTWKDIAGLLGIGASSSAAYTLRKHYTKNLLTFECHFDRGDIDPLPIIQQVEA 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1135 -----SSNSQDSFPA-PPGSAPNAAIDGYPGYPGGSPYPGAS-----GPQPDYAT 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1382 PGQPFGQGPG-----QYPPQNRNMYPPYGPEGEAPPTGANQYGPYGSRPYSQPPPGG 1433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1414 LVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGSITQGTPLKYDTGASTTGSKKHDV 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1521 SIARGAPVIVPELGKPRQSPLTYEDHGAPFAGHLPRGSP--------VTWREP 1565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1615 LRG-----VSGVDLYRSHIPLAFDP--TSIPRGIPLDAAAAYYLPRHLAPNPTYPHLY 1665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTPATAMDRLAYLPTAPQPFSSRHSSSPLSPGGPTHLTKPTTTSSSERERDRDRERDRDR 1808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGTGPG-----PGQGP-----GPGAASGGA------GAVGAVGGGPQPHP 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2099 EAAHLPHIRPLPESQPSSSPLLQTAPGVKGHQRVVTLAQHISEVITQDYTRHHPQQLSAP 2158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2159 LPAPLYSFPGASCPVLDLRRPPSDLYL-PP--PDHGAPARGS-----PHSEGGKRS 2206
1239 YKGTITRIIGEDSPSRLDRGREDSLPKGHVIYEGKKGHVLSYEGCMSVTQCSKEDGRSSS 1298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1566 TPRLQEGSLS-SSKASQDRKLTSTPREIAKSP----HSTVPEHHPHPI-----SPYEHL 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1179 AGOMORPPSONNPOTPHPGAAAVAAGD----NISVSNPFEDPIAAG-----GGPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPPHSPHTAAQQAAGQHQQQHPQHPGLPGPPPPQQQQGQQGQQPPP----SVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2043 YHGSSYSPE----GVEPVSPVSSPSLTHDKGLPKHLEELDKSHLEGELRPKQPGPVKLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----QQHVRPAAGAPYPPGG
                                                                                                                                                            GPPHETAAPKRTYDMMEGRVGRAISSASIEGLMGRAIPPE--RHSPHHL---KEQHHIRG
                                                                                                                                                                                                                                   675 GPP----PPPTSQAGAGGANSMPSGAQAGGYPGRGMPNHTGQYPPYQWVPPSPQQTVPG
                                                                                                                                                                                                                                                                                                                     1354 SITQGIPRSYVEAQEDYLRREAKLLKREGTPPPPPPPSRDLTEAYKTQALGPLKLKPAHEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----SGSPRPLNYL-KQHLQHKGGYGGSPTP-----PQG-PQGYGNG--PTGM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----HPGMPMGPPHHMGPPHGPTNMGPPTSTPPQSQMLQ------GGQPQGQGASGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :| :| : | : | DMSSPPNWPRPAGSPQVFNHVPVPQEPFRSTITITKKSDSLCKLY---EMDDNPDR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1809 EREKSILTSTTTVEHAPIWRPGTEQSSGSSGSGGGGGSSSRPASHAHQHSPISPRTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPVSGHATIARTPA---KNLAPHHASPDPPAPPASASDPHREKTQSKPFSIQELELRSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --- QYGSSDQYNATGP
                                                                          630 MHGGYK--MGGPGQSPGAQGYPPQQPQ------QYPPGNYPPRPQYPPGAYAT
                                                                                                                                                                                                                                                                                                                                                                                            730 ----GAPGGAMVGNH-----PQGKGTPPPPVVG-------GP----PPPQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------PLDVMADARALERACYEESLKSRPGTASSSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----PESGGPEH---ISQDNGISSSG--PTGAAGMHAVTSVVTTGPDGTSMDEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1106 GS-------KKKTAKAASVP-SPGG-GHLDAGTINSTG-
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	т т	OY 1092ARPULPRPTISORPEDPY OY 1092ARPULPRPPTISORPPL Db 694 ITGVVQEVEQLDSAGVTGRPPS OY 1138 SEHAKAPVGPVTMGLPLPMDPKKLAPFSGVK   1	1218 843 1265 890 1295	950 1338 1007 1394 1064	OY 1439 LPLAPRPLKEGSITGGTPLKYDTGASTTGSKI
2207 PEPNKTSYLGGGEDGIEPVSPPEGMTEPGHSRSAVYPLLYRDGEQTEPSRWGSKSPGNTS	155 242 160 246 166	R42761 Bassoon protein - rat Bassoon protein - rat Bassoon protein - rat Bassoon protein - rat C: Matternate names: brain-specific synapse-associated protein C: Species: Rattus norvegicus (Norway rat) C: Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000 C: Accession: 142761 C: Bassoon: A Sammarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex, J. Cell Biol. 142, 499-509, 1998 A; Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localized A; Reference number: 22249; MUID: 98345363 A; Accession: T42761 A; Scatus: preliminary; translated from GB/EMBL/DDBJ	A: Mosteure Lype: HIRNA A: Residues: 1-3938 CDIE> A: Cross-references: EMBL:Y16563; NID:g3413503; PIDN:CAA76287.1; PID:g3413504 A: Experimental source: strain Sprague Dawley; brain C: Function: May be involved in cytomatrix organization at the site of neurotransmitte A: Note: component of the presynaptic cytoskeleton C: Keywords: coiled coil; zinc finger Query Match 3938;	Best Local Similarity 19.5%; pred. No. 4.96-10; matches 506; conservative 257; Mismatches 918; Indels 918; Gaps 114; Qy 491 GKSQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ	QY         605 ASMELNESSERWTEEEMETAKKGLLEHGRNWSAIARWYGSKTVSQCKNFYFNYKKRON 661           1         : : : : : : : : : : : : : : : : : : :

ADKEAFAAEAQKLPGDPPCWT----- 1050 KKHDVRSLIGSPGRTFPPVHPLDVMADARA 1498 KRTYDMMEGRVGRAISSASIEGLMGRAIPP 1337 ASTPSYTSGISPISLSSLEED---SDSSPS 1006 PAHEGLVATVKEAGRSIHEIPREELRHTPE 1438 : :| | | | : :: | LDSEAETLDGGPTRLYKSGSEYNLPAFM-- 1154 SKASQDRKLTSTPREIAKSPHSTVPEHHPH 1606 :||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : FSYAPPGHPLPLGLHDT------ 1091 LISSAKHPSVLERQIGAISQGMSVQLHVPY 1137 KQEQLSPRGQAGPPES-----LGVPTAQE 1191 -----GI-----1217 IVPELG --- KPRQSPLTYEDHGAPFAGHLP 1555 TSIPRGIPLDAAAAYYLPRHLAPNPTYPHL 1664 VTKVHEPPREDAAPTKPAPPAPPPQNLQP 1007 -----PSELHKVGSSMRPSLEAQAVAPS 740 DVLYKGTITRIIGEDSPSRLDRGRED-SLP 1264 : ! :!! ------ASARPRESSQESVALP 889 GENPTPHLVEKTEWLCLNCQTKRLLEGSLG 523 | :|: :| || EKKTGIPVKAEPVPRETAVPPGTPKAK 633 EDQKRRPHSLSIMPEAFDSDEELGDILEED 782 GGLRRFKTIGLNSTGRLWSTSLDLGQGSDP 949 GKLFGLGASLLTQASTLMSVQPEADTQGQP 374 NKPPAAEELAVDTGKAEEPVKSECTEEAEEG 873 ---GRA-----TTAKSSGAPQDSDSSAT 920 PKHGRADHQAASKAAAKPKTMPKERAACPL 464 -LSPRPSLLTPT-----G 949 KPYSQDLSRSPQSLSDTGYSSDGVSSSQSE 693 EDSSEGGLSPLPPQPPARADMTDEEFMRRQ 842 ------GSGPGP-----G 404

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g	1253	3YEEILQTSQSIARMRQASSRDLAFTEDKKKEKQFLNAESAYMDPMKQNGGPLTPGT 1308	
οy	1665	ю	
g	1309	9 SPTQLAAPVSFPTSTSSDSSGGRVIPDVRVTQ 1340	
<u>ک</u> ج	1722	LNYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAMDRLAYLPTAPQPFSSRHS ::	
3	1 * 0 1	TREADER VERTAIN SOFT AND SOFT	
දු දු	1774	* SSPLSPGGPTHLTKPTTTSSSERERDRDREREKSILTSTTTVEHAPIWRPGTEQ 1833 ::	
δ	1834	SSGSSGSSGGGGGSSSRPASHSHAHQHSPISPR-TQDALQQ	
QQ	1441	:	
ογ	1874	RESVLHNTGMKGIITAVEPSKPTVLRSTSTSSPVRPAATFPPATHCPLGGTLDGVYPTLM 1933	
qq	1501	TPSLTPSS-DIPRSVGTPSPMVAQGTQTPHRPSTPRLVWQQSSQE 1544	
ογ	1934		
e G	1545	APVMVITLASDASSQTRMVHASASTSPLCSPTDSQP	
δ	1976	SK	
οg	1605	5GFPRAPSAGVDGPLALYGWGALPAENISLCRISSVPGTSRVEPGPRPPGTAVVDLRT 1661	
ογ	2025		
QQ	1662	2 AVKPTPILIDOGMDLTSLAVEARKYGLALDPVPGRQSTAVQPLVINLNAQEQTHT 1717	
δ	2082	2LEGELRPKOPGPVKLGGEAAHLPHLRPLPESQPSSSPL 2119	
g	1718	FLATATIVSITMASSVLMAQQRQPVVYGDPFQSRLDFGQGSGSPVCLAQVRQVEQ 1772	
οy	2120	-LQTAPGVKGHQRVVTLAQHISEVITQDYTRHHPQQLSAPLPAPLY 2164	
g	1773		
ογ	2165	S SFPGASCPVLDLRRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEPNKTSVLGGGE 2219	
g	1830	)PGAEPHRATPAELRAHALPGTRKPHTVVVQMGEGAAGT 1867	
ογ	2220	)	
g	1868	** VITILIPEEPAGALDLIGMRPESRLACCDMAYKFPFGSSCTGIFHPAPSAPDKSVTDAALP 1927	
οy	2235	GHSRSAVYPLLYRDGEQTEPSRMGSKSPGNTSQPPAFFSKLTESNSA 2281	
g G	1928	3 GQSSGPFYSPRDPEPPEPLTFRAQGVVGPGPHEEQRPYPQGLPGRLYSSMSDTNLAEA 1985	
δý	2282		
g G	1986	GENYHAQRIGQLFQGFGRDSAVDLSSLKHSYSLGFADGRYLGQGLQYGSFTDLRHPTDLL 2045	
ά	2307	SQP 2320	
g	2046	SHPLPMRPYSSVSNIYSDHRYGPRGDAVGFQEASLAQYSATTAREISRMCAALNSMDQYG 2105	
ρλ	2321		
qq	2106	GRHGGGSGGPDLVPYQPQHGPGLNAPQGL-ASLRSGLLGNPTYPEGQPSPGNLAQ- 2159	
à i	2368	FNPLNASASLPAAMPITAADGRSDHTLTSP	
g	2160		
à á	2398	GGGGKAKVSGRPSSRKAKSPAPGLASGDRPPSVSSVHSEGDCNRRT	
용	2220	) PYGSGGVTAVPLTSLTRVPMIAPRVPLGPAGLYRYPAPSRFPIASTIP 2267	

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A43359
microtubule-associated protein MAPIA - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 13-Aug-1999
C:Accession: A43359; S22108
C:Accession: A43359; S22108
C:Accession: A43359; S22108
A:Title: Microtubule-associated proteins IA and LC2. Two proteins encoded in one mess A:Recession: A43359; MUID:92355629
A:Accession: A43359; MUID:92355629
A:Molecule type: mRNA
A:Residues: 1-2774 < LANY
A:Residues: 1-2774 < LANY
A:Residues: C:Accession: A43396; NID:q205537; PIDN:AAB48069.1; PID:q205538
A:Cross-references: GB:M83196; NID:g205537; PIDN:AAB48069.1; PID:q205538
A:Cross-references: GB:M83196; NID:g205537; PIDN:ABB48069.1; PID:q205538
A:Cross-references: GB:M83196; NID:g205537; PIDN:ABB48069.1; PID:q205538
A:Crosy-references: GB:M83196; NID:q205537; PIDN:ABB48069.1; PID:q205538
A:Craychik, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Relecule type: mRNA
A;Residues: 73-364, 'NRIRS', 370, 'QKN', 374, 'PSPKGL', 381-751, 'RSMMSOMNAQRR', 764, 'D', 766, WIRESidues: 73-364, 'V', 853, 'NSL', 855, 'LPHRWIRTN', 865, 'W', 867, 'HSQLPDGGD', 877, 'Q', 87
A;Cross-references: EMBL: X66840
A;Experimental source: strain Sprague Dawley
C;Superfamily: microtubule-associated protein MAPIB
C;Keywords: microtubule binding; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps 132;
---YNPLIMRLQAGVMASPPPPG 2483
                                    2268 PAEGPVYLGKPAAAKASGAGGPPRPELPAGGAREEPLSTTAPPAVIKEAPVAQAPAPPPG 2327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 ERSQELHLRPESHSYLPELGKSEMEFIESKRPRLELLPDPLLRPSPLLATGQPAGSEDLT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 KDRSLTGKLEPVSPPSPPHTDPELELVPPRLSK --- EELIQNMDRVDREITMVEQQISKL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 KKKQQQLEEEAAKPPEPEKPVSPPPIESKHRSLV----QIIYDENRKKAEAAHRILE-- 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  398 DKAGKKHLK-EKISKLEE---KKDKEKKEIKKERKELKKE------
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2444 PLTNRVWEDRP----SSAGSTPFP----
                                                                                                                 2484 -LPA-----GSGPLAGP 2494
                                                                                                                                                                        2328 OKPAGDAAAGSGSGVLGRP 2346
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	Db 2594
m	Qy 220
DVCMADPEGLSSESGRVERLERGRPGRRAPGRAKFASPARRL	
.// VDXAGGVSGTHHPRVGHDPPPTPLPDPRPSPP	7152 du
V-KLGGEAAHLPHLRPLPESQPSSSPLLQTAPGVKGHQRVVTLAQHISEVITQ	7
57 VGRPGATGGPCPMADETPPTSASDSGSSQSDSDVPPETEECPSITAEAALDSDEDGDFLP 2516	Db 245
1. LGYHGSSYSPEGVEPVSPSPSLTHDKGLPKHLEELDKSHLEGELRPKQPGP 2093	Qy 2041
6 EAGPOGCATDPRPHCGELSPSFLNPPLPPSTDDSDLSTEEARLAGKGGRRR 2456	Db 2406
ю	Qy 199
	Db 235
ARPERPRADIGHAFLAKPPARSGLEPASSPSKGSEPRPLV	Qy 194
	Db 2291
.1 ATFPPATHCPLGGTLDGVYPTLMEPVLLPKEAPRV 1945	Qy 191
	Db 2264
PASHSHAHQHSPISPRTQDALQQRPSVLHNTGMKGIITAVEPSKPTVLRSTSTSSPV	Qy 1851
:	Db 2222
11 TSSSERERDRDRERERDRDREREKSILTSTTTVEHAPIWRPGTEOSSGSSGSGGGGSSSR 1850	Qy 179
:    :    :    :    :    :  :	Db 2164
PTAPOP	Qy 175
	Db 2108
8SSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAM 1755	Qy 1718
:  :     :     :     :     : :    : :      : :      : :	Db 2048
)7 HNTATAMAQR1717	Qy 1697
	Db 1991
64ALENROTITNDXITSQQMH 1696	Qy 1664
:  :	Db 193
:0 GVDLYRSHIPLAFDPTSIPRGIPLDAAAAYYLPRHLAPNPTYPH 1663	Qy 1620
:  : : :   :	Db 187
1 TMREPTPRLOEGSLSSSKASODRKLTSTPREIA-KSPHSTVPEHHPHPISPYEHLLRGVS 1619	Qy 1561
:	Db 182
8 SGGSIARGAPVIVPELGKPR	Qy 151
::   :    :    :	Db 176
ı,	Qy 148
EQEITPLOHTPRSPWTSDFKDFQEPLPQKGLEVERWLAESPVGLPPEEEDKLTRSPFEII 17	Db 1703
SI EEDRHIPELPLAPRPLREGSIIOGIPLKIDIGASIIGSKADVKSLIGSPGRIF 1484	C*T \O.

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Compugen Ltd
GenCore version 4.5
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OM protein - protein search, using sw model

8, 2001, 14:32:18; Search time 53.39 Seconds September Run on:

(without alignments) 1614.929 Million cell updates/sec

US-09-522-753-5

Perfect score:

13215 1 MSGSTQLVAQTWRATEPRYP......WDEEPKPLLCSQYETLSDSE 2517 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	Ω	NCR2_HUMAN	NCR2_MOUSE	NCR1_MOUSE	NCR1_HUMAN	NCR1_RAT	BAT2_HUMAN	MAPA_RAT	MAPA_HUMAN	TRX2_HUMAN	MAPB_MOUSE	YCS3_YEAST	MAPB_HUMAN	CA11_HUMAN	TCOF_HUMAN	CA11_CANFA	ANK2_HUMAN	CA17_HUMAN	HRX_MOUSE	CA34_HUMAN	HRX_HUMAN	CA54_HUMAN	DRPL_RAT	CA24_ASCSU	DRPL_HUMAN	NEST_HUMAN	APC_RAT	N214_HUMAN	CA11_CHICK	CA15_HUMAN	APC_HUMAN	CA13_MOUSE	CA14_MOUSE	KI67_HUMAN
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## ALIGNMENTS

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Sande S., Privalsky M.L.; "Identification of TRACS (T3 receptor-associating cofactors), a family of cofactors that associate with, and modulate the activity of,
                                 NCR2_HUMAN STANDARD; PRT; 2517 AA.

Q9Y618; Q9Y5010; Q13354; O00613; O15416;

Q1-OCT-2000 (Rel. 40, Created)

O1-OCT-2000 (Rel. 40, Last annotation update)

O1-OCT-2000 (Rel. 40, Last annotation update)

NUCLEAR RECEPTOR CO-REPRESSOR 2 (N-COR2) (SILENCING MEDIATOR OF RETINOIC ACID AND THYROID HORMONE RECEPTOR) (SMRT) (SMRTE) (THYROID-, RECEPTOR-ASSOCIANTED CO-REPRESSOR) (T3 RECEPTOR-ASSOCIANTED CO-REPRESSOR) (T3 RECEPTOR-ASSOCIANTED CO-REPRESSOR)
                                                                                                                                                                                                                                                                                                                                                                                 Ordentlich P., Downes M., Xie W., Genin A., Spinner N.B., Evans R.M.; "Unique forms of human and mouse nuclear receptor corepressor SMRT."; Proc. Natl. Acad. Sci. U.S.A. 96:2639-2644(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen J.D., Evans R.M.; "A transcriptional co-repressor that interacts with nuclear hormone
                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97369492; PubMed=9225980;
Margolis R.L., Abraham M.R., Gatchell S.B., Li S.H., Kidwai A.S.,
Breschel T.S., Stine O.C., Callahan C., McInnis M.G., Ross C.A.;
"CDNAs with long CAG trinucleotide repeats from human brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Cervix adenocarcinoma;
MEDLINE=99199215; PubWed=10097068;
Park E.J., Schroen D.J., Yang M., Li H., Li L., Chen J.D.;
"SMTPe, a silencing mediator for retinoid and thyroid hormone receptors-extended isoform that is more related to the nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor corepressor.";
Proc. Natl. Acad. Sci. U.S.A. 96:3519-3524(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM TRAC-1).
                                                                                                                                                                                                                                                                                                                                             TISSUE-Pituitary;
MEDLINE-99178941; PubMed-10077563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM SMRT).
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM SMRT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mol. Endocrinol. 10:813-825(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Cervix adenocarcinoma;
MEDLINE-96008552; PubMed=7566127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-96408715; PubMed-8813722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [3]
SEQUENCE OF 1023-2517 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [5]
SEQUENCE OF 428-613 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nuclear hormone receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptors.";
Nature 377:454-457(1995).
                                                                                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Brain cortex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Fetal liver;
                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
RESULT 1
NCR2_HUMAN
                                                                                                                                                                                                            NCOR2
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                            NUCLEAR RECEPTORS BY PROMOTING CHROMATIN CONDENSATION, THUS PREVENTING ACCESS OF THE BASAL TRANSCRIPTION.
SUBUNIT: FORMS A LARGE CORERESSOR COMPLEX THAT CONTAINS SIN3A/B AND HISTONE DEACETYLASE HEARD AND HEACT. THIS COMPLEX ASSOCIATES WITH THE THYROLD (TR) AND THE RETINOID ACID RECEPTORS (RAR) IN THE ABSENCE OF LIGAND, AND MAY STABILIZE THEIR INTERACTION WITH TFIIB. SUBCELLULAR LOCATION: NUCLEAR.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; SMRT/TRAC-2 (SHOWN HERE) AND TRAC-1, ARE PRODUCED BY ALTERNATIVE SPLICING. TRAC-1, CONTAINS ONLY THE C-TERMINAL RECEPTOR-INTERACTING DOMAIN AND ACTS AS AN
                -!- FUNCTION: MEDIATES THE TRANSCRIPTIONAL REPRESSION ACTIVITY OF SOME
                                                                                                                                                                                                        ANTAREAGON.

TISSUE SPECIFICITY: UBIQUITOUS. HIGH LEVELS OF EXPRESSION ARE DETECTED IN LUNG, SPLEEN AND BRAIN.
INDUCTION: REGULATED DURING CELL CYCLE PROGRESSION
DOMAIN: THE N-TERMINAL REGION CONTAINS REPRESSION FUNCTIONS THAT
ARE DIVIDED INTO THREE INDEPENDANT REPRESSION DOMAINS (RDI, RD2
AND RD3): THE C-FERMINAL REGION CONTAINS THE UNCLEAR RECEPPOR-
INTERACTING DOMAINS THAT ARE DIVIDED IN TWO SEPRARTE INTERACTION
DOMAINS (IDI AND ID2).
SEQUENCE THE TWO INTERACTION DOMAINS (ID) CONTAIN A CONSERVED
SEQUENCE REPERRED TO AS THE CORRE BOX. THIS MOTIF IS REQUIRED AND
SUFFICIENT TO PERMIT BINDING TO UNLIGANDED TR AND RARS. SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 1 SANT DOMAIN (COMPOSED OF SANT-A+SANT-B). SIMILARITY: CONTAINS 2 CORNR BOX. SIMILARITY: BELONGS TO THE N-COR NUCLEAR RECEPTOR COREPRESSORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00249; myb_DNA-binding; 2.
PROSITE; PS50090; MYB_3; 1.
Vacclear protein; Transcription regulation; DNA-binding; Repressor;
Colled coil; Alternative splicing.
DOMAIN 174 215 COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                        FLANKING THE CORNR BOX DETERMINE NUCLEAR HORMONE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COILED COIL (POTENTIAL). INTERACTION WITH SIN3A/B (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISSING (IN ISOFORM TRAC-1). MISSING (IN ISOFORM TRAC-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L -> P (IN REF. 2).
K -> E (IN REF. 2).
L -> W (IN REF. 2).
MISSING (IN REF. 2).
A -> P (IN REF. 2).
SS -> EF (IN REF. 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SANT-A (POTENTIAL).
SANT-B (POTENTIAL).
COILED COIL (POTENTI
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CORNR BOX OF ID2.
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MEDLINE-99178941; Pubmed-10077563;
Ordentlich P., Downes M., Xie W., Genin A., Spinner N.B., Evans R.M.;
Unique forms of human and mouse nuclear receptor corepressor SMRT.";
Proc. Natl. Acad. Sci. U.S.A. 96:2639-2644(1999).
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01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
NUCLEAR RECEPTOR CO-REPRESSOR 2 (N-COR2) (SILENCING MEDIATOR OF
RETINDIC ACID AND THYROLD HORMONE RECEPTOR) (SMRTE) (THYROID-,
RETINDIC-ACID-RECEPTOR-ASSOCIATED CO-REPRESSOR) (T3 RECEPTOR-
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MEDLINE=99199215; PubMed=10097068;
MEDLINE=99199215; PubMed=10097068;
Park E.J., Schroen D.J., Yang M., Li H., Li L., Chen J.D.;
"SMRTRe, a silencing mediator for retinoid and thyroid hormone receptors-extended isoform that is more related to the nuclear receptor orepressor.",
Proc. Natl. Acad. Sci. U.S.A. 96:3519-3524(1999).
-i- FUNCTION: MEDIATES THE TRANSCRIPTIONAL REPRESSION ACTIVITY OF 19
                                                                                                                                                                                                                                        2221 GIEPVSPPEGMTEPGHSRSAVYPLLYRDGEQTEPSRMGSKSPGNTSQPPAFFSKLTESNS
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
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SEQUENCE FROM N.A. (ISOFORM ALPHA AND ISOFORM BETA)
TISSUE-Spleen, and Brain;
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SEQUENCE FROM N.A. (ISOFORM ALPHA).
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
NUCLEAR RECEPTORS BY PROMOTING CHROMATIN CONDENSATION, THUS PREVENTING ACCESS OF THE BASAL TRANSCRIPTION.
SUBUNIT: FORMS A LARGE COREPRESSOR COMPLEX THAT CONTAINS SIN3A/B AND HISTONE DEACETLASES HDACI AND HDAC2. THIS COMPLEX ASSOCIATES WITH THE THYROID (TR) AND THE RETINOID ACID RECEPTORS (RAR) IN THE ABSENCE OF LIGAND, AND MAY STABILIZE THEIR INTERACTION WITH TFIIB.
                                                                                   SUBCELLULAR LOCATION: NUCLEAR.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA (SHOWN HERE) AND BETA; ARE
PRODUCED BY ALTERNATIVE SPLICING.
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HUCHPRILMTRANKKPRILQLPRQRWPRSRSLRPRRSMWE
-> PSPAAPPATVKRDENEY
                                                                                                                                                      DOMAIN: THE N-TERMINAL REGION CONTAINS REPRESSION FUNCTIONS THAT ARE DIVIDED INTO THREE INDEPENDANT REPRESSION DOMAINS (RDI, RDZ AND RD3): THE C'TERMINAL REGION CONTAINS THE NUCLEAR RECEPTOR-INTERACTING DOMAINS THAT ARE DIVIDED IN TWO SEPARATE INTERACTION DOMAINS (ID1 AND ID2).

DOMAINS (ID1 AND ID2).

SEQUENCE REFERRED TO AS THE CORNE BOX. THIS MOTIF IS REQUIRED AND SUFFICIENT TO PERMIT BINDING TO UNLIGANDED TR AND RARS. SEQUENCES FLANKING THE CORNE BOX DETERMINE NUCLEAR HORMONE RECEPTOR
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E -> K (IN AAD20945).
S -> F (IN AAD20944).
I -> IQ (IN AAD20944).
PKLPTEPPRWSSGLPFPI -> QSYRLSPHAGHRLPSH
                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 1 SANT DOMAIN (COMPOSED OF SANT-A+SANT-B). SIMILARITY: CONTAINS 2 CORNR BOX. SIMILARITY: BELONGS TO THE N-COR NUCLEAR RECEPTOR COREPRESSORS
                                                                                                                              TISSUE SPECIFICITY: UBIQUITOUS. ALSO WIDELY EXPRESSED IN EARLY EMBRYOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001005; --
Pfam; PF00249; myb_DNA-binding; 2.
PROSITE; PS50090; MYB_3; 1.
Nuclear protein; Transcription regulation; DNA-binding; Repressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COLLED COIL (POTENTIAL).
INTERACTION WITH SIN3A/B (BY
SANT-A (POTENTIAL).
SANT-B (POTENTIAL).
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EMBL; AF113002; AAD20945.1; -
EMBL; AF125671; AAD22972.1; -
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      PHAADEA -> TRADPL (IN REF. 2).
MISSING (IN REF. 2).
G -> E (IN REF. 2).
GSATSGSITKGLPSTRAADGPSYRGSITHG ->
SPRASOYPGCRRPOLQRLYHPR (IN REF. 2).
A -> S (IN REF. 2).
MISSING (IN REF. 2).
A -> G (IN REF. 2).
TA -> A (IN REF. 2).
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2A58F4DF7B79285B CRC64;
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84.0%; Pred. No. 0;
iive 90; Mismatches 200; I
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Matches 2145; Conservative
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update)
1) (N-COR) (RETINOID X RECEPTOR ; Vertebrata; Euteleostomi; athi; Muridae; Murinae; Mus. thyroid hormone receptor , Torchia J., Gloss B., stroem M., Glass C.K., E 2517 SHORT). 2472 53 AA.

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Mon Sep 10

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                                                                                             Seol W., Choi H.S., More D.D.;

Seol W., Choi H.S., More D.D.;

"Isolation of proteins that interact specifically with the retinoid X receptor: two novel orphan receptors.";

Mol. Endocrinol. 9:72-86(495).

-! FUNCTION: MEDIATES THE TRANSCRIPTIONAL REPRESSION ACTIVITY OF SOME NUCLEAR RECEPTORS BY PROMOTING CHROMATIN CONDENSATION, THUS PREVENTING ACCESS OF THE BAGAL TRANSCRIPTION.

-! SUBUNIT: FORMS A LARGE COREPRESSOR COMPLEX THAT CONTAINS SIN3A/B AND HISTONED DEACEFYLASES HDACI AND HDAC2. THIS COMPLEX ASSOCIATES WITH THE THYROID (TR) AND THE RETINOID ACID RECEPTORS (RAR) IN THE ABSENCE OF LIGAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN: THE TWO INTERACTION DOMAINS (ID) CONTAIN A CONSERVED SEQUENCE REFERRED TO AS THE CORN BOX. THIS MOTIF IS REQUIRED AND SUPFICIENT TO PERMIT BINDING TO UNLIGANDED TR AND RARS. SEQUENCES FLANKING THE CORNR BOX DETERMINE NUCLEAR HORMONE RECEPTOR
                                                                                                                                                                                                                                                                                 SUBCELLURAR LOCATION: NUCLEAR,
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
TILSSUE SPECIFICITY: UBLOUITOUS.
DOMAIN: THE N-TERMINAL REGION CONTAINS REPRESSION FUNCTIONS THAT
ARE DIVIDED INTO THREE INDEPENDANT REPRESSION DOMAINS (RDI, RD2
AND RD3): THE C-TERMINAL REGION CONTAINS THE NUCLEAR RECEPTOR-
INTERACTING DOMAINS THAT ARE DIVIDED IN TWO SEPARATE INTERACTION
DOMAINS (IDI AND ID2):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1349717; Ncorl.
InterPro; IPR01005;
Pfam; PF00249; myb_DNA-binding; 2.
PROSITE; PS50090; MYB_3; 1.
Nuclear protein; Transcription regulation; DNA-binding; Repressor; Coiled coil; Alternative splicing.
DOMAIN 174 216 COILED COIL (POTENTIAL).
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   co-repressor.";
                                             SEQUENCE OF 1792-2453 FROM N.A. (ISOFORM LONG)
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POLY-ALA.
POLY-PRO.
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POLY-SER.
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SANT-B
                                                                                MEDLINE=95280959; PubMed=7760852;
mediated by a nuclear receptor Nature 377:397-404(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U35312; AAB17125.1; -. EMBL; U22016; AAC52168.1; -.
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DB 1; Length 2453;

Score 4187;

31.7%;

Query Match

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--- QVIKVHEPPREDAAPIKPAPPAPPPQNLQPESDAPQQPGSSPRGK 1022
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                                                                                                                                                                     LEGLGPQVELPLYNQPSDTRQYHENIKINQAMRKKLILYFKRRNHARKQWKQKFCQRYDQ 304
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             444; Gaps
                                                          EPRYPPHSLSYPVQIARTHTDVGLLEYQ--HHSRDYASHLSPGSIIQPQRRRPSLLSEFQ 73
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             Indels
Pred. No. 2.3e-129;
; Mismatches 796;
Similarity 41.0%; Pr
13; Conservative 348;
 Best Local Sim
Matches 1103;
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1008	1082	1137	1197	1248	1308	1361	1421	1476 1417	1530	1584	1640	1699	1759	1818	1874	1930	1977	2024 1966
961 PIGTPVSGYALYQRHIKAMHESALLEEQRQRQEQVDLECRSSTSPCST	1023 SRSPAPPADKEAFAAEAQKLPGDPPCWTSGLPFPVPPREVIKASPHAPDPSAFSYAPPGH	1083 PLPLGLHDTARPVLPRPPTISNPPPLISSAKHPSVLERQIGAISQGMSVQLHVPY	1138 SEHAKAPVGPVTMGLPLPMDPKKLAPFSGVKQEQLSPRGQAGPPESLGVPTAQEASVLKG 1	1198 TALGSVPGGSITKGIPSTRVPSDSAITYRGSITHGTPADVLYKGTITRI-IG 	1249 EDSPSRLDRGREDSLPKGHVIYEGKKGHVLSYEGGMSVTQCSKEDGRSSSGPPHETAAPK	1309 RIYDHMEGRVGRAISSASIEGLMGRAIPPERHSPH-HLKEQHHIRGSITQGIPR  : ::  ::  ::   :	1362 SYVEAQEDYLRREAKLIKREGTPPPPPPRDITEAYKTQALGPLKLKPAHEGLVATVKEA : 1:	1422 GRSIHEIPREELRHTPELPLAPRPLKEGSITQGTPLKYDTGASTTGSKKHDVRSL 	1477 IGSPGRTFPPVHPLDVMAD-ARALERACYEESLKSRPGTASSSGGSIARGAPVIV	1531 PELGKPRQSPLTYEDHGAPFAGHLPRGSPVTMREPTPRLQEGSLSSSK-ASQDRK	1585 LTSTPREIAKSPHSTVPEHHPHPISPYEHLLRGVSGVDLYRSHIPLAFDPTSIPRG	1641 IPLDAAAAYYLPRHLAPNPTYPHLYPPYLIRGYPDTAALEN-RQTIINDYITSQQMHHNT	1700 ATAWAQRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAMDRLA	1760 YLPTAPQPFSSR-HSSSPLSPGGPTHLTKPTTTSSSERERDRDRERDREREKSILTST  :            ::::	1819 TTVEHAPIWRPGTEQSSGSSGSGGGGSSSRPASHSHAHQHSPISPRTQDA-LQQR :	1875 PSVLHNTGMKGIITAVEPSKPTVLRSTSSPVRPAATFPPATHCPLGGTLDGVYP	1931 TLMEPVLLPKEAPRVARPERPRADTGHAFLAKPPARSGLEPASSPSK	1978 GSEPRPLVPPVSGHATIARTPAKNLAPHHASPDPPAPPASASDPHRE 2024 
q	oy B	ç G	Oy Dp	Oy Dp	Qy Dp	Oy Op	oy Op	Oy Op	o P	g g	\$ B	Qy Dp	oy ag	OY Db	Oy Dp	Oy Dp	Q B	Oy Db

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2137
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                                                                                                                                                                                                                                                                                                                                                                             2190 --HGAPA-RGSPH----SEGGKRSPEPNKTSVLGGGEDGIEPVSPPEGMTEPG-HSRSA 2240
                                                                                                                                                                                                                                                                                                                                                                                                                    2124 VLHPRPGPRVSPENLVDKSRGSRPGRSPERSHI---PSEPYEPISPPQG---PAVHEKQD 2177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2301 EPEYNISQPGTEIFNMPAITGTGLMTYRSQAVQEHASTNMGLEAIIRKALMGKYDQWEE- 2359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2360 ----SPPLSANAFNPLNASASLPAAMPITAADGRSDHTLTSPGGG-GKAKVSGRPSSRK 2413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2296 HGVVMSHPV---GIMPGSASTSV----VTSSEARRDEGEPSPHAGVCKPKLINKSNSRK 2347
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2025 KTQSKPFSIQELELRSLGYHGSSYSPEGVEPVSPVSSPSLTHDKGLPKHLEELDKSHLEG 2084
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Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XIV
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
DNA Res. 6:197-205(1999).
[3]
SEQUENCE OF 974-2440 FROM N.A.
MEDLINE=99375328; PubMed=10444336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1967 GSQSSDSS-----SSLSSHRYETASDAIEVISPASSPAPPQEKPQAYQPDMVKANQAEN
                                                                                                                                                                   2085 ELRPKQPGPVKLGGEAAHLPHLR-----PLPESQPSSSPLLQT--APGVKGHQRVVTLAQ
                                                                                                                                                                                                                                                                                        TISSUE-Fetal brain;
MEDLINE-98393736; PubMed-9724795;
Wang J., Hoshino T., Redner R.L., Kajigaya S., Liu J.M.;
Wang J., Hoshino T., Redner R.L., active myeloid leukemia, represses "ETO, fusion partner in t(8;21) acute myeloid leukemia, represses transcription by interaction with the human N-COR/mSin3/HDAC1 complex.";
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bustaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2406 ----LSSTPPTQIACAPSAITQAAPHQONRIWEREPAPLLSAQYETLSDSD 2452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2472 QAGVMASPPPPGLPAGSGPL--AGPH---HAWDEEPKPLLCSQYETLSDSE 2517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCRI_HUMAN STANDARD; PRT; 2440 AA. 075376; Q9UPV5; Q9UQ18; Q9UC181. 40, Created) 01-OCT-2000 (Rel. 40, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) NUCLEAR RECEPTOR CO-REPRESSOR 1 (N-COR1) (N-COR).
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SEQUENCE FROM N.A.
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HUMAN
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
                              "Localization of the human nuclear receptor co-repressor (NN-COR) gene between the CMTIA and the SMS critical regions of chromosome
                                                                                                                                         SUBUNIT: FORMS A LARGE COREPRESSOR COMPLEX THAT CONTAINS SIN3A/B AND HISTONE DEACETYLASES HDACI AND HDAC2. THIS COMPLEX ASSOCIATES WITH THE THYROID (TR) AND THE RETINOID ACID RECEPTORS (RAR) IN THE
                                                                                               OF SOME
                                                                                                                                                                                       ABSENCE OF LIGAND.
SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DOMAIN: THE N-TERMINAL REGION CONTAINS REPRESSION FUNCTIONS THAT
ARE DIVIDED INTO THREE INDEPENDANT REPRESSION DOMAINS (RD1, RD2
AND RD3). THE C-TERMIRAL REGION CONTAINS THE NUCLEAR RECEPTOR-
INTERACTING DOMAINS THAT ARE DIVIDED IN TWO SEPARATE INTERACTION
DOMAIN: THE TWO INTERACTION DOMAINS (ID) CONTAIN A CONSERVED
SEQUENCE REPEREED TO AS THE CORNE BOX. THIS MOTIF IS REQUIRED AND
SUFFICIENT TO PERMIT BINDING TO UNLIGANDED TR AND RASS. SEQUENCES
FLAMKING THE CORNE BOX DETERMINE NUCLEAR HORMONE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 1 SANT DOMAIN (COMPOSED OF SANT-A+SANT-B). SIMILARITY: CONTAINS 2 CORNR BOX. SIMILARITY: BELONGS TO THE N-COR NUCLEAR RECEPTOR COREPRESSORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nuclear protein; Transcription regulation; DNA-binding; Repressor; Coiled coil.
                                                                                                             NUCLEAR RECEPTORS BY PROMOTING CHROMATIN CONDENSATION, THUS PREVENTING ACCESS OF THE BASAL TRANSCRIPTION.
                                                                             Genomics 59:339-341(1999).
-1- FUNCTION: MEDIATES THE TRANSCRIPTIONAL REPRESSION ACTIVITY
Nagaya T., Chen K.-S., Fujieda M., Ohmori S., Richer J.K., Horwitz K.B., Lupski J.R., Seo H.; "Localization of the human nuclear receptor co-repressor (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60A4D7964D00EDAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERACTION WITH SIN3A/B. COILED COIL (POTENTIAL). SANT-A (POTENTIAL).
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PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY - CLD.
POLY - ALA.
POLY - PRO.
POLY - SER.
L - > V (IN REF. 2).
PP - > SS (IN REF. 2).
V - > R (IN REF. 2).
C - > H (IN REF. 2).
C - > H (IN REF. 2).
S WW; 60A4D7964D00EDAB (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERACTION WITH ETO.
CORNR BOX OF ID1.
CORNR BOX OF ID2.
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Pfam: PF00249; myb_DNA-binding; 2.
PROSITE; PS50090; MYB_3; 1.
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                                                                                                                       --EGLRA-SADAKKDPAFGGKHEAPSSPISGQPCGDDQNASPSKLSKEELIQSMDRVDR 190
                                                                                                                                                                                HRILEGLGPQVELPLYNQPSDTRQYHENIKINQAMRKKLILYFKRRNHARKQWKQKFCQR 301
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TEEPPPPLPPPPEPISTEPVETSRWIEEEMEVAKKGLVEHGRNWAAIAKWVGTKSEAQCK 663
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EITMVEQQISKLKKKQQQLEEEAAKPPEPEKPVSPPPIESKHRSLVQIIYDENRKKAEAA
                                                                                                       LLATGQPAGSEDLTKDRSLTGKLE-PVSPPSPPHTDPELELVPPRLSKEELIQNMDRVDR
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                                            PGNERSQELHLRPESHSYLPELGKSEMEFIESKRPRLELLPD.
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LP 1019	113	NQ 1071	AS 1193 EG 1130	124	118	TA 1305 : IS 1242	og 1358	   0G 1299	TV 1418  : TI 1344	DV 1473	: I NV 1403	AP 1527 m- 1462	140 140	QD 1582 : HE 1516	IP 1638 :  MP 1573	169	 MQ 1624	MD 1756     MD 1676	IL 1815   IA 1730	QR 1874	 OR 1771	YP 1930	AS 1830	196	SG 1890	AS 2017	
CGTSKSPNREQLITNL	PGHPLPLGLHDTARPVLPRPPTISNPPPLISSAKHPSVLERQIGAISOGMSVOLH	EGVKLPTTKPTRPPPLIPSSKTTVASEK-PSFIMGGSISQGTPGTYLTSH	VPYSEHAKAP-VGPVTMGLPLPMDPKKLAPFSGVKQEQLSPRGQAGPPESLGVPTAQEAS   1:	VLRGTALGSVPGGSITKGIPSTRVPSDSAITYRGSITHGTPADVLYKGTITR  :      ::     :   :::: :  :	VVRGTA-GAIQEGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGIPTEALVKGSI	IIGEDSPSRLDRGREDSLPKGHVIYEGKKGHVLSYEGGMSVTQCSKEDGRSSSGPPHETA :     ::   ::	APKRTYDMMEGRVGRAISSASIEGLMGRAIPPERHSPH-HLKEQHHIRGSITOG		IPRSYVEAQEDYLRREAKLIKREGTPPPPPRDLTEAYKTQALGPLKIKPAHEGLVATV   :  -	KEAGRSIHEIPREELRHTPELPLAPRPLKEGSITQGTPLKYDTGASTTGSKKH	KEMGRSIHEIPRODILTQESRKTPEVVQSTRPIIEGSISQCTPIKEDNN-SGQSAIKHNV	RSLIGSPGRIFPPVHPLDVMAD-ARALERACYEESLKSRPGTASSSGGSIARGAP	AULITOFORDONGIFFELDIYFENINY YENGAL ELVANGEL VASARIISVYSSGFSVLRS	VIVFELGRERUSFLITEDHGAFFAGHLERGSPVIMREPTFRLQEGSLSSSRASQD :	RKLTSTPREIAKSPHSTVPEHHPHPISPYEHLLRGVSGVDLYRSHIPLAFDPTSIP 	RGIPLD-AAAAYYLPRHLAPNPTYPHLYPPYLIRGYPDJAALEN-RQTIINDY1FSQOMH	HRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQT1LNDY1TSQQ	HNTATAMAQRADMLKGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAMD 	RLAYLPTAPQPFSSR-HSSSPLSPGGPTHLTKPTTTSSSERERDRDRERDRDREREKSIL  :  :	TSTTTVEHAPIWRPGTEQSSGSSGSSGGGGSSSRPASHSHAHQHSPISPRTQDA-LQQR	::: :	PSVLHNTGMKGIITAVEPSKPTVLRSTSTSSPVRPAATFPPATHCPLGGTLDGVYP	. 년	TLMEPVLLPKEAPRVARPERPRADTGHAFLAK 	APQMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSG	PPARSGLEPASSPSKGSEPRPLVPPVSGHATIARTPAKNLAPHHASPDPPAPPAS 	THE STATE OF STATE OF THE PROPERTY OF THE PROP
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[1]
SEQUENCE FROM N.A.
TISSUE-Brain;
MEDLINE-99371771; PubWed-10441327;
Boutell J.M., Thomas P., Neal J.W., Weston V.J., Duce J., Harper P.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEAR RECEPTORS BY PROMOTING CHROMATIN CONDENSATION, THUS PREVENTING ACCESS OF THE BASAL TRANSCRIPTION.
SUBUNIT: FORMS A LARGE COREPRESSOR COMPLEX THAT CONTAINS SIN3A/B AND HISTONE DEACETYLASES HDACI AND HDAC2. THIS COMPLEX ASSOCIATES WITH THE THYROID (TR) AND THE RETINOID ACID RECEPTORS (RAR) IN THE ABSENCE OF LICAND (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DOMAIN: THE N-TERMINAL REGION CONTAINS REPRESSION FUNCTIONS THAT
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 --VKGH 2129
                        1998 KANQAENDPTRQYEGP-----LHHYRP---QQESPSPQQQLPPSSQAEGMGQVPRT 2045
                                                                                     2183 LYLPPPD-----HGAP-ARGSPH-----SEGGKRSPEPNKTSVLGGGEDGIEPVSPPEGM 2231
                                                                                                                                                                                                  2232 TEPGHSRSAVYPLLYRDGEQTEPSRMGSKSPGNTSQPPAFFSKLTESNSAMVKSKKQEIN 2291
                                                                                                                                                                                                                  2462 FPYNPLIMRLQAGVMASPPPPGLPAGSG-PLAGPH---HAWDEEPKPLLCSQYETLSDSE 2517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2383 FPYNPLTMRM---LSSTPPTPIACAPSAVNQAAPHQQNRIWEREPAPLLSAQYETLSDSD 2439
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"Aberrant interactions of transcriptional repressor proteins with the Huntington's disease gene product, huntingtin.";
Hum. Mol. Genet. 8:1647-1655(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biochem. 264:982-988(1999).
FUNCTION: MEDIATES THE TRANSCRIPTIONAL REPRESSION ACTIVITY OF
                                                                                                                                                        GKYDQWEE-----SPPLSANAFNPLNASASLPAAMPITAADGRSDHTLTSPGGGG--KA
                                                                                                                                                                                                                                                                                                                                                                                                    KVSGRPSSRKAKSPAP - - GLASGDRPPSVSSVHSEGDCNRRTPLTNRVWEDRPSSAGSTP
                                                                   QRVVTLAQHISEVITQDYTRHH----PQQLSAPLPAPLYSFPGA--SCPVLDLRRPPSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCRI_RAT STANDARD; PRT; 533 AA.

OG9WUB5; O70463;
01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
NUCLEAR RECEPTOR CO-REPRESSOR 1 (N-COR1) (FRAGMENT).
DKSHLEGELRPKQPGPVKLGGEAAHLPHLRPLPESQPSSSPLLQTAPG--
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SEQUENCE OF 476-528 FROM N.A.
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DIVIDED INTO THREE INDEPENDANT REPRESSION DOMAINS (RD1, RD2

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RESULT 6
BAT2_HUMAN
                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.ch).
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              AND RD3). THE C-TERMINAL REGION CONTAINS THE NUCLEAR RECEPTOR-INTERACTING DOMAINS THAT ARE DIVIDED IN TWO SEPARATE INTERACTION DOMAINS (IDI AND ID2).

DOMAIN: THE TWO INTERACTION DOMAINS (ID) CONTAIN A CONSERVED SEQUENCE REPERRED TO AS THE CORNR BOX. THIS MOTIF IS REQUIRED AND SUFFICIENT TO PERMIT BINDING TO UNLIGANDED TR AND RARS. SEQUENCES FLANKING THE CORNR BOX DETERMINE NUCLEAR HORMONE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 MVKANQAENESPQQYEGP------LTHYRSQQGSPSPQQQPPLPPSSQ-AEGMGQVP 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 AVHEKQDSMLLLSQRGMDPAEQRSDSRSPGSISYLPYFFTKL-ESTSPMVKSKKQEIFRK 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FDDKVEDHGVVMPHPVGVVPGSASTSV---VTSSETRRDEGDPSPHSGVCKPKLINKSNS 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 2 CORNR BOX.
SIMILARITY: BELONGS TO THE N-COR NUCLEAR RECEPTOR COREPRESSORS
                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF059311; AAC14567.1; -.
PROSITE; PS50090; MYB_3; PARTIAL.
Nuclear protein; Transcription regulation; DNA-binding; Repressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPPD----HGAPA-RGSPH-----SEGGKRSPEPNKTSVLGGGEDGIEPVSPPEGMTEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 PESQSQTVLHPRPGPRVSPENLVDKSRGSRPGKSPERSHI---PSEPYEPISPPGG---P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RLQAGVMASPPPPGLPAGSG-PLAGPH---HAWDEEPKPLLCSQYETLSDSE 2517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.4%; Score 714.5; DB 1; Length 533; 38.5%; Pred. No. 3e-17; Live 68; Mismatches 192; Indels 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> W (IN REF. 2).
-> V (IN REF. 2).
7DF60F8228227EC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORNR BOX OF ID1.
                                                                                                                                                                                                                                                                                                                                                              EMBL; AF124821; AAD32566.1; -.
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Best Local Similarity 38.5%
Matches 205; Conservative
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157
361
484
497
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357 3
484 4
497 4
533 AA;
                                                                                                                                       SPECIFICITY.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                               Banerji J., Sands J., Strominger J.L., Spies T.;
"A gene pair from the human major histocompatibility complex encodes large proline rich proteins with multiple repeated motifs and a single ubiquitin-like domain."
                                                                                                                                                                                                                                                                                                                      Claverie J.-M., Dausset J.,
                                                                                                                                                                                                                                                                                                                                             "Dense Alu clustering and a potential new member of the NF kappa B family within a 90 kilobase HLA class III segment.";
Nat. Genet. 3:137-145(1993).
-!- FUNCTION: UNKNOWN.
                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                  -!- TISSUE SPECIFICITY: LIMITED TO CELL-LINES OF LEUKEMIC ORIGIN
                                    01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2),
                                                                                                                                                                                                                                                                                                        Iris F.J.M., Bougueleret L., Prieur S., Caterina D., Primas G.,
Perrot V., Jurka J., Rodriguez-Tome P., Claverie J.-M., Dausset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2-2.
3 x 50 AA TYPE C REPEATS.
3-1.
3-2.
3-3.
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                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 87:2374-2378(1990)
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2142 AA
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POLY-PRO.
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POLY-GLY.
POLY-PRO.
POLY-PRO.
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EMBL; M33518; AAA35586.1; -.
EMBL; M33512; AAA35586.1; JOINED.
EMBL; Z15025; CAA78744.1; -.
PIR; B35098; B35098.
PIR; S36152; S36152.
MIM; 142580; -.
                                                                                                                                                                         TISSUE=T-cell;
MEDLINE=90192810; Pubmed=2156268;
                                                                                                                                                                                                                                                                                            MEDLINE=93272029; PubMed=8499947;
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                          (Rel. 33, Created)
(Rel. 33, Last seq
                                                                                                                                                                                                                                                                              SEQUENCE OF 1-1860 FROM N.A.
STANDARD;
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1345
1442
1442
1991
1795
154
337
1795
549
                                                                                          Homo sapiens (Human).
                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1340
1398
1436
1982
                       01-FEB-1996
01-FEB-1996
BAT2_HUMAN
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            P48634;
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DOMAIN
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OY 1103 SNPPPLISSAKHPSVLERQIGAISQGMSVQLHVPYSEHAKAPVGPVTMGLPLPMDPKKLA 1162	0 y 1335   IPPERHESENTETRACEPICTRENCHANGEDILARREALKIKEROTPP 1386	Qy 2009 -PDPPAPPASASDPHREKTQSKPFSIQELE 2037
FT CONFLICT 57 57 R -> A (IN REF. 2).  FT CONFLICT 109 109 Q -> S (IN REF. 2).  FT CONFLICT 414 414 P -> PPHRRAGANWRPP (IN REF. 2).  FT CONFLICT 532 532 T -> K (IN REF. 2).  FT CONFLICT 682 682 Q -> K (IN REF. 2).  FT CONFLICT 750 750 E -> D (IN REF. 2).  FT CONFLICT 1055 1035 G -> A (IN REF. 2).  FT CONFLICT 1068 1068 M -> T (IN REF. 2).  FT CONFLICT 1068 1285 P -> K (IN REF. 2).  FT CONFLICT 1068 1285 P -> K (IN REF. 2).  FT CONFLICT 1610 1400 G -> A (IN REF. 2).  FT CONFLICT 1285 1285 P -> A (IN REF. 2).  FT CONFLICT 1400 1400 G -> A (IN REF. 2).  FT CONFLICT 1611 1611 T -> S (IN REF. 2).  FT CONFLICT 1285 1285 M -> C (IN REF. 2).  FT CONFLICT 1611 1611 T -> S (IN REF. 2).  FT CONFLICT 1729 1729 G -> A (IN REF. 2).  FT CONFLICT 1611 1611 T -> S (IN REF. 2).  FT CONFLICT 1729 1729 G -> A (IN REF. 2).	Length 2142;  13. Indels 912; Ge 13. Indels 912; Ge 14. Indels 912; Ge 14. Indels 912; Ge 14. Indels 912; Ge 15. Indels 912; Ge 16. Indels 912; Ge 17. Indels 912; Ge 18. Indels 912; Ge 18. Indels 912; Ge 18. Indels 912; Ge 19. Indels 912; Ge	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2

DOMAIN: THE BASIC REGION CONTAINING THE REPEATS MAY BE RESPONSIBLE FOR THE BINDING OF MAPIA TO MICROTUBULES.

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J. Biol. Chem. 267:16561-16566(1992).

-! FUCUTION: STRUCTURAL PROTEIN INVOLVED IN THE FILAMENTOUS

-! CROSS-BRIDGING BETWEEN MICROTUBULES AND OTHER SKELETAL ELEMENTS.

-! SUBDINT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE

WITH MAPLA AND MAPLB PROTEINS.

-! TSSUE SPECIFICITY: BRAIN, HERRT AND MUSCLE.

-! DEVELOPMENTAL STAGE: EXPRESSED LATE DURING NEURONAL DEVELOPMENT

-! APPEARING WHEN AXONS AND DENDRITES BEGIN TO SOLIDIFY AND STABILIZE
----- PPS-DL 2183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------EPVSPPEGMTEPGHSRSAV-YPLLYRDGEQTEPSRMGSKS 2261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1902 AGGVLYPPPSFLYSPAFCPSPLPDTSLLQVRQ--------DLPSP-SDF 1941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1993 SLLPVGPALQPPSLA------RPFPAS 2029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1727 DRGTEPGPIRPS-HRPGPPVQF-GTSDKDSDLRLVVGDSLKAEKELTASVTEAIPVSRDW 1784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1785 ELLP---SAAASAEPQSKNLDSGHCVPEPSSSGQRLYPEVFYGSAGPSSSQISGGSHGLS 1841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1842 ITSKQWRLRPGTPSLHPYRSQPLYLPPGPAPPSALLSGVALKGQFLDFSTMQATELGKLP 1901
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Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Langkopf A., Hammarback J.A., Mueller R., Vallee R.B., Garner C.C., "Microtubule-associated proteins lA and LC2. Two proteins encoded in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2262 PGNTSQPPAFF----SKLTESNSAMVKSKKQEINKKLNTHNRNEPEYNISQPGTEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NASASLPAAMPITAADGRSDHTLTSPGGGGKAKVSGRPSSRKAKSPAPGLASGDRPPSVS
                                                                                                                                                                          1633 QSDSGVDLSGDSQVSSGPCSQRSSP----DGGLKGAAEGPPKRPGGSSPLNAVPCEGPPG
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                                                                                                  LRSLGYHGSSYSPEGVEPVSPVSSPSLTHDKGL-----PKH-----LEELDKSHLEG
                                                                                                                                                                                                                                                   ELRPKOPGPVKLGGEAAHLPHLRPLPESQPSSSPLLQTAPGVKGHORVVTLAQHISEVIT
                                                                                                                                                                                                                                                                                                                                                                                                   QDYTRHHPQQLSAPLPAPLYSFPGASCPVLDLRR-------
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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01-FEB-1994
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P34926;
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THEIR MORPHOLOGY

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132;
                        PTM: VARIOUS SERINE RESIDUES MAY BE PHOSPHORYLATED BY CAMP KINASE. PTM: LC2 IS COEXPRESSED WITH MAPIA. IT IS A POLYPEPTIDE GENERATED FROM MAPIA BY PROTEOLYTIC PROCESSING. IT IS FREE TO ASSOCIATE WITH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---EGRKEEK 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDAKKDEKRKDTKPEVKKLSKPDLKPFTPEVRKTLYKAKAPGRVKVDK------GRA 491
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2465 2774 MAPI LIGHT CHAIN LC2.
309 496 LYS-RICH (BASIC).
336 541 11 X 3 AA REPEATS OF K-K-[DE].
415 417 2.
424 426 4.
431 433 6.
440 442 9.
440 445 9.
440 445 9.
539 541 11.
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20.5%; Pred. No. 2.4e-09;
ive 278; Mismatches 1002;
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                                                                        BOTH MAPIA AND MAPIB. SIMILARITY: TO MAPIB.
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2774 AA;
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Matches 553; Conserv
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q	752	:     :     :     :     :     :     :     :     :
οy	580	
q	812	NMVAAPLAEEEHVSSATSITECDKLSSFATSVAEDQSVASLTAPQTEETGKSSLL 866
λo δ	634	VSQCKNFYFNYKRQNLDEILQQHKLKMEKERNARRKKKKRAPAAASEE
9	98	LDTVTSIPSSRTBATQGLDYVPSAGTISPTSSLEE 901
ýo.	694	VVEDEEMEASGVSGNEEEMVEEAEALHASGNEVPRGECSGPATVNNSSDTES 75
g	905	DKGFKSPPCEDFSVTGESEKKGETVGRG-LSGEKAVGKEEKYV- 943
οχ	751	IPSPHTEAAKDTGONGPKPPATLGADGPPPGPPTPPRRTSRAPIEPTPASEATGAPTP 808
q	944	VTSEKLSGQYAAVFGAPGHTLPPGEPALGEVEERC-LSPDDSTVKMASP-P 992
δ,	808	854
g	993	PSGPPSAAHTPFHQSPVEDKSEPRDFQEDSWGETKHSPGVSKEDSEEQTVKPGPEEGTSE 1052
λο i	855	
2	1053	
δ,	903	TPTGDPRANASPQKPLD 962 :  : :
g	1112	TSTEEATEPQKDEVLRFTDQSLSPEDAESLSVLSVVSPDTTKQEATPRSPCS 1163
οy	963	LKQLKQRAAAIPPIQVTKVHEPPREDAAPTKPAPPAPPPPQNLQPESDAPQQPGSSPRGK 1022
q	1164	LKEQQPHKDLWPMVSPEDTQSLSFSEESPSKET-SLDISSKQLSPESLGTLQFGELNLGK 1222
οy	1023	EAFAAEAQKLPGDPPCWTSGLPFPVPPREVIKASPHAPDP-SAF
qq	1223	EERGPVMKAEDDSCHLAPVSIPEPHRATVSPSTDETPAGTLPGGSFS 1269
ογ	1077	YAPPGHPLPLGLHDTARPVLPRPTISNPPP 1107
q	1270	HSALSVDRKHSPGEITGPGGHFMTSDSSLTKSPESLSSPAMEDLAVEWEGKAPGKEKEPE 1329
ò	1108	LISSAKHPSVLERQIGAISOGMSVQLHVPYSEHAKAP 1144
Q	1330	L   : : : : : : : : : : : : : : : :
Οy	1145	VGPVTMGLPLPMDPKKLAPFSGVKQEQLSPRGQ-AGPPESLGVPTAQEASVLRGTA 1199
g	1390	AELDKGPEPKEKDLDREDQGQRAGPPAEKDKASEQRUTD 1428
οy	1200	LGSVPGGSITKGIPSTRVPSDSAITYRGSITHGTPADVLYKGTITRIIGED- 1250
QQ	1429	
οy	1251	RLDRGREDSLPKGHVIYE
qq	1474	
δy	1285	SVTQCSKEDGRSSSGPPHETAAPKRTYDMMEGRVGRAISSASIEGLMG 1332
QQ	1534	:      :    :
δ	1333	IPRSYVEAQ
qq	1592	EESPAEGSKAREQEKKYWKEQDVVQGWRETSPIRGEPVGGQKEPVPAWEGK 1642
δý	1384	PPPPPPSRDLTEAYKTQALGPLKLKPAHEGLVATVKEAGRSIHEIPR 1430
qq	1643	SPEQEVRYWRDRDITLQQDAYWRELSCDRKVWFPHELDGQGARPRYCEERESTFLDEGFD 1702
οy	1431	EELRHTPELPLAPRPLKEGSITOGTPLKYDTGSGTTGSKKHDVRSLIGSPGRTF 1484

qq	1703	EQEITPLQHTPRSPWTSDFKDFQEPLPQKGLEVERWLAESPVGLPPEEEDKLTRSPFEII 1762
οy	1485	-PPVHPLDVMADARALERACYEESLKSRPCTASS 1517
qq	1763	SPPASSPPEMTGQRVPSAPGQESPVPDTESTAPMRNEPTTPSWLAEIPPWVPKDRPLPP 1820
δλ	1518	SGGSIARGAPVIVPELGKPRQSPLTYEDHGAPFAGHLPRGSPV 1560
QQ	1821	APLSPAPAPPTPAPEPHTPVPFSWGLAEYDSVVAAVQEGAAELEGGPYSPLGKDY 1875
οy	1561	TWREPTPRLQEGSLSSSKASQDRKLJSTPREIA-KSPHSTVPEHHPHPISPYEHLLRGVS 1619
qq	1876	RKAEGEREGEGGAGAPDSSSFSPKVPEAGESLATRDTEQTEPEQREPTPYPDERSFQ 1932
δλ	1620	GVDLYRSHIPLAFDPTSIPRGIPLDAAAAYYLPRHLAPNPTYPH 1663
Q	1933	YADIYEQMMLTGLGPACPTREPPLGASGDWPPHLSTKEEAAGCNTSAEKETSSPASPQ 1990
Qy	1664	LYPPYLIRGYPDTAALENROTIINDYITSQOMH 1696
qo ·	1991	NLQSDTPAFSYASLAGPAVPPRQEPDPGPNVEPSITPPAVPPRAPISLSKDLSPPLN 2047
δλ	1697	HNTATAMAQR1717
qq	2048	GSTVSCSPDRRTPSPKETGRGHWDDGTNDSDLEKGAREQPEKETRSPSPHHPMPMGHSSL 2107
δy	1718	HLPVLV
qq	2108	WPETEAYSSLSSDSHLGSVRPSLDFPASAFGFSSLQPAPPQLPSPAEPRSAPCGSL 2163
Qy	1756	E
ΩD	2164	AFSGDRALALVPGTPTRTRHDEYLEVTKAPSLDSSLPQLPSPSSPGGPLLSNLPRPAS 2221
ΟŅ	1791	TSSSERERDRDRERERSILTSTITVEHAPIWRPGTEQSSGSSGSGGGGSSSR 1850
qq	2222	PALSEGSSSEATTPVISSVAERFPPGLEAAEQSAEGLGSGKE 2263
οy	1851	PASHSHAHQHSPISPRTQDALQQRPSVLHNTGMKGIITAVEPSKPTVLRSTSTSSPVRPA 1910
qq	2264	S-LWDLTPL
ΟŊ	1911	ATFPPATHCPLGGTLDGVYPTLMEPVLLPKEAPRV 1945
qq	2291	PAPAPAPGLP-GDLGDGTLPCRPECTGELTKKPSPFLSPSGDHEANGPGETSLNPPGFVT 2349
Óγ	1946	RPL
qq	2350	ATAEKEEAEAPHAWERGSWPEGAERSSRPDTLLSSEQPLRPGKSSGGPPCSLSSEV 2405
Qy	1995	ARTPAKNLAPHHASPDPPAPPASASDPHREKTQSKPFSIQELELRS 2040
QQ	2406	EAGPGCATDPRPHCGELSPSFLNPPLPPSTDDSDLSTEFARLAGKGGRRR 2456
δy	2041	LGYHGSSYSPEGVEPVSPVSPSITHDKGLPKHLEELDKSHLEGELRPKQPGP 2093
Ωp	2457	VGRPGATGGPCPMADETPPTSASDSGSSQSDSDVPPETEECPSITAEAALDSDEDGDFLP 2516
ΟŊ	2094	ES.
Dp	2517	VDKAGGVSGTHHPRPGHDPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP
ΟŊ	2146	DYTRHHPQQLSAPLPAPLYSFPGASCPVLDLRRPPSDLYLPPPDHGAPARGSPHSEG 2202
QQ	2551	DVCMADPEGLSSESGRVERLREKGRPGRRAPGRAKPASPARRL 2593
δy	2203	GRRSPEPNKTSVLGGEDGIEPVSPPGGMTEPGHSRSAVYPLLYRDGEGT 2252
qq	2594	DIRGKRSPIPGKGPVDRISRIVPRPRSIPSQVISAEEKDGHSPMSKGLVNGLKA 2647
ΟŊ	2253	EPSRMGSKSPGNTSQPPAFFSKLTESNSAMVKSKKQEINKKLNTHNRNEP 2302
qq	2648	GSTALGSKGGSGPPVYVDLAYIPNHCSGKTADQDFFRRVRASYYVVSGNDP 2698

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                                                                                                                                                                                                                                                                                                                                                                                                                     (MAP1A) gene and its assignment to human chromosome 15.";
J. Neurosci. Res. 40:820-825(1995).
-!- FUNCTION: STRUCTURAL PROTEIN INVOLVED IN THE FILAMENTOUS
CROSS-BRIDGING BETWEEN MICROTUBULES AND OTHER SKELETAL ELEMENTS.
-!- SUBUNTI: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE WITH MAP1A AND MAP1B PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: BRAIN. DOMAIN: THE BASIC REGION CONTAINING THE REPEATS MAY BE RESPONSIBLE FOR THE BINDING OF MAPIA TO MICROTUBULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PTM: VARIOUS SERINE RESIDUES MAY BE PHOSPHORYLATED BY CAMP KINASE.
-!- PTM: LC2 IS COEXPRESSED WITH MAPIA. IT IS A POLYPEPTIDE GENERATED FROM MAPIA BY PROTEOLYTIC PROCESSING. IT IS FREE TO ASSOCIATE WITH BOTH MAPIA AND MAPIB.
-!- SIMILARITY: TO MAPIB.
                                                                                                                                                                                                                                                                                                                                                                                               Fukuyama R., Rapoport S.I.;
"Brain-specific expression of human microtubule-associated protein 1A
                                                                                                                                                                                                    MEDLINE-97001161; PubMed-8812494;
Fink J.K., Jones S.M., Esposito C., Wilkowski J.;
"Human microtubule-associated protein la (MAPIA) gene: genomic
organization, CDNA sequence, and developmental- and tissue-specific
                                          MAPA_HUMAN STANDARD; PRT; 2805 AA.
P78559; Q15882; Q12973;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2].
                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAP1 LIGHT CHAIN LC2.
LYS-RICH (BASIC).
1.
2.
3.
4.
5.
                                                                                                                                                                                                                                                                                               TISSUE-Fetal muscle;
Chiannilkulchai N., Pasturaud P., Richard I., Auffray C.
                                                                                                                                                                                                                                                                                                                                   Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-95356255; PubMed-7629894;
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1607-1883 FROM N.A.
                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                    SEQUENCE OF 134-419 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U38292; AAB41133.1; --
EMBL; 247038; CAA87104.1; --
EMBL; U14577; AAA81362.1; --
MIM; 600178; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U38291; AAB41132.1; -.
                                                                                                                                                                                                                                                               Genomics 35:577-585(1996).
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422
429
433
4438
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                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                   NCBI_TaxID=9606;
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309
415
415
420
427
431
440
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                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Brain;
                                                                                                                                                                                                                                                     expression
                                                                                                                                                                                                                                                                                                                         Beckmann
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                                                                                                                    MAP1A.
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                                MAPA_HUMAN
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                     RESULT
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91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1139 RYPDRSLSPEDXESLSVLSVPSPDTXXQEPTPKSPCGLXEQXLHKDRWXE-----VSP 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : : ||| | | | : | || | | EDTQSLGTLQFGELNLGKEEMGHLMQAEDTSHHTA 1251
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Indels
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9027AF693EFFBE3A CRC64;
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ilarity 21.5%; Pred. No. 9.4e-08;
Conservative 188; Mismatches 756;
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1650
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1650
1690
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Matches 420;
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	713 NEEEMVEEAEALHASGNEVPRGECSGPATVNNSSDTESIPSPHTEAAKDTGONGPKPPAT	1801	773 LGADGPPFGPPTRTSRAPIEPTPASEATGAPTPPPAPPSPSAP 818	819 PPVVPKEEKEEETAAAPPVEEGEEOKPPAAEELAVDTGKAE-EPVKSECTEEAEE 872		873GPAKGKDAEAAEATAEGALKAEKKEGGSGRATTAKSSGAPQDSD 916	1968 ADIYEQMMLTGLGPACPTREPPLGAAGDWPPCLSTKEAAAGRNTSAEKELSSPISPKSLQ 2027	917 SSATCSADEVDEAEGGDKNRLLSPRPSLLIPTGDPRANASPQKPLDL 963 17 SSATCSADEVDEAEGGDKNRLLSPRPSLLIPTGDPRA	964 KQLKQRAAAIPPIQVTKVHEPPREDAAPTKPAPPAPPPQNLQPES 1009	2083 SCSPDRRSPSPKESGRSHWDDSTSDSELEKGAREQAEKEAQSPSPPHPIPMGSPTLWPET 2142	1010 DAPQOPG-SSPRGKSRSPAPPADKEAFAAEAQKLPGDPPCWTSGLPF- 1055	2143 EAHVSPPLXSHLGXARPSLDFPASAFGFSSLEXAPPQXPSPAEPRSAPCGSLAFS 2197	1056PVPPREVIKASPHAPDPSAFSYAPPGHPLPLGLHDTAR 1093	2198 GDRALALAPGPPTRTRYDEYLEVIKAPSLDSSLPQLPSPSSPGXPLLSNLPRPAS 2252	1094 PVLPRPPTISNPPPLISSAKHPSVLERQIGAISQGMSVQLHVPYSEHAKAPVGPV 1148	TEMOTO TO THE PROPERTY OF THE	2313 SIDLALAPAPSIPGDMGDGILPCHLECSEAATEKPSPFQ-VPSEDCAANGPTETSPNPPX	1185 GVPTAOEASVLRGTALGSVPGGSITKGIPSTRVPSDSAITYRGSITHGTPADVLYKG 1241		1242 TITRIIGEDSPSRLDRGREDSLPKGHVIYEGKKGHVLSYEGGMSVTQCSKEDGRSSSGPP 1301	2414GSGGPP 2423	1302 HETAAPKRIYDMMEGRVGRAISSASIEGLMGRAIPPERHSPHHLKEQHHIRGSITQG 1358	2424RELSPS 2451	1359IPRSYVEAQEDYLRREAKLIKREGTPPPPPPPPRDLTEAYKTQALGPL 1405	2452 FLNPPLPPSIDDRDLSTEEVRLVGRGGRRRVGGPGTTGXPXPVTDETPPTSASDSG 2507	1406 KLKPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGSITQGTPLKYDTGAST 1465	2508SGSDSDVPPETEECPSITAEAALDSDEDGDFLPVDKXGGV 2548	1466 TGSKKHDVRSLIGSPGRTFPPVHPLDVMADARALERACYEESLKSRPGT 1514	2549 SGTHHPRPGHDPPPLPQPDXRPSPP-RPDVCMADPEGLSSESGRXERLRXKEKVQGRVG- 2606	ASSSGGSIARGAPVIVPELGKPRQSPLTYEDHGAPFAGHLPRGSPVTMREPTPRLQEGSL		1575 SSSKASQDRKLTSTPREIAKSPHSTVPEHHPHPISPYEHLLRGVSGVDLYRSHIPL 1630
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1631 AFDPTS-IPRGIPLD----AAAAYYLPRHLAPNPTYPHLYPPYLIRGYPDTAAL----- 1679
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MEDLINE-20105772; PubMed-10637508;
HUNTSMBD D.G., Chin S.-F., Muleris M., Batley S.J., Collins V.P.,
Wiedemann L.M., Aparicio S., Caldas C.;
Willer, the second human homolog of the Drosophila trithorax gene, maps to 19q13.1 and is amplified in solid tumor cell lines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2640 VSRXPXRSRSXTSQVTPAE-EKDGHSPMSKGLVNGLKAGPXALSSKGSSGAPVY---VDL 2695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (LONG ISOFORM).
Lamardin J.E., McCready P.M., Adamson A.W., Burkhart-Schultz K.,
Garcia E., Kyle A., Ramirez M., Stilwagen S., Garnes J., Danganan L.,
Bruce R., Quan G., Montgomery M., Ow D., Kobayashi A., Olsen A.O.,
Carrano A.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can
                                                                                                                                                                                                                             TEX2_HUMAN STANDARD; PRT; 2715 AA.

QUUNNS; QOSK25; O95836; QOY669; QOY668; O15022;

Q10-0CT-2000 (Rel. 40, created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last sequence update)
TRITHORAX HOMOLOG 2 (MIXED LINEAGE LEUKEMIA GENE HOMOLOG 2 PROTEIN).
TRX2 OR HRX2 OR MLL2 OR KIAA0340.
HOMO Sapiens (Human).
BUKATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TAXID=9606;
                                                                         ---ANGEPSRAVLDALLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Angrand P.O., Valvatne H., Jeanmougin F., Adamson A., van der Hoeven F., Olsen L., Tekotte H., Huang N., Poch O., Lamerdin J., Chambon P., Losson R., Stewart A., Aasland R.; Mammalian trithorax- and ASHI-like proteins: putative chromatin regulators which contain PHD fingers and SET domains."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARTIAL SEQUENCE FROM N.A. (LONG AND TRUNCATED ISOFORMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence analysis of a 1 Mb region in human 19q13.1."; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 816-2715 FROM N.A. (LONG ISOFORM).
TISSUE-Brain;
MEDLINE-97349984; PubMed-9205841;
                                                          2696 AYIPNHWSGKTADLDFFRRVRASYYVVSGNDP----
                                                                                                        1680 -----ENRQ---TIINDYITS-----QQMH 1696
                                                                                                                               2744 KAQWGENLQVKVTLIPTHDTEVTREWYQQTH 2774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     code for large proteins in vitro.";
DNA Res. 4:141-150(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (LONG ISOFORM).
                                                                                                                                                                                                                   TRX2_HUMAN
                                                                     g
                                                                                                        δy
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPQEPAPVPS -> PLSQSLLLPMTLQLSLSLGQWAAPTTS
ACLDSPLWSPLLLRPRCPLFGLQL (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSARSSRVIKTPRRFMDEDPPKPPKVEVSPVLRPPITTSPP
                                                                                                                                                                                                                                                                                                                                                                         Nuclear protein; Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---EA----EKEEEKPEVENDKEDL--LKEKTDDTSGEDNDEKEAVASKGRKTANSQGRR 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RKRGEBGTERMVQALTELLRRAQAPQAPRSRACEPSTPRRSRGRPPGRPAGPCRRKQQAV
          DISEASE: OFTEN AMPLIFIED IN PANCREATIC CARCINOMAS.
SIMILARITY: BELONGS TO THE TRITHORAX FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 1171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISOFORM TRUNCATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . H (IN REF. 5).
C0615B981BBEB7BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRRGKSQQQQQQQ----QQQQQQQQQPMPRSSQEEKDEKEKEK----
                                                                                                                                                                                                                                                                                                                                                                                    (DIVERGENT)
                                              SIMILARITY: CONTAINS 1 BROMODOMAIN.
SIMILARITY: CONTAINS 1 SET DOMAIN.
SIMILARITY: CONTAINS 3 PHD ZINC-FINGER DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-PRO.
ASP/GLU-RICH (ACIDIC)
PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.2%; Score 428.5; DB 1; ilarity 19.0%; Pred. No. 2.8e-07; Conservative 223; Mismatches 798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> ( IN REF. 5).

-> Y (IN REF. 5).

-> Q (IN REF. 5).

-> Y (IN REF. 5).

-> Y (IN REF. 5).

-> H (IN REF. 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BROMODOMAIN
                                                                                                                                                                                              EMBL; AJ007041; CAB45385.1; -.
EMBL; AD006071. -; NOT_ANNOTATED_CDS.
EMBL; AB002302; BAA20763.2; -.
EMBL; AF108605; AAD56420.1; -.
EMBL; AF104918; AAD1332.1; -.
EMBL; AF10529; AAD26113.1; -.
EMBL; AF105280; AAD26112.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRUNCATED)
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LYMPHOCYTES, AND PLACENTA.
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941
17 1317
2 1362
1 1438
2622
; 293511 M
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InterPro; IPR001965;
InterPro; IPR002857;
Pfam; PF00628; PHD; 3.
Pfam; PF00865; SET; 1.
Pfam; PF02008; Zf-CXX; 1.
PROSITE; PS50280; SET; 1.
                                                                                                                                                                                                                                                                                                                                                                         DNA-binding; Bromodomain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
Les 515; Conserv
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1362
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CONFLICT
SEQUENCE
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VVAEAAVTIPKPEPPPPVVPVKHQTGSWKCKEGPGPGPGTPRRGGQSSRGGRGRGRGRG 298

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1112 AKHPSVLERQIGAISQGMSVQLHVPYSEHAKAPVGPVTMGLPLPMDPKKLA-----PFSG 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLPKGHVIYEGKK-----GHVLSYEGGMSVTQCSK----EDGRSSSGP-PHETAAPKRT 1310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YDMMEGR-----VGRAI----SSASIEGLMGRAIPPERHSPHHLKEQHHIRGSI 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDKIEARKMERLAKKGRTIVKTLLPWDSDESPEASPG---PP---GPR-----RGAG 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---KLLKR 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1051 AGG-PREEVVAHPGPEEQDSLLQRKSARRCVKQRPSYDIFEDSDDSEPGGPPAPRRTPR 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENELPLPEPEEQSRPRKPTLQPVLQLKARRLDKDALAPGPFASFPNGWTGKQKSPDGVH 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------DLTEAYKTQALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPELPL 1441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDAPQQPGSSPRGKSRSP---AP---PADKEAFAAEAQKLPGDPPCWTSGLPFPVPPRE 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .062 VIKASPHAPDPSAFSYAPPGHPLPLGLHDTARPVLPRP------PTISNPPLISS 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----AGPPESLGVP----TAQEASVLRGTALGSVPGGSITKGIPSTRVPSDSAIT 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLPSHH----GKKMRMARCGHC---RGCLRVQDCGSCVNCLDKPKFGGPNTKKQCCVYRK 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               518 TTFL-----KNIRQFIMPVVSARSSRVIKTPRRFMDEDPPRPFRVEVSPVLRPPITTS 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               628 PPAPSPP-PAPATSSRRPLLLRAPQFTPSEAHLKIYESVLTP--PPLGAPEAPEPEPP-- 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    683 PADDSPAEPEPRAV----GRTNHLSLPRFA-PVVTTPVKAEVSPHGAPALSNGPQTQAQ 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVEAKRERPSGPESPVQGPRIKHVCRHAAVALGQARAMVP------EDVPRLSALP 897
579 KGR-----ITRSMANEANSEEAITPQQSAELASMELNESSRWTEEEMETAKKGLLEHGR 632
                                                                                                                                                                                                                                                                                                        805 APTPP--PAPPSPSAPPPVVPKEEKEEETAAAPPVEEGEEQKPPAAEELAVDTGKAEEPV 862
                                                                                                                                                                                                                                                                                                                                T------PSQRAEREAARAGPEGTSPPTP-----TPSTATGGPPEDSPTVAPKS 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRDR-----QDLATEDTSSASETESVPSRSRRGKVEAAGPGGESEPTGSGGTLAHTPRR 951
                                                                                                                                                       --PAAASEEAAFPPVVEDEEMEASGVSGNEEEMVEEAEALHASGNEVPRGECSGPATVNN 744
                                     ---KKVKMGQLSLGLES------GQGQGQHEE
                                                                                                               SWODVPORRVGSGOGGSPCWK-----KQEQKLDDEEEEKKKEEEEKDKEGEEKEERAVAEE
                                                                                                                                                                                                                                 SSDTESIPSPHTEAAKDTGQNGPKPPATLGADGPPPGPPTPPRRTSRAPIEPTPASEATG
                                                                                                                                                                                                                                                                                                                                                                                      863 KSECTEEAEEGPAKGKDAEAAEATAEGALKAEKKEGGSGRATTAKSSGAPQDSDSSATCS
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                                                                           NWSAI-ARMVGS-KTVSQCKNFYFNYKKRQNLDEILQQHKLKMEKERNARRKKKKA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEEKMFSLLKRAKVQLFKIDQQQQKVAASMPLSPGGQMEEVAGAVKQISDRGPVRSEDE
                                                                                                                                                                                                                                                      ------LSPRGQ-----
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                                   GGLPFVIKFVSRA---
                                                                                                                                                                                         MMPAAEKEEAKLPP
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ą	1170	:
ķ	1442	APRPLKEGSITQGTPLKYDTGASTTGSK1469
ð	1229	CLEEAERPLPQHHDTWCCRRCKFCHVCGRKGRGSKHLLECERCRHAYHPAC 1279
Ż.	1470	
ą	1280	LGPSYPTRATRKRHWICSACVRCKSCGATPGKNWDVEWSGDYSLCPRCTQLYEKGNYCP 1339
7,	1501	RACYE
q	1340	ICTRCYEDNDYESKMMQCAQCDHWVHAKCEGLSDEDYEILSGLPDSVLYTGGPCAGAAQP 1399
ζ	1527	PVIVPELGKPRQSPLTYEDHGAPFAGHLPRGSPVTWREPTPRLQE 1571
ą	1400	RWREALSGALQGGLRQVLQGLLSSKVVGPLLLCTQCGPDGKQLHPG-PCGLQAVSQRFED 1458
λ	1572	
ą	1459	
ķ	1619	SGVDLYRSHIPLAF-DPTSIPRGIPLDAAAAY
ą	1500	LLE
ķ	1666	
ą	1550	TPESGQPPGDPSAAFQGKDPAAFSHLEDPRQCALCLKYGDADSKEAGRLLYIGQNE 1605
λ	1683	QTIINDYITSQQMHH17709
q	1606	WIHUNCAIWSAEVFEENDGSLKNVHAAVARGROMRCELCLKPGAIVGCCLSSCLSNFHFM 1665
.×.	1710	1715
ą	1666	CARASYCIFQDDKKVFCQKHTDLLDGKEIVNPDGFDVLRRVYVDFEGINFKRKFLTGLEP 1725
à	1716	RESSLALNYAAGPRGIIDLSQVPHLPVLV 1744
ą	1726	:
ž	1745	PPTPGTPAT
g	1782	
λλ	1803	ER
á	1818	EDPPLDTDVLVPGAPERHSPIQNLDPPLRPDSGSA
<b>≿</b>	1861	SPISPR
ą	1853	:  :   PPPAPRS
λ.	1921	LGGTLDGVY PTLMEPVLLPKEAPRVARPERPRADTGHAFL
ą	1877	LGGVSFGPLPSPGSPSSLTHHIPTVGDPDFPAPPRRSRRPSPLAPRPPPS 1926
λ	1977	
ą	1927	R. S. P. P. RETSPOLRVPPPTSVVTALTPTSGELAPPGPAPSPPPPEDLGPDFEDMEVVSG 1985
λ̈	2015	-PASASDPHREKTQSKPFSIQELELRSLGYHGSSYSPEGVEPVSPV 2059
ą	1986	
λ,	2060	
ą	2043	SAPGLAPSATPGAPR-IEQLDGVDDGTDSEAEAVQQPRGQGTPPSGPGVVRAGVLGAAGD 2101
≿	2105	HLRPLPESQPSSSPLLQTAPGVKGHQRVVTLAQHISEVITQDYTRHHPQQLSAPLPAPLY 2164

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-1-FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.
PHOSPHORYLATED MADIB MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES
THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MADIB BINDS TO AT LEAST
TWO TUBULIN SUBUNITS IN THE POLYMER, AND THIS BRIDGING OF SUBUNITS
MIGHT BE INVOLVED IN NUCLEATING MICROTUBULE POLYMERIZATION AND IN
STABILIZING MICROTUBULES.

-1-SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LCI, LC2 AND LC3, CAN ASSOCIATE
WITH MAPLA AND MAPIB PROTEINS.

-1-SUBUNIT: 3 AND MAPIB PROTEINS.

-1-DOMAIN: HAS A HIGHLY BASIC REGION WITH MANY COPIES OF THE SEQUENCE
KKEE AND KKELY, REPEATED BUT NOT AT FIXED INTERVALS. THIS LATTER
REGION IS RESPONSIBLE FOR THE BINDING OF MAPIB TO MICROTUBULES 2171 2220 2246 2379 2295 2437 2296 KAPRLDEDGEASEDTPQVPGLG----SGGFSRVRMKTPTVRGVLDLDRPGEPAGEESPG 2350 BOTH IN VITRO AND IN VIVO.

PHY LCI IS CORKPRESEED WITH MAPIB. IT IS A POLYPEPTIDE GENERATED FROM MAPIB BY PROTEOLYTIC PROCESSING. IT IS FREE TO ASSOCIATE WITH BOTH MAPIA AND MAPIB. IT INTERACTS WITH THE AMINO-TERMINAL REGION 2438 DCNRRIPLINRVWEDRPSSAGSTPFPYNPLIMRLQ----AGVMAS----PPPPGLPAGSG 2489 2165 SFPGASCPVLDLRRPPSDLYLPPPDHGAP--ARGSPHSEGGKRSP-EPNKTSVLGGGEDG 2221 01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
115-UUL-1999 (Rel. 38, Last annotation update)
MICROTUBLE-ASSOCIATED PROTEIN 1B (MAPI.2) (MAPI(X)) [CONTAINS: MAPI SEQUENCE FROM N.A.
STRAIN-SWISS WEBSTER; TISSUE-Brain;
MFDLINE-90094539; PubMed-2480963;
Noble M., Lewis S.A., Cowan N.J.;
"The microcubule binding domain of microtubule-associated protein MAPIB contains a repeated sequence motif unrelated to that of MAP2 and tau."; 2172 VRVLSLGPAPEPPKPATSKIILVNKLGQVFVKMAGEGEPVPPP-----VKQPPL--2333 QEHASTNMGLEAIIRKA-----LMGKYDQWEESPPLSA-----NAFNPLNASASLPA 2380 AMPITAADGR-SDHTLTSPGGGGKAKVSGRPSSRKAKSP-APGLASGDRPPSVSSVHSEG ---SEIV--DFVL---KNLGGP----2222 IEPVS-----PPEGMTEP---GHSRSAVYPLLYRDGEQTEPSRMGSKSPGNTSQPPAFF SKLTESNSAMVKSKKQEINKKLNTHNRNEPEYNISQPGTEIFNMPAITGTGLMTYRSQAV Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus NCBI\_TaxID=10090; PRT; 2464 AA. OF MAP1B. SIMILARITY: TO NEURAXIN. STANDARD; 2490 P-LAGPH 2495 2102 RARP-PEDLP-MAPB\_MOUSE P14873; RESULT 10 MAPB\_MOUSE 2273 2247 ò g ò g δy 셤 ŏ 셤 ò ద δy g ò g 

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 between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                       MGD; MGI:97179; Mtap...

A MGD; MGI:97179; Mtap...

A nterpro; IRRO00102;

B fam: PF00414; MAPIB_neuraxin; 10.

DR PROSITE; PS00230; MaPIB_neuraxin; 7.

KW Microtubules; Repeat; Phosphorylation.

FT CHAIN ? 2464 MAPI LIGHT CHAIN LCI.

CHAIN 589 787 KKEE AND KKEI/V REPEATS.

12 X 17 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                         FBD3DD99CFDBDA87 CRC64;
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                                                                                 EMBL; X51396; CAA35761.1;
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Gaps 114; 190 263 YIFPGGRGDSALFAVNGFNMLINGGSERKSCFWKLIRHLDRVD---SILLTHIGDDNLPG 319 68 LLSEFQPGNERSQELHLRPESHSYLPELG-----KSEMEFIESKRPRLELLPDPLL 118 119 RPSPLLATGQPAGSEDLTKDRSLIGKLEPVSPPSPPHTDPELELVPP-----RLSKE-- 170 -----EMEGLSEFTEYLS----ESVEVPSPFDI-----LEPPTSGGFLKLSKPCC 262 ---SKLKKKQQQLEEEAAKPPEPEKPVSPPPIESKHRSLVQIIYDENRKKAEAAHRILEGL 248 ------350 249 GPQVELPLYNQPSDTRQYHENIKINQAMRKKLILYFKRRNHARKQWKQKFCQRYDQLMEA 308 LEKKVE------RIENNPRRRAKESKVREYYEKQFPEIRKQR-ELQERMQSRVGQ 356 462 PISYLTSVSSLIVWHPANPAEKIIRVLFPGNSTQYNILEGLEKLKHLDFLKQPLATQKDL 521 ----IPPMLYDADQQRIKFINMNGLMADPMKVYKDRQVMNMWSEQEKE-TFREKFMQHP 448 KNFGLIASFLERKTVAECVLYYYLTKKNENYKSLVRRSYRRGKSQQQQQ--QQQQQQQ 402 VGNTIEPVILFQKMGVGKLEMYVLNPVKSSKEMQYFMQQWTGTNKDKAELILPNGQEVDI 461 RGSGL-SMSAARSEHEVS----- 394 -----ELIQNMDRVDREITMVEQQI-----Ouery Match 3.2%; Score 424.5; DB 1; Length 2464; Best Local Similarity 19.3%; Pred. No. 3.4e-07; Matches 521; Conservative 314; Mismatches 996; Indels 869; 320 INSMLQRKIAELEEE------222 191 309 357 449 579 171 395 셤 δ qq à g δ g ò qq ŏ 셤 ŏ g ò g

Qy	507	QQQQPMPRSSQEEKDEKE-KEKEAEKEEEKPEVENDKEDLLKEKTDDTSGEDNDEKEAVA 565 
Qy	995	SKGRKTANSQGRRKGRITRSMANEANSEEAITPQQSAELASMELN 610
qq	680	KEIKKEIKKEERKEEKKEVKKETPLKDAKKEVKKEEKKEVKKEEK-EPKKEIKKISKDIK 738
ې وړ	611	67
2		FUSUIRRFSALKPRVARKEESTKK-
yo da	671	LKMEKERNARRKKKKAPAAASEEAAFPPVVEDEEMEASGVSGNEEEWVEEAEALHA 726  LI :
ò	727	PATLGADGPPPGPPTPP 78
ු අ	823	86
Qy	787	RRTSRAPIEPTPASEATGAPTPPPAPPSPSAPPVVPKEEKEEETAAAPPVEEGE 841
qq	861	::
ΟŊ	842	EQKPPAAEELAVDTGKAEEPVKSECTEEAEEGPAKGKDAEAAEATAEGALKAEKKEG 898
qq	006	GECEQTPEELEPVEKQGVDDIEKFEDEGAGFEESSETGDYEEKAETEEAEEP 951
Oy	899	VDEAEGGDKNRLLSPRPSLLTPTGDPRANA 95:
qq	952	EEDGEDNASGSASKHSPTEDDESAKAEADVHLKEKRESVVSGDDRAEE 999
οy	926	SPQKPLDLKQLKQRAAAIPPIQVTKVHEPPREDAAPTKPAPPAPPPPQNLQPESD 1010
qq	1000	DMDDVLEKGEAEQSEEEGEEEDKAEDAREEGYEPDKTEAEDYVMAVADKAAEA 1052
οy	1011	ADKEAFAAEAQKG-SSPRGKSRSPAPADKEAFAAEAQKLFGDPPC 1048
Op	1053	IQSPSREPASSIHDETLPGGSES
Qy	1049	WTSGLPFPVPPREVIKASPHAPDPSAFSYAPPGHPLPLGLHDTARPVLPRPPTISN 1104
QQ	1110	FTATSGYTQSTIEISSEPTPMDEMSTPRDVMSDETNNEETESP 1152
δλ	1105	PPPLISSAKHPSVLERQIGAISQGMSVQLHVPYSEHAKAPVGPVTMGLPLP 1155
οg	1153	SQEFVNITKYESSLYSQEYSKPAVASFNGLSEGSKTDATDGKDYNASASTISPPSS 1208
οy	1156	MDFKKLAPESGVKQEQLSPRGQAGPPESLGVPTAQEASV 1194
qq	1209	MEEDKFSKSALRDAYCSEEKELKASAELDIKDVSDERLSPAKSPSLSPSPPSP 1261
οy	1195	LRGTALGSVPGGSITKGIPSTRVPSDSAITYRGSITHGTPADVLYKGTITRIIGEDSPSR 1254
qq	1262	IEKTPLGERSVNFSLTPNEIKVSAEGEARSVSPGVTQAVVEEHCASP 1308
Qγ	1255	LDRGREDSLPKGHVIYEGKKGHVLSYEGGMSVTQCSKEDGRSSSGPPHETAAPKRT 1310
qq	1309	EEKTLEVVSPSQSVTGSAGHTPYYQSPTDEKSSHLPTEVSENAQAVP 1355
Οy	1311	YDMMEGRYGRAISSASIEGLMGRAIPPERHSPHHLKEQHHIRGSITQGIPRSYVE 1365
qq	1356	VSFEFSEAKDENERASLSPMDEPVPDSESPVE-KVLSPLRSPPLLGSESPY 1405
Qy	1366	AQEDVLRREAKLLKREGTPPPPPPSRDLTEAYKTQALGPLKLKPAHEG 1413
qq	1406	LSADSK
Qy		QGTPLKYDTGASTTGSKKHDV 147
qq	0	FIPIKEDFGPEKKTSDVETMSSQSALALDERKL-GGDVSPTQIDVSQFGSFKEDT 1513
οy	1474	RSLIGSPGRTFPPVHPLDVMADARALERACYEESLKSRPGTASSSGGSIARGAPVIVPEL 1533

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SDISPLTPRESSPLYSPGFSDSTSAAKETAAAHQASSSP------PIDAATAEPYG 1827
1650 YLPRHLAPNPTYPHLYPPYLIRGYPDTAALENRQTIINDYITSQQMHHNTATAMAQRADM 1709
                                                                                                                                                                                                                                                                                                                                                                                   1722 VEASPSTSSAHTPSQIASPLQEDTLSDVVPPREMSLYASLASEKVQSLEGE----KLSPK 1777
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                                                                              TIDDVSPSLHAEVGSPHSTEVDDSLSVSVVQTPTTFQETEMSPSKEECPRPMSISPPDFS
                                                                                                                           ---AKSPHSTVPEHHPHPISPYEHLLRGVSGVDLYRSHIPLAFDPTSIPRGIPLDAAAAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NPLEWFAGE------EPTEESE---KPLTQSGGAPPPSGGKQ---QGRQCDETPPTSVS
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                                                     GKPRQSPLTYEDHGAPFAGHLPRGSPVTMREPTPRLQEGSLSSSKASQDRKLTSTPREI -
                                                                                                                                                              -----OSSMSIEFGQESPEHSFAMDFS---
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PKTAKS-RTPVQDHRSE------
               1514 KMSISEGTVSDKSATPVD-
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                                                                                                                                                                                                                                                                                                        Yeast 7:413-424 (1991).
Yeast 7:413-424 (1991).
-!- MISCELLANEOUS: THIS PROTEIN IS ENCODED BY A NON-ESSENTIAL GENE.
-!- SIMILARITY: SOME, TO S.POMBE SPACZE12.01.
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                                                                                                                                                                                                                                               MEDLINE-91335897; PubMed-1872032;
Jia Y., Slonimski P.P., Herbert C.J.;
"The complete sequence of the unit YCR59, situated between CRY1 ar
MAT, reveals two long open reading frames, which cover 91% of the
                                                                                                                                                                       Wicksteed B.L., Roberts A.B., Sagliocco F.A., Brown A.J.P.; "The complete sequence of a 7.5 kb region of chromosome III from Saccharomyces cerevisiae that lies between CRY1 and MAT."; Yeast 7:761-772(1991)
                                                                                              Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                           INTERGENIC REGION
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8D133A0918658E53 CRC64;
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                                    01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYPOTHETICAL 138.5 KDA PROTEIN IN RPS14A-GNS1
YCRO33W OR YCR33W OR YCR592.
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                                                                                    Saccharomyces cerevisiae (Baker's
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Pfam; PF00249; myb_DNA-binding;
PROSITE; PS50090; MYB_3; 1.
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                        22, Created)
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19.5%;
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Matches 240; Conserv
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145	79	205	112	152	176	383	441	266	319	379	427	486	537	584	631 908	691	738	790	1034	845	905
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                                                                          01-NOV-1995 (Rel. 32, Created)
UNOV-1995 (Rel. 32, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: MAP1 LIGHT CHAIN LC1].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAPI LIGHT CHAIN LC1.
LYS-RICH (HIGHLY BASIC, CONTAINS MANY
KKEE AND KKEI/V REPEATS).
12 x 17 AA TANDEM REPEATS.
                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
           PRT; 2468 AA
965 QLKQRAAAIPPIQVTKVHEPPREDAAPTKPAPP 997
                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000102; --
Pfam; PF00414; MAPIB_neuraxin; 10.
PROSITE; PS00230; MAPIB_NEURAXIN; 6.
Microtubules; Repeat; Phosphorylation.
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MIM; 157129; -.
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q	947	ETEEAEEPEEDGEEHVCVSASKHSPTEDEESAKAEADAYIREKRESVA 994
δy	948	TGDPRANASPQKPLDLKQLKQRAAAIPPIQVTKVHEPPREDAAPTKPAPPAPPPQNLQP 1007
qq	995	DDRAEEDMDEAIEKGEA
δy	1008	
q	1042	EDYVMAVVDKAAREAGGAEEQYGFLTTPTKQLGAQSPGREPASSIHDETLPGGSESEATAS 1101
Qy	1038	
q	1102	DEENREDQPEEFTATSGYTQSTIEISSEPTPMDEMSTPRDVMS 1144
Qy	1098	RPPISNPPPLISSAKHPSVLERQIGAISQGMSVQLHVPYSEHAKA 1143
Q	1145	DETINNEETESPSQEFVNITKYESSLYSQEYSKPADVTPLNGFSEGSKTDATDGKDYNASA 1204
Οy	1144	PVGPVTMGLPLPMDPKKLA
qq	1205	STISPPSSMEEDKFSRSALRDAYCSEVKASTTLDIKDSISAVSSEKVSPSKSPS 1258
οy	1182	ESLGVPTAQEASVLRGTALGSVPGGSITKGIPSTRVPSDSAITYRGSITHGTPADVLYKG
QQ	1259	TSPSP
δ	1242	н
qq	1301	VTQEVVEEHCASPEDKTLEVVSPSQSVTGSAGHTPYYQSPTDEKSSHLPT 1350
Qy	1302	HETAAPKRIYDMMEGRVGRAISSASIEGLMGRAIPPERHSPHHLKEQHHIRGSITQGIPR 1361
qq	1351	EVIEKPPVSF 1363
οy	1362	SYVEAQEDYLRREAKLLKREGTPPPPPPSRDLTEAYKTQALGPLKLKPAHEG-L 1414
q	1364	ESTORANDENERASVSPMDEPVPD-SESPIEKVLSPLRSPPLIGSESAYESFL 1414
Qy	1415	
qq	1415	SADDKASGRGA-ESPFEEKSGKQGSPDQVSPVSEMTSTSLYQDKQEGKSTDFAPIKEDFG 1473
δλ	1463	ASTIGSKKHDVRSLIGSPGADVPVHP-LDVMAD 1495
QQ	1474	QEKKTDDVEAMSSQPALALDERKLGDVSPTQIDVSQFGSFKEDTKMSISEGTVSDKS 1530
οy	1496	ARALERACYEESLKSRPGTASSSGGSIARGAPVIVPELGKPRQSPLTYEDHGAPFAGHLP 1555
qq	1531	ATPVDEGVAEDTYSHMEGVASVSTASVATSSFPEPTTDDVSPSLHAEVGSPHSTEVD 1587
Οy	1556	RGSPVTMREPTPRLQEGSLSSSKASQDRKLTSTPREIAKSPHSTVPEHHPHPISPY 1611
qq	1588	DSLSVSVVQTPTTFQETEMSPSKEECPRPMSISPPDFSPKTAKS-RTPVQDHRSE 1641
δy	1612	EHLLRGVSGVDLYRSHIPLAFDPTSIPRGIPLDAAAAYYLPRHLAPNPTYPHLYPPYLIR 1671
QQ	1642	QSSMSIEFGQESPEGSLAMDFSRQSPDHPTV 1672
δy	1672	MHHNTATAMAQRADMLRGLSPRESSLA
qq	1673	GAGVLHITENGPTEV-DYSPSDMQDSSLSHKIPPMEEPSYTQDN 1715
ογ	1732	IDLSQVPHLPVLVPPTPGTPATAMDRLAYLPTAPQPFSSRHSSSPLSPGGPTHLTK 1787
QQ	1716	-DLSELISVSQVEASPSTSSAHTPSQIASPLQEDTLSDVAP 1755
٥y	1788	RDRD
QQ	1756	PRDMSLYASLISEKVQSLEGEKLSPKSDISPLIPRESSPLYSPIFSDSTSAVKEKT 1811
ΟŊ	1843	аѕнѕнанонѕ
qa	1812	ATCHSSSSPPIDAASAEPYGFRASVLFDTMQHHLALNRDLSTPGLEKDSG 1861

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                                                                                                 SEQUENCE OF 1-181 FROM N.A.
MEDLINE-84270697; PubMed-6462220;
MEDLINE-84270697; PubMed-6462220;
MEDLINE-1, de Wet W.J., Bernard M.P., Ding J.-F., Morabito M.,
Myers J., Williams C., Ramirez F.;
"Human pro alpha 1(I) collagen gene structure reveals evolutionary
                                                                                                                                                                                                                             2060 SSPSLTHDKGLPKHLEELDKSHLEGELRPKQPGPVKLGGEAAHLPHLRPLPESQPSSSPL
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                                                                        1943 -PRVARPERPRADTGHAF--LAKPPARSGLEPASSPSKGSEPRPLVPPVSGHATIARTPA
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                                   GKTP-------GDFSYAYQKPEETTRSPDEEDYDYESYEKTTRTSDVGGYY
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                                                                                                                                                                                       EGGYSYDISEKTISPP-EVSGYSYEKTERSRRLLDDI---SNGYDDSE---DG-----
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Catarrhini, Hominidae, Homo.
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"Structure of a full-length cDNA clone for the prepro alpha 1(I) chain of human type I procollagen.";
Biochem. J. 253:919-922(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2445 LINRVWEDRPSSAGSTPFPYNPLIMRLQAGVMASPPPPGLPAGSGPLAGPHHA 2497
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1903 TSSPVRPAATFPPATHCPLGGTLDGVYPTLMEPVLLPKEA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-89025644; PubMed-3178743;
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Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID-9606;
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Click E.M., Bornstein P.;
"Insolution and characterization of the cyanogen bromide peptides from the alpha 1 and alpha 2 chains of human skin collagen.";
Biochemistry 9:4699-4706(1970).
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MEDLINE-91184577; Pubmed-2010058;
Kuivaniemi H., Tromp G., Prockop D.J.;
Mutations in collagen genes: causes of rare and some common diseases
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MEDLINE=97255959; PubMed=9101290;
Kuivaniemi H., Tromp G., Prockop D.J.;
"Mutations in fibrillar collagens (types I, II, III, and XI), fibril-
associated collagen (type IX), and network-forming collagen (type X)
cause a spectrum of diseases of bone, cartilage, and blood vessels.";
Hum. Mutat. 9:300-315(1997).
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vertebrate collagens. A possible role of the carbohydrate in fibril
formation.";
J. Biol. Chem. 245:5042-5048(1970).
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MEDLINE-88033098; PubMed-2822714;
Rossouw C.M.S., Vergeer W.P., du Plooy S.J., Bernard M.P., Ramirez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-88124208; PubMed-3340531;
Maekelae J.K., Raassina M., Virta A., Vuorio E.;
"Human pro alpha 1(I) collagen: cDNA sequence for the C-propeptide
                                                                                                                                                                                                                                                                                                                                                                                                                     Ramirez F., Eikenberry E.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-34 FROM N.A.
MEDLINE-85130970; PubMed-2857713;
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Fine structural analysis of the human pro-alpha 1 (1) collagen promoter structure, Alul repeats, and polymorphic transcripts.";
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conservation of a pattern of introns and exons."; Nature 310:337-340(1984).
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J. Biol. Chem. 262:15151-15157(1987).
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MEDLINE-84080385; PubMed=6689127;
Bernard M.P., Chu M.-L., Myers J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 16:349-349(1988)
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                                                                                           MEDLINE=71038625; PubMed=5529814;
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                                                     SEQUENCE OF 162-301.
TISSUE-Skin:
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"The human typ
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Pack M., Constantinou C.D., Kalia K., Nielsen K.B., Prockop D.J.;
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Weiss L., Graham J.M., Byers P.H.;
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VARIANT OI-II CYS-422.
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                                          560 GODGRPGPPGPPGARGOAGVMGFPGPKGAAGEPGKAG----ERGVPGPPGAVGPAGKDG
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-1- DISEASE: DEFECTS IN TCOF1 ARE THE CAUSE OF TREACHER COLLINS SYNDROME (TCS). TCS IS A AUTOSOMAL DOMINANT DISORDER OF CRANIOFACIAL DEVELOPMENT THAT OCCURS WITH AN INCIDENCE OF 1/50,000 LIVE BIRTHS. THE CLINICAL FEATURES OF TCS ARE BILATERALLY SYMMETRICAL AND INCLUDE: (1) ABNORMALITIES OF THE EXTERNAL EARS, ATRESIA OF THE EXTERNAL EAR CANALS, AND MALPORMATION OF THE MIDDLE RAR OSSICLES, WHICH MAY RESULT IN CONDUCTIVE HEARING LOSS: (1) LATERAL DOWNWARD SLOPING OF PALPEBRAL FISSURES, FREQUENTLY WITH COLOBOMAS OF THE LOWER EYELIDS: (3) HYPOPLASIA OF THE MANDIBLE AND ZIGOMATIC COMPLEX; (4) CLEFT PALATE.
                                        1304 QPSVAQKNWYISKNPKDKRHVWFGESMTDGFQFEYG-----GQGSDPADVAIQLT--- 1353
2226 SPPEGM-----TEPGHSRSAVYPLLYRDGEQTEPSRMGSKSPGNTSQPPAFFSKLTESN 2279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97250498; PubMed-9096354; Wise C.A., Chiang L.C., Paznekas W.A., Sharma M., Musy M.M., Ashley J.A., Lovett M., Jabs B.W.; "TCOF1 gene encodes a putative nucleolar phosphoprotein that exhibits mutations in Treacher Collins syndrome throughout its coding
                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata, Vertebrata; Euteleostomi;
Catarrhin1; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-96154183; PubMed-8563749;
Dixon J., Edwards S.J., Gladwin A.J., Dixon M.J., Loftus S.K., Bonner C.A., Koprivnikar K., Wasmuth J.J.;
"Positional cloning of a gene involved in the pathogenesis of Treacher Collins Syndrome. The Treacher Collins Syndrome Collaborative Group.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS L-439; V-810; V-1313 & G-1355, AND VARIANT TCS R-53. MEDLINE-97195537; PubMed-9042910; Edwards S-J., Gladwin A.J., Dixon M.J.; Edwards S-J., Gladwin Treacher Collins syndrome reveals predominance of mutations that create a premature-termination
                                                                                                                                                                                                                                      TCOF_HUMAN STANDARD; PRT; 1411 AA. 013428; 099408; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-CCT-2000 (Rel. 40, Last annotation update) TREACLE PROTEIN (TREACHER COLLINS SYNDROME PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 94:3110-3115(1997)
                                                                                                                1354 --FERLMSTEASQNITYHCKNSVAYMDQQTG 1382
                                                                                   2280 SAMVKSKKQEINKKLNTHNRNEPEYNISOPG 2310
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U84664; AAC51185.1; -.
U84640; AAC51185.1; JOINED.
U84641; AAC51185.1; JOINED.
U84642; AAC51185.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                      TCOF1.
Homo sapiens (Human)
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TCOF_HUMAN
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1411 AA; 144312 MW; 3880203D985C2699 CRC64;
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W -> R (IN TCS).
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D -> G.
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                                                                                                                                                       AAC51185.1;
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OKPLDLKQLKORAAAIPPIOVTKVHEPPREDAAPTKPAPPAPPPPQNLOPESDAPQQPGS 1017

1119 ASPHA-----PDPSAFSYAPPGHPLPLGLHDTARPVLPRPPTISNPPPLISSAKHPSVL 1118 1234 PADVLYKGTITRIIGEDSPSRLDRGREDSLPKGHVIYEGKKGHVLSYEGGMSV----TQC 1289 1402 1403 GPLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGSITQGTPLKYDTG 1462 1512 PGTASSSGGSIARGAPVIVPE-LGKPRQSPLTYEDHG--APFAGHLPRGSPVTMREPTPR 1568 LQEGSLSSSKASQDRKLTSTPREIAKSPHSTVPEHHPPHPISPYEHLLRGVSGVDLYRSHI 1628 1732 IDLSQVPHLPVLVPPTPGTPATAMDRLAYLPTAPQPFSSR--HSSSPLSPGGPTHLTKPT 1789 VSKKNPASLPL-----TQAALKVLAQKASEAQPPVARTQPSSGVDSAVGTLPATSPQ 1036 TISSSERERDRDRERDRDREREKSILISTITVEHAPIWRPGTEQSSGSSGGGGGSSS 1849 RPASHSHAHQHSPISPRTQDALQQRPSVLHNTGMKGIITAVEPSKPTVLRSTSTSSPVRP 1909 1910 AATFPPATHCPLGGTLDGVYPTLMEPVLLPKEAPRVARPERPRADTGHAFLAKPPARSGL 1969 1159 AAKDDPDGKQEAKPQQAAGMLSPKTGGKEAASGTTPOKSRKPKKGAGNPQASTLALQSNI 1218 1174 PRGQAGPPESLGVPTAQEASVLRGTALGSVPGGSITKGIPSTRVPSDSAITYRGSITHGT 1233 1290 SKEDGRSSSGPPHETAAPKRTYDMMEGR---VGRAI----SSASIEGLMGRAIPPERHSP 1342 STSVQAKGTNKLR-----KPKLPEVQQATKAP---ESSDDSEDSSDSSGSEEDGE 1084 ASTTGSKKHDVRSLIGSPGRTFPPVH-------PLDVMADARALERACYEESLKSR 1511 PLAF-DPTSIPRG---IPLDAAAAYYLPRHLAPNPTYPHLYPPYLIRGYPDTAALENRGT 1684 1685 IINDYITSQQ-----MHHNTAT-----AMAQRADMLRGLSPRESSLALN--YAAGPRGI 1731 1970 EPASSPSKGSEPRP-----LVPPVSG-HATIARTPAKNLAPHHASPDPPAPPASASDPH 2022 1018 SPRGKSRSPAPPADKEAFAA--EAQ-----KLPGDPPCWTSGL-PF-----PVPPREVIK 1064 714 ---KANPA-----APGKVVTA 738 AAQAKQR-----SPSKVKPPVRNPQNSTVLARGPASVPSVGKAVATAA----QAQ 784 785 TGPEEDSGSSEEESDSEEEAETLAQAKPSGKTHQIRAALAP----AKESPRKGAAPTPP 839 --- PPRKTGPAAAQVQVGKQ 394 455 ATPSAQVGKWEEDSESSS------EESSDSSDGEVPTAVAP-----AQ ERQIGAISQGMSVQLHVPYSEHAKAP---VGPVTMGLPL--PMDPKKLAPFSGVKQEQLS 1343 HHLKEQHHIRGSITQGIPRSYVEAQEDYLRREAKLLKREGTPPPPPPSRDLTEAYKTQAL PLIFVDPNRSPAGPAATPAQAQAA------STPRKARASESTARSSSSES GPQGAKSAHTLGPTPSRTETLVEE-------TAAESSEDDVV-----------APSQSLLSG----YMTPGLTP--ANSQASKATPKLD-----SSPSVSSTL 534 SEESSDSADSEEAPAAMTAAQAK-------PALKIPQTKACPKKTNTTASA 578 KVAPVRVGT-----QPPR-----QPPR------KAGTATSPAGSSPAVAGGTQR 840 GKTGPSAAQAGKQDDS-GSSSEESDSDGEAPAAVTSAQVIKP---------AKESPRKGAAPA--------KAPQVRAASAP-1065 492 1463 739 1629 985 1790 1850 1085 1569 1119 925 1037 ò g à g à g ò g οy g δ 셤 δy 셤 á g ò g ò Ω ò g ò g ò g ò 셤 ò a à g δ g à g 82;

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                                                                                                         2202
2023 REKTQSKPFSIQELELRSLGYHGSSYSPEGVEPVSPVSSPSLTHDKGLPKHLEELDKSHL 2082
                                                                                                                                                          GKRSPEPNKTSVLGGGEDGIEPVSPPEGMTEPGHSRSAVYPLLYRDGEOTEPSR----M 2257
                                                                                                                                                                                 1296 GEASVSPEKTSTTSKGKAKRDKAS---GDVKEKKGKGS----LGSQGAKDEPEEELQKGM 1348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----SWWKVLTEL----L
                                                                                                      2143 ITQDYTRHHPQQLSAPLPAPLYSFPGASCPVLDLRRPPSDLYLPPPDHGAPARGSPHSEG
                                                                                                                                   -----GA-----GEG
                                                    EGELRPKQPGPVKLGGEAAHLPHLRPLPESQPSSSPLLQTAPGVKGHQRVVTLAQHISEV
                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
Canis.
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PROSITE; PS01208; VWFC; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
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CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
                                                                            EQE-RKKVVDTTKESSRKGWESRKRKLSGDQPAA----RTPRSKKKKKL----
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COLLAGEN ALPHA 1(1) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE.
                                                                                                                                                                                                             GSKSPGNTSQPPAFFSKLTESNSAMVKSKKQEIN--KKLNTHNRNEP 2302
                                                                                                                                                                                                                                     1349 GTVEGGDQSNPKSKKEKKKSDKRKKDKEKKEKKKAKKAKKASTKDSESP 1395
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
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Last annotation update)
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                        TQCLLGQPWPLNEAQVQA-----
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30-MAY-2000 (Rel. 39, Last seq
30-MAY-2000 (Rel. 39, Last ann
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InterPro; IPR001007;
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Q9XSJ7;
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975 PIQVTKVHEPPREDAAPTKPA-PPAPPPPQNLQPESDAPQQPGS-SPRGKSRSPAPP--- 1029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1199 A--LGSVPGGSITKGIP-STRVPSDSAITYRGSITHGTPADVLYKGTITRIIGEDSPSRL 1255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1079 PPGHPLPLGLHDTARPVLPRPPTISNPPPLISSAKHPSVLERQIGAISQGMSVQLHVPYS 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D-----RGREDSL----PKGHVIYEGKKGHVLSYEGGM-----SVTQCSKEDGR 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITQGIPRSYVEAQEDYLRREAKLLKREGTPPPPPPSRDLTEAYKTQALGPLKLK--PAHE 1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1413 GLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGSITQGTP----LKYDTGASTTGS 1468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKHD-----VRSLIGSPGR----TFP--PVHPLDVMADARALERACYEESLKSRPGTA 1515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSSGGSIARGAPVIVPELGKPRQSPLTYEDHGAPFAGHLPRGSPVTMREPTPRLQEGSLS 1575
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                                                                                                                                                                                           | : | :|| |||
ETKNCPGAQVPPGECCPVCPDGEASPTDQETTGVEGPKGDTGPRGPRGPPGTPGTPG 132
                                                                                                                                                                   EALHASGNEVPRGECSGPATVNNSSDTESIPSPHTEAAKDTGQNGPKPPA-TLGADGPP- 779
                                                                                                                                                                                                                                                                                         133 QPGLPGPPGPP------GPPGPPGLGGNFAPQMSYGYDEKSTGGISVPG 175
                                                                                                                                                                                                                                                                                                                                                                                                                    859 EEPVKSECTEEAEEGPAKGKDAEAAEATAEGALKAEKKEGGSGRATTAKSSGAPQDSDSS 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 919 ATCSADEVDEAEGGDKNRLLSP----RPSLLTPTGDPRANASPQKPLDLKQLKQRAAAIP 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 NDGATGAAGPP----GPTGPAGPPGFPGAVGAKGEAGPQGARGSEGPQGVRGEPGPPGPA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         376 GAAGPAGNPGADGQPGAKGANGAPG----IAGAPGFPGARGPSGPGGPSGPPGPKGNSG 430
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                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                  PPSPSAP-----PPVVPKEEKEETAAAPPVEEGE------EQKPPAAEELAVDTGKA
                                                                                                                                                                                                                                                                                                                                                                         176 PMGPSGPRGLPGPPGAPGPQGFQ----GPPGEPGEPGASGPMGPRGPPGPPGKNCDDGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GKPGR-----PGERGPPGPQGARGLPGTA--GLPGMKGHRGFSGLDGAKGDAGP-----
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1361 N-LINKED (GLCNAC. . .) (POTENTIAL)
AA; 138762 MW; 58E3674D2B570697 CRC64;
                                                                                                                          643;
                                                                                   Length 1460;
                                                                                                                            Indels
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                                                                                                                          Mismatches 645;
                                                                                 Score 391.5; DB Pred. No. 2.5e-06
                                                                                                                                                                                                                                                   ----PGPPTPPRRTSRAPIEPTPASEATGAPTPP---
                                                                                                                          Conservative 102;
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                                                                                                       Similarity
1361
1460
                                                                                                                        Matches 379;
CARBOHYD
SEQUENCE
                                                                                 Query Match
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1692 SOOMHHATATAAAGRADML	Db 834 Qy 1632 Db 867		866 1691 908
PULUPPT - PGTPATAMDRIAYLPTAPQDFSSRHSSSPLSPGGPTHLTKPTTTSSSBERB PGGRGERGFPGLAGPPGSAGS PGGRGERGPPGLAGPPGBAGPGPAGPPGLAGPPGSRAS	169		1740 959
DEDREEDEDEREKEKSILISTITVEHAPIWRPGTEQSSGSSGSGGGGGGSSSRPAS	174	PVLVPPTPGTPATAMDRLAYLPTAPQPFSSRHSSSPLSPGGPTHLTKPTTTSSSERER	1798 1009
HSHAHQHSPISPRTQDALQQRPSVLHNTGMKGIITAVEPSKPTVLRSTSTSSPVRPAATF	175	DRDRERDRDREREKSILTSTTTVEHAPIWRPGTEQSSGSSGSSGSGGGGSSSRPAS	1853 1043
PPATHCPLGGTLDGVYPTLMEBVILPKEAPRVARPERPRADTGH	185	HSHAHQHSPISPRTQDALQQRPSVLHNTGMKGIITAVEPSKPTVLRSTSTSSPVRPAATF	1913 1072
FLAKPPARSGLEPASSPSKGSEPRPLVPPVSGHATIARTPAKNLAPHHASPDPPAPPASR	191	PPATHCPLGGTLDGVYPTLMEPVLLPREAPRVARPERPRADTGHA	1958
SDPHREKTQSKPESIQELELRSLGYHGSSYSPEGVEPVSPVSSPSLTHDKGLPKHLEELD	195	FLAKPPARSGLEPASSPSKGSEPRPLVPPVSGHATIARTPAKNLAPHHASPDPPAPPASA	2018
KSHLEGELRPKQPGVKLGGEAAHLPPLLPESQPSSSPLLQTAPGVKGHQ PPGPPGPPSGGFDFSFLP	20 <u>1</u>	SDPHREKTQSKPFSIQELELRSLGYHGSSYSPEGVEPVSPVSSPSITHDKGLPKHLEELD   ::	2078
DANVYRDRDLEVDTTLAQHISEVITQDVTRHHPQQLSAPLPAPLYSFPGASCPVLDL :::::::::::::::::::::::::::::::::::	20%	KSHLEGELRPKQPGPVKLGGEAAHLPHLRPLPESQPSSSPLLQTAPGVKGHQ	2130
RRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEPNKTSVLGGGEDGIEPVSP:	21:	DANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDL	2176 1258
PEGMTEPGHSRSAVYPLLYRDGEQTEPSRMGSKSPGNTSQPPAFFSKLTESNSA	21;	RRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEPNKTSVLGGGEDGIEPVSP :	2227 1301
MVKSKKQEINKKLNTHNRNEPEYNISQPG  ::                    FLRLMSTEASQNITYHCKNSVAYMDQQTG	22;	PEGMTEPGHSRSAVYPLLYRDGEQTEPSRMGSKSPGNTSQPPAFFSKLTESNSA	2281 1349
	135	MVKSKKQEINKKLNTHNRNEPEYNISQPG  ::                    FLRLMSTEASQNITYHCKNSVAYMDQQTG	

Search completed: September 8, 2001, 14:39:31 Job time: 433 sec

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088778 rattus norv

caenorhabdi drosophila

Sequence:

Run on:

Searched:

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Q61479 mus musculu Q61479 mus musculu Q4161 homo sapien Q9wpa5 homo sapien Q9w02 drosophila Q9vp1 drosophila Q9vq2 drosophila
                                                            Q9uha8 homo sapien
Q9n541 caenorhabdi
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EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 113.8 KDA PROTEIN (FRAGMENT).
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Submitted (JAN-2000) to the 1
EMBL, AL137641; CAB70854.1;
Hypothetical protein.
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1 MSGSTQLVAQTWRATEPRXP......WDEEPKPLLCSQYETLSDSE 2517
                                                                                                                                           ; Search time 92.74 Seconds
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                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
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                                                                            279 TPPMDRITYIPGTQITFPPRPYNSASMSPGHPTHL---AAAASAEREREREKERERERER
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  ----AMENTROTILNDYIT
                                                                                                           EKSILTSTTTVEHAPIWRPGTEQSSGSSGSGGGGSSSRPASHSHAHQHSPISPRTQDA
                                                                                                                                                                                                                                                                                   2013 APPASASDPHREKTQSKPFSIQELELRSLGYHGSSYSPEGVEPVSPVSSPSLTHDKGLPK
                                                                                                                                                                                                                                                                                                  546 RQIASDKDARERGSQSSDSS-----SSLSSHRYETPSDAIEVISPASSPAPPQEKLQTY
                     SQQMHHNTATAMAQRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGTP
                                  ATAMDRIAYLPTAPQPFSSR-HSSSPLSPGGPTHLTKPTTTSSSERERDRDRERDRDRER
                                                                                                                                                                   AFLAKPPARSGLEPASS --- PSKGSEPRPLVPPVSGHATIARTPAKN -- LAPHHASPDPP
                                                                                                                                                                                                                                                       600 QPEVVKANQAENDPTRQYEGP-----LHHYRP---QQESPSPQQQLPPSSQAEGMG
                                                                                                                                                                                                                                                                                                                                                                         2126 -VKGHQRVVTLAQHISEVITQDYTRHH-----PQQLSAPLPAPLYSFPGA--SCPVLDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KQEINKKLNTHNRNEPEYNISQPGTEIFNMPAITGTGLMTYRSQAVQEHASTNMGLEAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RKALMGKYDQWEE-----SPPLSANAFNPLNASASLPAAMPITAADGRSDHTLTSPGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         875 RKALMGSFDDKVEDHGVVMSQPMGV---VPGTANTSV----VTSGETRREEGDPSPHSG
                                                                                                                                                                                                                                                                                                                               HLEELDKSHLEGELRPKQPGPVKLGGEAAHLPHLRPLPESQPSSSPLLQTAPG----
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Last sequence update)
 P-AMPFHRALDPAAAYLFQRQLSPTPGYPSQYQLY---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QE-----LHLRPESHSYLPELGKSEMEFIESKRPRLELLPDPLLRPSPLLATGQPAGS 132
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SEQUENCE FROM N.A.
MEDLINE=99417957; PubMed=10488333;
TSai C.-C., Kao H.-Y., Yao T.-P., McKeown M., Evans R.M.;
"SMRTER, a Drosophila nuclear receptor coregulator, reveals that ECR-mediated repression is critical for development.";
Mol. Cell 4:175-186(1999)
Mol. Cell 4:175-186(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPHSLSYPVQIARTHTDVGLLEYQHHSRDYASHLSPGSIIQPQRRRPSLLSEFQPGNERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 RLSKEELIQNMDRVDREITMVEQQISKLKKKQQQLEEEA--AKPPEPEKPVS----PP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIESKHRS--LVQIIYDENRKKAEAAHRILEGLGPQVE-----LPLYNQPSDTRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     266 YHENIKINQA-MRKKLILYFKRRNHARKOWKOKFCORYDQLMEALEKKVERIENNPRRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     713 LAMLIRQHQSQIRAPLLLHIRKLKAERWAHNQGLVEKYTKDQADWQRRCERMEASAKRKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KESKVREYYEKQFPEIRKQRELQERMQSRVGQRGSGLSMSAARSEHEVSEIIDGLSEQEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOHPKNFGLIASFLERKTVAECVLYYYLTKKNENYKSLVRRSYRRGKSOQOQOQOQO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         479 ROVVTTPMGMOLKVET---LPQQQQKQQQHQQQQQQQQGRSQPVV-SSMSTVVSQPVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 1232;
       SANT DOMAIN PROTEIN SMRTER.

SMR OR SMRTER OR CG4013.

Drosophila melanogaster (Fruit fly).

Brayota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6284E14C5C247CD9 CRC64;
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 8.1%; Score 1075; DB 5; Best Local Similarity 21.0%; Pred. No. 9.4e-46; Matches 712; Conservative 361; Mismatches 1078;
                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000104; -.
InterPro; IPR001005; -.
InterPro; IPR002086; -.
Ffam: PF00249; myb_DNA-binding; 1.
PRIWTS; PR00308; ANTIFREEZEI.
PROSTIE; PS000887; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
SMART; SM00395; SANT; 1.
SEQUENCE 3469 AA; 364115 WW; 6284E14C5C247CD9
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Пр	1004	AEKASAATKAVEATAAGEKVAKAAAAAAAAAATTATTATTTTSSSTSSSSASSASTAS	1063
ò	538	VENDKEDLLKEKTDDTSGVENDKEDLLK	555
qq	1064	SSTASPATLAGIAADKTDAGKTASASDKNAATAGGPTATGTPTAATTPATATAPPEISAG	1123
οy	556	ELA (ELA (ELA (ELA (	605
qq	1124	GEAKSKNAEEEAAATAGAATVATAGTPATGASAASAGEATTATGATATAAAKGVGKPETA 1	1183
οy	909	RMVGSKTVSQCKN	651
g	1184	TEPAGTAAKGADSRPDANDPLAKTASKAINAEGYNAIGGNSSSSSNATGASAP 1	1237
δ	652		211
qq	1238	VQGVTLNGFKPGYQTVVWANVKASTGGDDSGANAGGAAPGSLAATNASIATSGDKIVKTT 1	1297
δγ	678	PVVEDEEMEASGVEEEMVE	719
qq	1298	PSSRAPNSTSSTAANESSSGAGVNTYGHTATTAGNYLGQKLKAAQVEGLG	1347
ογ	720		992
g	1348	AGNELHSDVSESKRKRFELNSGEAGGNATSAMTNSSTSGSMNISNSHGLKANAKDGSMMA 1	1407
οy	167	PKPPAT	772
qq	1408	KTSMASTSSASVVVTSTPSASSSSLSSASSMLLISAASVMSTAAGATSSSTATTTATASA 1	1467
οy	773	LGADGPPPGPIEP 7	962
q	1468	ISLPLLADGSGNSMVNANEILALDGKDKLASCFVCKAEACPRTRPLKKGRGQQYGIPDET 1	1527
δ	197	TAAAPPVEE	839
ପ୍ର	1528	IPAGARVCNSCQCKSVRSRYPNCPLPTCPNPKDRAQRLRNIPSRLFELAPEVRDPL 1	1583
ογ	840		872
g	1584	MAEFQIPPHATRCCSACLMRIRRKLDPQLNLTDGSSGGAGSGSGGDETDVSTSSCDEREP 1	1643
ογ	873	GPAKGKDAEAABATAEGALKAEK	895
QQ	1644	GGSDIASVESPENLQRHKSLTMVKQQQQQQQQQQQQQQQQQQQQQQQQLSQPPP 1	1698
οy	968		912
q	1699	PAPQQQKGSSGRGGDQCTPLITPTRMSSKSGSGAQTAGDNERLLPPAAGQAPKKQKTS 1	1758
δ			951
යු	1759		1818
δý		PPAPPPPONLO	1006
අ	1819		1859
δ	1001	PESDAPQQPGSSPRGKSRSPAPPADKEAFAAEAQKLPGDPPCWISGLPFPV 1	1057
qq	1860		1904
ο.			1105
8			1962
o d	1106	PPLISSAKHPSVLERQIGAISQGMSVQLHVPYSEHAKAPVGPVTMGLPLPMDPKKLAPFS 1 	1165 2016
λo	1166	GVKQEQLSPRGQAGPPESLGVPTAQEASVL-RGTALGSVPGGSITKGIPSTRVPSDSA 1	1222
q	2017		2073

ç qa	1223 ITYRGSITHGTPADVLYKGTITRI- : :          :: 2074 VHPAHPSHTQHPAHPQHSSHGQHTQLQ	IGEDSPSRLDRGREDSLPKGHVIYEGKKGHVLS 12:	279
οy	1280 YEGGMSVTQCSKEDGRSSSGPPHETAAPK	RTYDMMEGRVGRAISSA 13	325
qq	Db 2127AGGSSSGGGGPSSSDRHHGPPPPTMSMKHIVRSGGMYRGDT		184
ò	1326SIEGLMGRAIPPERHSPHHLKEQHHIRG  :::  :	RSYVEAQEDYLRREAK 137 : : :	376
đ	2185 PTRSVKSIGGGGVVP	GVLPGVPGIALYLQPVPVPVPISISGQGQ 222	228
οy	1377 LLKREGTPPPPPPSRDLTEAYKTQALGPLKLKP	AHEGLVATVKEAGRSIHEIPREE 14	432
QΩ	2229 LPPKAGQPPPAQPPSGRGVAKV	PPKLSPQQAHHLHPSHGHSPSQQQQQQQQQQQ	281
QY	1433 LRHTPELPLAPRPL	KEGSITQGTPLKYDTGASTTGSKKHDVRSLIGSPGRTFPPVHPL 14	490
g	2282 QQQQQQAAAAQQQLLVKSGSIIHGTP	ANSAQQQIIVHAPATAAAAPSSLFSPKFD- 23	336
οy	1491 DVMADAR	- 15	531
Ωp	Db 2337GLVRQTTPEGVGSVGPGGASGSGKHGSITQGTPLHMPPHHLESKRPYESYYK	TPLHMPPHHLESKRPYESYYKS 238	389
ΟŊ	QY 1532ELGKPRQSPLTYEDHG	APFAG 15	552
qq	2390 SQRHSPAQQPGGNQQLPPPPQQSSPQAPPPQGYGVGV	SSPYARSPFAGVVEQPQVLSTRQ 24	449
QY	Qy 1553HLPRGSPVT	MREPTPRLQEGSLS- 157	575
qq	Db 2450 IVMHDYITSQQMQGQQQQQQQQQQQRNMSRGSSASGGGGGGGSDKESPSPRNSVGSASG	GGGGSDKESPSPRNSVGSASG 250	509
δλ	QY 1576SSKASQDRKLTSTPREIAKSPHSTVP	HSTVP	605
Ωp	2510 FAYGGDKESAPRGRPEYSSRASPADHVNSTP	SPHRIPPPQRQGVIQRHNTGSKPP 250	564
оу.	1606 HPISPYEHLLRGVS	RGIPLDAAAYY 1	650
Q	Db 2565 SPAAPPPSRMHMPPYQYAPSGHDALASFVDVAVQQPQLPV	PSQKDDKSPGPSTAPGQ 26	621
QY	1651 LPRHLAPNPTYPHLYPP	YLIRGYPDTAALENROTIINDYITSQQMHHN 16	869
QQ	2622 VPGSGPPLGP	тгнинитгуоог-аоонтк 268	680
οy	QY 1699 TATAMAQRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAMDRL	17	758
QQ	Db 2681 SLNVAAQ-VDMQRQMDQAKRVMRHQQHQVQQQQQQQQQQ	NHALERDR- 27	728
Qy	1759 AYLPTAPOPFSSRHSSSPLSPGGPTHLTKPTTTSSS	ERDRDRERDRDREREKSILTST 181	818
q	2729EMQERMRERDRE	REREREREGEREREREREREREGORA 277	772
QY	1819 TTVEHAPIWRPGTEQSSGS	SGSSGGGGSSSRPASHSHAHQHSPISPRTQDAL 187	871
qq	2773 RRVVAEEREHDSRRMERMFAGNVV	-PGQFLRA 281	815
Qy	QY 1872 QQRPSVLHNTGMKGIITAVEPSKPTVLRSTSTSSPVRPAATFPPATHCPLGGTLDGVY	PT 1	931
q	Db 2816SVPETGPPRSIPDRERESYYRQAHGGPAPEDIP	AHGGPAPEDIPGQLSAQS 285	855
Qy	OY 1932 IMEPVLLPKEAPRVARPERPRADTGHAFLAKPPARS	GLEPASSPSKGSEP- 1	981
QQ	2856 LIDAIIKHEINRSNDATAGPGREFPRPSFVHAPL-	-PPRGSGSGGGTGTRSSPANVLHPM 291	913
οy	1982RPLVPPVSGHATIARTPAKNLAPHH	PPASASDPHREKTOS 202	028
qq	2914 YLRDLRQPLDGGAGSMLTAENNGKP	SSSGSPSVINIDEDQERISAAAAAVAQQQQQQQ 29:	971
οy	2029 KPFSIQELELRSLGYHGSSYSPEGVEPVSPVSSP	SLTHDKGLPKHLEELDKSHLEGELRP 200	088
qq	Db 2972 APPPSQSSQSRSVHGQLRTPTS-QSGGSAPSPQQIHTKSIT	TKSITFGELTDSIITSDYGT 3020	026

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Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., In P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Brandon R.C., Moyteman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Hell G., Nelson C.R., Miklos G.L.G.,
A Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Berman B.P., Bhandari D., Botshakov S.,
Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Daviez S.M.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAVY------PLLYRDGEQTEPS-RMGSKSPGNTSQPPAFFSKLTESNSA 2281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3253 AAVHAAHVAHAAHVAHAAAMELQHRSKEPPPPEISVSRKTPNQYEVVDASGRRSAGSGSV 3312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2282 MVKSKKQEINKKLNTHNRNEPEYNISQPGTEIF-----NMPAITGTGLMTYRSQAVQEHA 2336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3313 SV----SVSGANSHHSPYHPPAAAYAPSTYAFPYSALNVPGAAG-----GLPPHQ 3358
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    --LLQTAPGVKGH----QR 2131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2397 PG--GGGKAKVSGRPSSRKAKSPAPGLASGDRPPSVSSVHSEGDCNRRTPLTNRVWEDRP 2454
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Eukaryota: Metazoa; Arthropoda; Trachesta: Hexapoda; Insecta;
Ptersygota: Neoptera: Endopterygota: Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                            N------PHIRPPYMAYLQETQSILPPDRWKQNRRMQQKAEEANDHSQQQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2189 DHGAPARGSPHSEGGKRSPEPN-KTSV-----LGGGEDGIEPVSPPEGMTEP--GHSR
                                                                                                                                                                                                                                         3073 ООНОООННАООООООООННАООННАООННРОМРСТСЅСЅАРССАСССССССССССССССССССАСКАЅ
                                                                                                                                                                                                                                                                                                                                                                                                          3133 TPGEDGRNIIRMPQAVSPRKFNHEMMLHHVMGTTGAGGEAGQFFLPSRVVLPEQRGTPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STINMGLEAIIRKALMGKYDQWEESPPLSANAFNPLNASASLPAAMPITAADGRSDHTLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3385 LGAVGGGVSLVVGGGSG-----GIAGG--PGCVS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2455 SSAGSTPFPYNPLIMRLQAGVMASPPPPGLPAGSGPLA-----GPHH------
                                                                                                                                                        2132 VVTLAQHISEVITQDYTRHHPQQLSAPLPAP-LYSFPG------
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Last annotation update)
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2089 KOPGPVKLGGEAAHLPHLRP----LPESQPSSSP-
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MEDLINE-20196006; PubMed-10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2497 -- AWDEEPKPLLCSQYETLSDSE 2517
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SMR OR CG4013.
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RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Goler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K., Glogk A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harvey D., Heiman T.J., Wel M.-H., Ibeqwam C., Alaris N.L., Harvey D., Heiman T.J., Wel M.-H., Ibeqwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Mattei B.E., McIntosh T.C., McLeod M.P., McPherson D., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Moshredi A., Monnt S.M., Moy W., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Ra Merkulov G., Milshina N.Y., Moharry C., Morris J., Moshrefi A., Monnt S.M., Moy W., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Ra Palazzolo M., Pittnan G.S., Pan S., Pollard J., Puri V., Reses M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Smith T., Shier E., Spradling A.C., Stapleton M., Strong R., Sun E., Syradling A.C., Stapleton M., Strong R., Sun E., Syradling A.C., Stapleton M., Strong R., Sun S., Modage T., Worley K.C., Wu D., Yang S., Yao Q.A., Walliams S.M., Myers E.W., Rubin G.M., Venter E., Wang S., Yao Q.A., Milliams S.M., Myers E.W., Rubin G.M., Venter J.C.; R. The genome sequence of Drosophila melanogaster.; Science 287:2185-2195(2000).

EMBL; Abdoll A.F. F., Zach M., Thong W., Zhou X., Zhu X., Zhu X., Zhu K., Thong W., Thong W., Zhou X., Zhu S., Zhu X., Smith H.O., R. Therbro., Trandon. A., Thong W., Thon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----PPPIESKHRS--LVQIIYDENRKKAEAAHRILEGLGPQVE------LPLYN 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369068 MW; 74C8004F9DA8F8D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 21.0%; Pred. No. 5.4e-45;
Matches 699; Conservative 346; Mismatches 1056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.0%; Score 1060; DB 5; 21.0%; Pred. No. 5.4e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00249; myb_DNA-binding; 1.
PRINTS; PR00308; ANTIFREEZEI.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
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SEQUENCE 3502 AA; 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001005;
InterPro; IPR002086;
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7.	498		
ð	1076	KAQAAQPQCIIDSMTTGVWTRLQREQQQKSGGRSSAVAERERAERAARAERERAABA 1135	
<b>≥</b>	529	AEKEEERPE	
ą	1136	AKAAESAAEKASAATKAVEATAAGEKVAKAAAAAAAAAATTATTATTTTSSSTSSSSSA 1195	
<u></u>	538	555 VENDKEDLLK EKTDDTSG 555	
ą	1196	SSASTASSSTASPATLAGIAADKTDAGKTASASDKNAATAGGPTATGTPTAATTPATATA 1255	
<u>⊁</u>	556	EDNDEKEAVASKGRKTANSQGRRKGRITRSMANEANSEEAITPQQSA 602	
۾	1256	PPEISAGGEAKSKNAE	
<u>~</u>	603	ELASMELNESSRWTEEEMETAKKGLLEHGRNWSAIARWVGSKTVSQCKN 651	
ą	1316	VGKPETATEPAGTAAKGADSRPDANDPLAKTASKAINAEGYNAIGGNSSSSSSN 1369	
ž.	652	ILQQHK           :	
ð	1370	ATGASAPVQGVTLNGFKPGYQTVVMANVKASTGGDDSGANAGGAAPGSLAATNASIATSG 1429	
≿	671	LKMEKERNARRKKKKAPAAASEEAAFPPV	
ð	1430	DKIVKTTPSSRAPNSTSSTAANESSSGAGVNTYGHTATTAGNYLGQKLKA 1479	
≿	714	-EEEMVEEAEALHASGNEVPRGECSGPATVNNSSDTESIPSPHTEAAKDTG 763	
ą	1480	AQVEGLGAGNELHSDVSESKRKRFELNSGEAGGNATSAMTNSSTSGSMNISNSHGLKANA 1539	
⋩	764	QNG	
ą	1540	::  KDGSMMAKTSMASTSSASVVVTSTPSASSSLSSASSMLLISAASVMSTAAGATSSSTAT 1599	
<u>&gt;</u>	773		
ă	1600	TTATASAISLPLLADGSGNSMVNANEILALDGKDKLASCFVCKAEACPRTRPLKKGRGQQ 1659	
λ	793	PIEPTPASEATGAPTPPPAPPSPSAPPVVPKEEKEEETAAA 834	
ą	1660	YGIPDETIPAGARVCNSCQCKSVRSRYPNCPLPTCPNPKDRAQRLRNIPSRLFELA 1715	
<b>≿</b>	835	PPVEEGEEGKPPAAEELAVDTGKAEEP	
ą	1716	:	
λ	866	CTEEAEEGPAKGKDAEAAEATAEGALKAEK895	
ą	1776	SCDEREPGGSDTASVESPENLQRHKSLTMVKQQQQQQQQQQQQQQQQQQQQQQL 1830	
Ż.	968		
ð	1831	SQPQPPPPPAPQQQKGSSGRGGDQGTPLIITPTRMSSKSGSGGAQTAGDNERLLPPAAGQA 1890	
<u>⊁</u>	907		
ą	1891		
Ā	945	LIPTGDPRANASPQKPLDLKQLKQRAAAIPPIQVTKVHEPPREDAAPTK	
۾	1951	GTGGGVQPGGAAGQOVNGPISMRREA	
<u>≻</u> ,	1000	PPPQNL	
٩	1998	QPKGGQGQQQQQQQQQQQQQQQQQQQQQQQQQQQQ	
¥	1051	SGLPFPVPPREVIKASPHAPDPSAFSYAPPGHPLPLGLHDTARPVLPR 1098	

g	2044ERKELT	IVREYRODPGILKQQQQQQQQQQGAPPTSAAGSLPHGTSVQKLTTR	50 50 50
Qy	1099 PPTISNPPPLISSAKHPSVLERQ	IGAISQGMSVQLHVPYSEHAKAPVGPVTMGLPLPMDP	1158
qq	::       ::     ::     ::   ::     ::     ::     ::     ::     ::     ::     ::     ::     ::     ::     ::     ::	:     :	2148
δλ	1159 KKLAPFSGVKQEQLSPRGQ	PESLGVPTAQEASVL-RGTALGSVPGGSITKGIPST	121
QQ	2149 ASSAGGIGVDKATITPVVKSS	SGSSKSGGGSASSHSTATPPETIIYNVPVAHPQRGIPP-	220.
ΟŊ	y 1216 RVPSDSAITYRGSITHGTPADVLYKGTITRI	LYKGTITRI-IGEDSPSRLDRGREDSLPKGHVIYEG	127
qq	2208	LQVPEPEPQTL	226
ΟY	1273 KKGHVLSYE	SSGPPHETAAPKRTYDMMEGRVGRAISSA	132
qq	2266	AGGSSSGSGSGGPSSSDRHHGPPPPTMSMKHIVRSGGMYRGDTVTVPSLA	231
οy	1326	SIEGLMGRAIPPERHSPHHLKEQHHIRGSITQGIPRSYVEAQED	136
qq	o 2317 APSSYLYPTRŠVKTIGGGGVVP	GVLPGVPGSALYLQPVPVPI	236(
δy	1370 YLRREAKLLKREGTPPP	PPPSRDLTEAYKTQALGPLKLKPAHEGLVATVKEAGRSI	142
qq	b 2361 SISGQQQLPPRAGQPPPAQPPSGRGVAKV	GVAKVPPKLSPQQAHHLHPSHGHSPSQQQ	241
QY	1426 HEIPREELRHTPELPLAPRPL	KEGSITQGTPLKYDTGASTTGSKKHDVRSLIGSPGRT	148
qq	b 2414 QQQQQQQQQQQAAAAQQQLLVKSGSITHGTP	SGSITHGTPANSAQQQIIVHAPATAAAAPSSL	246
QY	Y 1484 FPPVHPLDVMADARALERACYEESLKS	-RPGTASSSG GSIARGAPVIVPELGKPR	153
qq	2470 LSPKFD	GLVRQTTPEGVGSVGPGGASGSGKHGSITQGTPLHMPPHHLE	251
Oy	Y 1539 SPLTYEDHGAPFAGHLPRGSPVTMREPTPRLQEGSLS	REPTPRLQEGSLSSSKASQDRKLTSTPREIAKSPHS	159
QQ	b 2518 SKRPYESYYKSSQRHSPAQQPGGNQQLPP	00LPPPQQSS	255
δy	1599 TVPEHHPHPIS	PYEHLLRGVSGVDLYRSHIPLAFDPTSIPRGIPLDAAAAYYLPRHLAPN	165
qq	b 2553PQAPP	:   :   :   :   :   :   :   :   :   :	257
οy	1659 PTYPHLYPPYLIRGYPDTAALEN	ITSQQMHHNTATAMAQRA	171
qq	2573 PFAGVVEQPQV	LSTRQIVMHDYITSQQMQGQQQQQQQQQQQQRRMSRGSSA	262
Qy	1714SPRES-	SLALNYAAGPRG	173
qq	2624		268
οy	1731 -IIDLS-QVPHLPVLVP	T.	178
ΟP			274
ΟŊ	y 1782 pr		178
qq	2741	 РТАННDQRYRDLTLHHHHHTLVQQQIAQQQHYRSLNVAAQVDMQRQMDQAKRVMRHQQHQ	280
δλ	1787	KPTTTSSSERERDRDREREKS	181
qq	2801	: :	286
δλ	Y 1814 ILTSTTTVEHAPIWRPGTEOSSGS	OSSGSSGSSGGGGSSSRPASHAHQHSPISPR	186
qq	2861 EQDRARRVVAEEREHDS	REMERMFAGNVVTGSGGAGGGGPS-PGQFLRA	2908
Οy	1867 TQDALQQRPSVLHNTGMKG	IITAVEPSKPTVLRSTSTSSPVRPAATFPPATHCPLGGTLD	192
qq	5909	SVPETGPPRSIPDRERESYYRQAHGGPAPEDTPGQLS	294
οy	1927 GV	PERPRADTGHAFLAKPPARSGLEPASSPSK	1977
qq	2946 A-	-QSLIDAIIKHEINKSNDATAGPGREFPRPSFVHAPLPPRGSGSGGTGTRSSPAN	300]

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3002 VLHPMYLRDLRQPLDGGAGSMLTAENNGKP--SSSGSPSVINIDLDQERISAAAAAVAQQ 3059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3304 IEKYVKTRIAEVMRDDIGYGKNRTVEVRTEDEV------TADMVAHSHA 3346
                                                                                                                   3060 QQQQQAPPPSQSSQSRSV--HGQLRTPTS-QAGGSAPSPQQIHTKSIT--FGELTDSIIT 3114
                                                                                                                                                                   GELRPKQPGPVKLGGEAAHLPHLRP-----LPESQPSSSP-----LLQTAPGVKGH- 2129
                                                                                                                                                                                                                                                      2130 ---QRVVTLAQHISEVITQDYTRHHPQQLSAPLPAP-LYSFPGASCPVLDLRRPPSDLYL 2185
                                                                                                                                                                                                                                                                                                                                                                            3206 ---GOGG-GSGGPGSGGGAGRASTP-----GEDGRNIIRMPO-----AVSP 3243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2385 AADGRSDHTLTSPG--GGGKAKVSGRPSSRKAKSPAPGLASGDRPPSVSSVHSEGDCNRR 2442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2443 TPLTNRVWEDRPSSAGSTPFPYNPLIMRLQAGVMASPPPPGLPAGSGPLA----GPHH- 2496
    ---PPASASDPHR 2023
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MEDLINE=99379811; PubMed=10451362;
MEDLINE=99379811; PubMed=10451362;
Mewberry E.P., Latifi T., Towler D.A.;
The RRM domain of MINT, a novel msx2 binding protein, recognizes and regulates the rat osteocalcin promoter.";
Biochemistry 38:10678-10690(1999).
EMBLA AR156529; AAD55931.1; -...
InterPro; IPR000504; -...
                                                                                                                                                                                             SDYGTN------PHLRPPYMAYLQETQSILPPDRWKQNRRMQQKAEEAKHHS
                                                                                  EKTQSKPFSIQELELRSLGYHGSSYSPEGVEPVSPVSSPSLTHDKGLPKHLEELDKSHLE
                                                                                                                                                                                                                                                                                                                                         PPPDHGAPARGSPHSEGG--KRSPEPNKTSVLGGGEDGIEPVSPPEGMTEPGHSRSAVYP
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2272 FSKLTESNSAMVKSKKQEINKKLNTHNRNEPEYNISQPGTEIFNMPAITGTGLMTYRSQA
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                                                                                                                                                                                                                                                                                                3161 ОООООООНОООННАООООООООННАООННРОМРЕТСЯЗВАРССА---
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TEMBLrel. 16, Last annotation update)
MSX2 INTERACTING NUCLEAR TARGET PROFEEN.
1978 GSEP --- RPLVPPVSGHATIARTPAKNLAPHHASPDPPA-
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PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
SMART; SM00360; RRM; 1.
SEQUENCE 3576 AA; 390966 MW; 9B56855D8A8
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                                                                                                                                                                                  SEDLTKD--RSL-----TGKLEPVSPP------SPPHTDPELELVPPRLS 168
                                                                                                                                                                                                                                                                                                                                                                                   RYDQLMEALEKKVERIENNPRRRAKESKVREYYEKQFPEIRK------- 342
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                                                                                --RSQELHLRPESHSYLPELGKSEMEFIESKRPR----LELLPDPLLRPSPLLATGQPAG 131
                                                                                                                                                   EYRSDPYEQDIREYSYRQRERERERERFESDRDHERRPIERSQSPVHLRRPQSPGVSPAH 697
                                                                                                                                                                                                             SERLPSDSERRLYRRSSERSGSCSSVSPPRYDKLEKARLERYTKNEKADKERTFDPERVE 757
                                                                                                                                                                                                                                             KEELIQNMDRVDREITMVEQQISKLK----KKQQQLEEEAAKPPEPEKPVSPPPIESKH 223
                                                                                                                                                                                                                                                                                                       RSLVQIIYDENRKKAEAAH--------RILEGLGPQVELP---------------------255
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                               Gaps
                                                                                                                                                                                                                                                              -LYNQP-----SDTRQYHENIKINQAMRKKLILYFKRRNHA----RKQWKQKFCQ--
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                              Indels 1042;
Length 3576;
                          Conservative 347; Mismatches 1114;
4.4%; Score 576; DB 11;
19.1%; Pred. No. 1.5e-20;
                                                            GLLEYQHHSRDYASHLSPGSIIQPQRR-RPSLLSEFQPGNE-
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              Similarity
    Local 590;
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Matches
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	4 GECSGPATVNNSSDTESIPSPHTEAAKDTGQNGPKPPATLGADGPPPG		0 SSAPEKAEEAAEAPSPAGEKPAEPAPVSEETKLVSEPVSVPVEQPROSDVPPGEDSRDSO			4 DTGKAEEPVKSECTEEAEEGPAKGKDAEAAEATAEGALKAEKKEGGSGRAT :	S TAKSSGAPQDSDSSATCSADEVDGG  TAKSSGAPQDSDSSATCSADEVD			3 KPAPPAPPPPQNLQPESDAPQQPGSSPRGKSRSPAPPADKEAFAA		BAQKLPGDPPCWTSGLPPPVPREVI-KASPHADDPSAFSYAPPGHPLPLGL		TARPVLPRPPTISNPPPLISSAKHPSVLERQIGAISQGMSVQLHVPYSEHAKAPVGPVTM	. 19			:       : :     : :   : :   : :   : :   : : :   : : :   : : :   : : : :   :	1 GITTRIIGEDSPSRLDRGREDSLPKGHVIYEGKKGHVLSYEGGMSVTQCSKEDGRSSSGP	PHETAAPKRTYDMMEGRVGRAISSASIEGLMGRAIPPERH		RSYVEAQEDY	7QEAKGSKAEVTPPRKDKGRQKTTRRKRNANKKVVAITETRASEAEQT		S QSESPAAEEATAATPEAPQ EEKPSEKPPSPPAECTFDPSKTPPAESLSQENSAAEKTP	7 LKYDTGASTTGSKKHDVRSLIGSPGRTFPPVHPLDVMADARALERACYEESLKSRPGT	ACCOUNT OF THE POST OF THE POS	> ASSGGSTANGAPYLVPELGKRQSPLTYEDHGAPPAGHLPRGS	PVTMREPTPRLQEGSLSSSKASQDRKLTSTPREIAKSPHSTV	
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δί	09	PISPYEHLLRGVSGVDLYRSHIPLAFDPTSIPRGIPLDAAAAYYLPRHL 1659
g	2498	Apv
Oy Dp	1656	APNPTYPHLYPPYLIRGYPDTAALENRQTIINDYITSQQMHHNTATAMAQRADMLRGLSP 1715
δ <sub>γ</sub>	1716	RESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAMDRLAYLPTAPQPFSSRHSSS 1775 :     : : :       :       ::       :       :
οy	1776	ERERDRORERDRORE
QQ	2614	TPAGPVNLLKGPVNVLTGPVNVLTTPVSATVGTVNAAPGP 2653
δλ	1830	GTEQSSGSSGSSGGGGGSSSRPASHAHAHQHSPISPRTQDALQQRPSVLHNTGMK 1884
qq	2654	VTAACGVTATTGTAAVTGAVTAPAAKGKQRASSNENSRFHPGSMSVIDDRPADTG-S 2709
ογ	1885	GGTLDGVYPTLMEPVLL 193
q	2710	GAGLRVNTSEGVVLLSYSGQKTEGPQRISAKISQIPPASAMDI 2752
g oy	1939	PKEAPRVARPERPRADTGHAFLAKPPARSGLEPASSPSKGSEPRPLVPPVSGHATIARTP 1998
Qy	1999	ASASDPHREKTQSK PFSIQELELRSLGYHGSSYSPEGVEPVSP
qq	2797	
ογ	2059	VSSPSIJTHDKGLPKHLEELDKSHLEGELRPKQPGPVKLGGEAAHLPHLRPLPESQPSSSP 2118
Ωp	2805	VIS-SVKTDRPSLEKPEPIHLSVSTPVTQGGTVKVLTQGINTPPVLVHNQLVLTP 2858
ογ	2119	LLQTAPGVKGHQRVVTLAQHISEVITQDYTRHHPQQLSAPLPAPLY 2164
qq	2859	SIVITNKKLADPVILKIETKVLQPANLGPTLIPHHPPALPSKLPAEVN 2906
δλ	2165	SFP-GASCPVLDLRRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEPNKTSVLG 2216
qq	2907	HVPSGPSTPADRIIAHLATPKPDTHSPRPTGPTPGLPPRPCHPSSTTSTALSTNATVMLA 2966
δy	2217	GGEDGIEPVSPPEGMTEPGHSR 2239
q	2967	AGIPVPQFISSIHPEGSVIMPPHSITQTVSLGHLSQGEVRMSTPTLPSITYSIRPETLHS 3026
δλ	2240	AVYPLLYRDGEQTEPSRMGSKSPGNTSQPPAFFSKLTESNSAWVKSKKQE 2289
qq	3027	PRAPLQPQQIEARAPQRVGTPQPATTGVPALATQHPPEEEVHYHLPVARAAAPVQSEVLV 3086
δλ	2290	INKKLNTHNRNEPEYNISQPGTEIFNMPAITGTGLMTYRSQAVQEHASTNMGLEAIIRKA 2349
QΩ	3087	MQSEYRLHPYTVPRDVRIMVHPHVTAVSEQPRATEGVVKVPPANKAPQQLVKEA 3140
δy	2350	EMGKYDQWEESPPLSANAFNPLNASASLPAAMPITAADGRSDHTLTSPGGGGKAKV-SGR 2408
qq	3141	YKTSDAKAVPAPAPVPVPVPYTPAPPPHGEARILTVT 3178
οy	2409	RKAKSPAPGLASG
qq	3179	PSSQLQGLPLTPPVVVTHGVQIVHSSGELFQEYRYGDVRTYHAPAQQLTHTQF 3231
δλ	2463	PY-NPLIMRLQAGVMASPPPPGLPAGSGPLAGP 2494
qq	3232	PVASSISLASRIKTSAQVPPEGEPLQSTQSAQP 3264
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Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
Pteryyota: Neotera: Endopterygota: Diptera: Brachycera: Muscomorpha:
Ephydroidea: Drosophilidae: Drosophila.
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                                                                                                                                                                                                                                                                                                                          Papagiannakis G., Spanos L., Siden-Klamos I., Louis C., "Sequencing the distal X chromosome of Drosophila melanogaster."; Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
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4.3%; Score 574; DB 5; Length 5327;
Best Local Similarity 19.4%; Pred. No. 3.1e-20;
Matches 531; Conservative 332; Mismatches 1123; Indels 752;
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Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AL031128; CAA20006.1; -.
FlyBase; FB900025392; futsch.
SEQUENCE 5327 AA; 575942 MW; FEFEE23A118FF38A CRC64
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                                                                                                                                                                                              EMVEEAEALHASGNEVPRGECSGPATVNNSSDTESI ----PSPHTEAA----KDTGQNGP
                                                                                                                                                                                                                                                                                                              ---PPR----RTSRAPIEPTPASEAT
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                                                                               RQNLDEILQQHKLKMEKERNARRKKKKAPAAASEEAAFPPVVED----EEMEASGVSGNEE
                                                                                                                  ------SECTEEAEEGPAKGKDAEAAEATAEGALK-AEKKEGGSGRATTAKSSGA
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AESIKSDITKGEKSPLPSKEVSRPESVVGSIKDEKAESRRESVAESVKPESSKDATSAPP 2964	-EHHPHPISPYEHLLRGVSGVDLYRSHIPLAFDPTSIPRGIPLDAAA 1647 :	AYYLPRHLAPNPTYPHLYPPYLIRGYPDTAALENRQTIINDYITSQQMHHNTATAMAQRA 1707	:     :     :     :       :			AUDAL - ALLETANDETS SONDSTELS OF STATEMENT TO STATEMENT MENTAL TO STATEMENT TO STAT	EKSILTSTTTVEHAPIWRPGTEQSSGSSGSGGGGSSSRPASHSHAHQHSPISPRTQDA 1870	EKSPLPSKEASRPASVAESVKDEADKSKEESRRESGAEKSPLASKEASRPASVAESIKDE 3234	LQQRPSVLHNTGMKGIITAVEPSKPTVLRSTSTSSPVRPAATFPPATHC 1919  : :     :     :     :     :	S		KGSEPRPLVPPVSGHATIARTPAKNLAPHHASPDPPAPASASDPHREKTQSKPFSIQEL 2036	ESVAEKSPLASKEAS	ELRSLGYHGSSXSPEGVEPVSPVSSPSLTHDKGLPKHL-EELDKSHLEGELRPKQPG 2092		PARLOGGEMANILPHIKPLPESORSSPPLIQIAPGYKGHOKVYLAGHISEV 2142 	ITQDYTRHHPQQLSAPLPAPLYSFPGASCPVLDLRRPPSDLYLPPPDHGAPARGSPHS 2200	SPLPSKEASRPTSVAESVKD 3529	EGGKRSPEPNKTSVLGGGEDGIEPVSPPEGMTEPGHSRSAVYPLLYRDGEQTEPSRMGSK 2260			FNMPAITGTGLMTYRSQAVQEHASTNMGLEAIIRKALMGKYDQWEESPPLSANAFNPLNA 2373	TSVAESVKDEADKSK	SASLPAAMPITAADGRSDHTLTSPGGGGKAKVSGRPSSRKAKSPAPGLASGDRPPSVS-S 2432	KDETEKSKEESRRESVTEKSPLPS-KEASRPTSVAES 3711	RTPLTNRVWEDRPSSAGST 2460 	RY; PRT; 3261 AA.	1. 12, Created) 1. 12, Last sequence update)
	-EHHPHPISPYEHL		:     :     :     :     :       :										EASRPASVAESIKDEAEKSKEESRR					AEKSKEESRRESVAEKSPLPSK			Spds		TSVAESVKDE	SASLPAAMPITAADGRSDHTLTS	-ASMEASRPTSVAESVKDET	VHSEGDCNR   ::   XNDEAEKSKEESRRESV	RESULT 6 Q9Y556 ID Q9Y556 PRELIMINARY;	(TrEMBLrel.
2905	1602	1648	3024	1708	3073	3125	1811	3175	1871	1920	3290	1977	3331	2037	2000	3439	2143	3494	2201	2261	3584	2314	3632	2374	3661	2433 3712	LT ( 56 Q9Y5!	03455 01-R 01-R
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996 YESSRLSFLLRDREDKLRERDERLSSSLERNKFYSFALDKTITPDTKALLERAKSLSSSR 1055
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01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 357.0 KDA PROTEIN.
HOWO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        797 DEYERRSLVHEVGKP--PQDVTDD-----SPPSKK-------K
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                                                                                                                                                                                                                                                                                                            Rhodes S., Huckle E.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AA1096858; CAB51072.1; -
InterPro: IPR000504; -
Pfam; PF00076; rrm; 2.
SWART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 3261 AA; 357039 MW; F8BB6A645DD9B6BC CRC64;
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                   NCBI_TaxID=9606;
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Qy Dp	1329	GADGPPGPPTPPRRTSRAPIEPTPASEATGAPTPPPAAPPSPSAPPPVVPKEEKEEET	831 1377
Oy Dp	832 1378	AAAPPVEEGEEQKPPAAEELAVDTGKAEEFPVKSECTEEAEEGPAKGKDAEAA	883 1437
oy op	884 1438	EATAEGALKAEKKEGGSGRATTAKSSGAPQDSDS-SATCSADEVDEAEGGDKNRLLSPRP :	942 1489
oy Dp	943	SL-LTPTGDPRANASPQK-PLDLKQLKQRAAIPPIQVTK	980 1546
O.y	981	VHEPPR	1012
oy d	1013	-	1067
ko da	1068		1327
QY Db	1128		1172
S &	1173	; ; &	1203
o v	1204	PGGSITKGIPSTRVPSDSAITYRGSITHGTPADVLXKGTI-TRIIGED	1250
ργ	1251	SPSRLDRGREDSLPKGHVIYEGKKGH	1298
oy e	1299	GPPHETAAPKRTYDMMEGRVGRAISSASIEGIMGRAIPPERHSPHHL	1355
3 6 2	1356	TQGIPRSYVEAQEDYLRREAKLLKREGTPPPPPPSRDLTEAYKTQ  1     :     :     :     :     :     :       :	1966 1415 2006
λō	1416	ATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGSITQGTPLKYDTGASTTGS	1470
<u>අ</u>	2007	ROSSQEISVEERTPTKASVPPDLPPPPQPAPVDEEPQAR HDVRSLIGSPGRTFPPVHPLDVMADARALERACYEESIKSRPGTASSSGGSTARGADV	2044 1528
7 g	2045		2084
yo d	1529	IVPELGKPRQSPLTYEDHGAPFAGHLPRGSPVTMREPTPRLQEGSLSSSK	1578
δò	1579	HLLRGVSGVDLYR	1625
qq	2128	SSTERKILMDPKYVSATSVTSTSVTTAIAEPVSAAPCLHEAPPPPVDSKRPLEE	2181
Oy Dp	1626 2182	SHIPLAFDPTSIPRGIPLDAAAAYYLPRHLAPNPTYPHLYPPYLIRGYDDTAALENRQTI	1685 2234

ΟŽ	PRESSLA	
qq	2235TLAKPAPQTLTGLVSALTGLVNVSLVP-VNALKG 2267	7
. vo	YLPTAPQPFSSRHSSSP	2
qq	2268 PVKGSVTTLKSLVS 2294	4
Qy	REREK	-
QQ	2295NVLTGPVNVLTTPVNATVGTVNAAPGTVNAAASAVNATASAVTVTAGAVTAAS 2347	7
Qy	1842 GGGGGSSSRPASHSHAHQHSPISPRTQDALQQRPSVLHNTGMKGIIT 1888	80
qa `	2348 GGVTATTGTVTWAGAVIAPSTKCKQRASANENSRFHPGSMPVIDDRPADAG-SGAGL 2403	e
Qy	1889 AVEPSKPTVLRSTSTSSPVRPAATFPPATHCPLGGTLDGVYPTLMEPVLLPKEA 1942	2
qq	2404 RVNTSEGVVLLSYSGQKTEGPQRISAKISQIPPASAMDIEFQQSVSKSQVKPDS 2457	7
δλ	1943 PRVARPERPRADTGHAFLA	4
QQ	2458 VTASQPPSKGPQAPAGYANVATHSTLVLTAQTYNASPVISSVK-ADRPSL-EKPEPIHLS 2515	2
οy	1985 1999 1999 1999 1999	6
qq	2516 VSTPVTQGGTVKVLTQGINTPPVLVHNQLVLTPSIVTTNKKLADPVTLKIETKVLQPANL 2575	2
Qy	2000 -KNLAPHHASPDPPAPAPASASDPHREKTQSKPFSIQELELRSLGYHGSSYSPEGVE 2054	4
qq	VNHVP	1
δλ	2055 PVSPVSSPSLTHDKGL	2
qq	2632 SFPRASHPSSTASTALSTNATVMLAAGIPVPQFISSIHPEQSVIMPPHSITQTVSLSHLS 2691	1
δλ	2083 EGELRPKQPGPVKLGGEAAHLPHLRPLPESQPSSSPLLQTAPGVKGHQRVVTLAQH 2138	80
qq	2692 QGEVRANTPILPSITYSIRPEALHSPR-APLQPQQIEVRA 2730	0
Qy	2139 ISEVITQDYTRHHPQQLSAPLPAPLYSFPGASCPVLDLRRPPSDLYLPPPDHGAPAR 2195	2
qq	2731PQRASTPQPAPAGVPALASQHPPEEEVHYHLPVARATAPVQ 2771	1
δλ	2196 GS	н
q	2772 SEVLVMQSEYRLHPYTVPRDVRIMVHPHVTAVSEQPRAADGVVKVPPASKAPQQPG 2827	7
ŏ	2222 IEPVSPPEGMTEPGHSRSAVYPLLYRDGEQTEPSRMGSKSPGNTSQPP 2269	6
ф	2828 KEAAKTPDAKAAPTPTPAVPVPVPVPLPAPAPAPHGEARILTVTPSNQLQGLPLTPP 2883	е
οy	2270 AFFSKLTESNSAMVKSKKQEINKKLNTHNRNEPEYNISQPGTEIFNMPAITGTGLMTY 2327	7
q	2884VVVIHGVQIVHSSGELFQEYRYGDIRTY 2911	н
QY	2328 RSQAVQEHASTINMGLEALIRKALMGKYDQWEE-SPPLSANAFNPLNASASLPAAMP 2382	0
q	2912 HPPAQLTHTQFPAASSVGLPSRTKTAAQGPPPEGEPLQPPQPVQSTQPAQPAPPCPPSQ- 2970	0
δλ	2383 ITAADGRSDHTLTSPGGGGKAKVSGRPSSRKAKSPAPGLASGDRPPSVSSV 2433	m
QQ	2971LGQPGQPPSSKMPQVSQEAKGTQTGVEQPRLPAGPANRPPEPHTQVQRA 3019	on
δλ	2434 HSE-GDCNRRTPLTNRVWEDRPSSAGSTPFPYNPLIMRLQAGVMASPPPPGLPAGSGPLA 2492	0
qq	3020 QAETGPTSFPSPVSVSMKPDLPVSLPTQTAPKQPLFVPTTSGPSTPPGLV 3069	0
οy	2493 GPHHAWDEEPKPLICSQ 2509	
qq	3070 LPHTEFQPAPKQDSSPHLTSQ 3090	

RESULT	1 110		
E E	HX6 QOHIX6 PRELIMINARY; PRT; 1966 AA.	δŏ	928
	(TrEMBLrel.	qa	533
	(TremBirel, 15, (TremBirel, 16,	QY	988
DE		qa	579
886	ous on coords. Drosophila melanogaster (Fruit fly). Bukarvota Motanoa, Arthonoga, manhott, Houseda, Trootta	Qy	1040
388	Lunarjota, metazda; Athiopoda; Machedia; hexapoda; Insecta; Pterygota: Neoptera; Endopterygota: Diptera; Brachycera; Muscomorpha; Enhudrojdas: Drocophilidae: Drocophil	qa	639
3 × ×	brigatorada, brosopiittidae, brosopiitta.   CEL_TaxID=7227;   11	QY	1098
RP 40	M N.A.	q	657
R R	for provinel and westral log describerant	Qy	1157
RT	T Goodson's Anno	qq	691
3 25 25		Qy	1216
88	SEQUENCE 1966 AA; 208033 MW; 96AF90E2082E770C CRC64;	qu	728 (
ć	A 29. CANYA EES. NO E. TANATH	Qy	1275 (
N Be	900	qu	753
إ	TOPWVPVOPDBTTDVODET OPDBANCE	Qy	1330
3 6	AVKEITER VEEELKAAKAKELOEKMASK	qa	794
3 8	TINGLERORISEROMDOLANTEDBALVARACODERSTRANGIANDARANGERAKNY	Qy	1373
; A	:	qu	832
2	NAMACEÓ PER PREDEVENDA UNO TANGENTA DA COL EDUNA A COLOR A	Qγ	1433
5 A		ପୁ	869
3	BROK COOLOO MARKA	Qy	1477
; a	ANGUN CACCACACACACACACACACACACACACACACACACAC	QΩ	929
2	THE THE THE THE TABLE THE THE THE THE THE THE THE THE THE TH	Qy	1537
;	A COLOR DE LA COLO	<b>q</b> 0	973
3 8	TABE CONTRACT TO DESCRIPTION TABLET CONTRACT TO DESCRIPTION OF THE CONTRACT TO DESCRIPTION OF	Οy	1567
5 6	THE THE TEST WAS CONTROLLED ON THE TANK TO CAN THE TENT TO CONTROLL TO CONTROL	qa	1033
3 8	OWE WERE FOUND DEFECT TO BE A SEPTIAL CONTINUE OF THE CONTINUE	Qy	1624
; £		qa	1087
}	THE THE THE THE TREE TO COLUMN CONTRACT TO COLUMN THE TREE TO COLUMN T	Qy	1684
3 6	CKENERGER DOLCE THE THE CONTROL OF THE CANADA TARGET OF THE CANADA TARGE	qa	1115 (
3 8	CONTRACTOR TO COCCAST TO FAIR TANAMED SANDAL FOR THE TANAMED SANDAL FOR THE SANDA	Qy	1725
; f	NKERPOSNIPS-AHERNATKEKERPDOSUKSMNKOKORDOGU INGERALITARIA	qa	1175
}	DVERGERANDDAARDE AVONCKARDDAYGONEDARDARDARDARDARDARDARDARDAARDAARDAARDAA	Οy	1765
, a		QQ	1234
λ̈́α	895 KKEGGSGRATTAKSSGAPQDSDSSATCSADEVD 927	δλ	1793
· 8	:   :   :   :   DEETHIQAPSSADTSLYDGPNPNALPSPVAAPITMKVPTIATVEALNASVD	qa	1294

οy	928 EAEGGDKNF	KVHEPPRE	987
qq	] :  533 RKEAIEKME	:	578
ογ	80		1039
qq	579 QLAPVGIPC	QLAPVGIPQPPSCPPSESVYIKKEPMEDSMDATCNQNSNEPQDLKVKIEIKNEDALKHSA (	638
Qy	1040 QKLPGDPPC	TISGLPFPVPPREVIKASPHAPDPSAFSYAPPGHPLPLGLHDTARPVLP	1097
<del>Q</del>	639 GGLPPSGPC-	APPSALHPL	959
Οy	1098 RPPTISNPE	SNPPPLISSAKHPSVLERQIGAISQGMSVQLHVPXSE-HAKAPVGPVTMGLPLPM	1156
g	657SGAF	HMPHGQVTTQPPPGYLIDG	069
Qy	1157 DPKKLAPFS	ESLGVPTAQEASVLRGTALGSVPGGSITKGIPST-	1215
qq	691	Д	727
ΟŊ	1216 -RVPSDSAI	RGSITHGTPADVLYKGTITRIIGEDSPSRLDRGREDSLPKGHVIYEGKK	1274
qq	728 QKYPPEMEMKF	APQDLKYPPPPPLD	752
Qy	1275 GHVLSYEGG	KEDGRSSSGPPHETAAPKRTYDMMEGRVGRAISSASIEG	1329
QQ	753ALKYSQE	ALKYSQEMQAAAAAAAAAGKYDMKYMMEQQGKYNVELSAAH	793
Οy	1330 LMGRAIPPER	HSPHHLKEQHHIRGSITQGIPRSYVEAQEDYLR	1372
q	794 VPPS	AAHKY	831
δy	1373 REAKLLKRE	ALGPLKLKPAHEGLVATVKEAGRSIHEIPREE	1432
qq	832	GPPPTSQESQQQQPQPPAHQVPPGATPPPGIAMPKPH	868
οy	1433 LRHTPELPI	LRHTPELPLAPRPLKEGSITQGTPLKYDTGASTTGSKKHDVRSL	1476
ф	869 ҮСНБИСТРЕ	PLAAKCGPPODLKYPMPPVSQAGPADVKPYGGENL	928
οy	1477 IGSPGRTFF		1536
ф	929 IKSSPYGPE	SNSNSQPPSMPPQPQQ	972
Qy	1537 ROSPLTYED	RQSPLTYEDHGAPFAGHLPRGSPVTMREPT	1566
QO	973 FQSPHPSPH	FÖSPHPSPHMPSPAGGGLPPGMHPQNLIHGPPPGAAGGSGPQPPPPPTSLHQPTPTSAGP	1032
ΟŸ	1567 PRLQEGSLS	PRLQEGSLSSSKASQDRKLTSTPREIAKSPHSTVPEHHPHP-ISPYEHLLRGVSGVDL	1623
qq	1033 РЅГОНСГНЕ		1086
0y	1624 YRSHIPLAFDPT	SIPRGIPLDAAAAYYLPRHLAPNPTYPHLYPPYLIRGYPDTAALENRO	1683
đ	1087HRP		1114
Qy	1684 TIINDYITS		1724
qq	1115 GLPPSHTSC	GLPPSHTSQQQQQQQQQQQQQPGGPAGTVRTSSPAQQPPRSMHDPQSSREPPTSQPSTTWAG	1174
Qy		LPVLVPPTPGTPATAMDRLAYLPTA	1764
QQ	1175 SSGPGG-PF	PPPGLIGHPMAIHPHLAHLPPGHPAHAALA	1233
ογ	1765 -PQPFSSRH	TKPTTTS	1792
qq	1234 нРСНИССЯ	GPIALLAGPGGLGGIPESALSRRTPPSHLPHSHASSAPLTAH	1293
ΟŊ	1793 SSERERDRU	SSERERDRDRERENDREREKSILTSTTTVEHAPIWRPGTEQSSGSSGSGGGG	1846
q	1294 SVA		1341

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92;
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967 LLAIPTVEENEETSFLRPEPQPKMEEMDTGGSGLPPLPTVEEHKVVDQDVDWVD----- 1020
                                                                                                                                                                                                                                                                                                                                                        1174 ---NQFSQSDKDKVSGGKGHSGSDNHGKEGGRRTTSRFSTELDVEYAIQESIREAQEKKE 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :: | :: | :: | :: | 1.231 REERAQREKYRTDKEAVIPEMIWTDEEKDHQLFVDTSGLL--PLE-----KLVETWQAVP 1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1461 AIAPTPPAASGKGTNARSRSNSTRVQNPEWMPPKTPAELGARVQNPMFDVPPGSMQPPLA 1520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1521 PAQQTPLASPERAPPTLASTTISEVMAPPSLRPEPPAPPASLPTFEIGQSSGPERIRTPQ 1580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1685 -POPAKSEAAPPANQPFSRFQVTPIQASPVLHTLVQRSPTVMPAPLPPAPVAASASASAAPS 1743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          487
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                                                                                                                                                                                                                       -------RILEGLGPQVELPLYNQPSDTRQYHENIKINQAMRKK--LILY 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       332 YYEKQFPEIRKQRELQERMQS----RVGQRGSGLSMSAARSEHEVSEII-DGLSE-QENLE 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KQMR-----QLAVIPPMLY-DADQQRIKFINMNGLMADPMKVYKDRQVMNMW---- 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 728 GNEVPRGECSGPATVNNS----SDTESIPSPHTEAAKD-TGONGPKPPATLGAD-GPPPG 781
                                                                                                                                   QPQRRRPSLLSEFQPG--NERSQELHLRPESHSYLPELGKSEM--EFIESKRPRLELLPD 115
                                                                                                                                                       :| :: | | :| | :| | 848 KPVQKPAQKLDELPPEKLPEPEQIPR 907
                                                                                                                                                                                                    PLLRPSP---------LLATGQPAGSEDLTKDRSLTGKLEPVSPPSPPHTDPE 159
                                                                                                                                                                                                                                                                  LELVP------PRLSKEEL------1QNMDRVDREITMVEQQISKL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F------KRRNHARKQWKQKFCQRYDQLMEALEKKVERIENNPRRRAKESKVRE 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --SSRWTEEEMETAKKGLLEHGRNWSAIARMYGSKTVSQCKNFYFNYKK--RQNLDEILQ 667
                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   782 PPTPPRRTSRAPIEPTPASEATGAPTPPPAPPSPSAPPPWPKEEKEEETAAAPPVEEGE 841
                                                                                                                                                                                                                                                                                                                                                                                                                       1073 EERTEDDASVSGSVEHVRELSTTPPTDELPVEN----VKPWHQSSKVRKLSEQSPGFGAF
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                                                                                                                                                                                                                                                                                                                                    194 KKKQQQLEEE---AAKPPEPEKPVSPPPIESKHRSLVQIIYDENRKKAEAAH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----SEQEKETFREKFMQHPKNFGLIASFLERKTVAECVLYYYLTKKNENYKSLVRRSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      END------KEDLLKEKTDDTSGEDNDEKEAVASKGRKTANSQGRRKGRI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.2%; Score 552; DB 3; Length 2649;
Best Local Similarity 19.3%; Pred. No. 1.7e-19;
Matches 406; Conservative 268; Mismatches 771; Indels 658;
PROSITE; PS50090; MYB_3; 1.
SEQUENCE 2649 AA; 294398 MW; 36FB50BF3917F2AB CRC64;
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us-09-522-753-5.rspt

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RC STRAIN—EBERKELEY,
RATIN—EBERKELEY,
RATIN—EGROUPENCE FOR IN R. A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Richards S., Ashbuner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.H.C., Blazej K.G., Channe M., Hefelfer B.D.,
RA Ballew R.M., Basu A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Beeson K.Y. Bence P.V., Barenda B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Bultler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Dalle C., Davenport L.B., Davies P.,
RA Burtis K.C., Busam D.A., Dalle C., Perraz C., Ferriac C., Perriac S.,
RA Burtis K.C., Busam D.A., Balke C., Perraz C., Perriac S., Dunkov B.C., Dunn P.,
RA Burtis K.C., Busam D.A., Balle C., Perraz C., Perriac S., Dunkov B.C.,
RA Burtis K.C., Busam D.A., Balle K.C., Perraz C., Perriac S., Dunkov B.C.,
RA Godon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Well M.-H., Ibegwan C.,
Alalli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Retchum K.A.,
Alalli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Mattei B., McIntosh T.C., Morris J., Mosheri A.
Merkulov G., Milshina N.V., Modary C., Morris J., Mosheri A.,
Raloson D.R., Noly M., Murphy B., Murphy L., Murshy D., Melson D.R.,
Reinert K., Remington K., Stunders R., Duri V., Santh H.,
Rheiner E.C., Siden-Kiamos I., Singbson M., Strong R., Subelsenbach J.,
Rheiner K., Tectro C., Turner R., Venter E., Wang S., Yao Q.A.,
Randy S.Y., Tach M., Worley B., Worley K.C., Wu D., Yang S., Zhu X., Smith H.O.,
Rheiner S.H., Woodage T., Singbson M., Strong R., Santh H.O.,
Rheiner S.H., Myers E.W., Rholin G.M., Venter J.C.;
Rheiner S., Siden-Kamos I. S., Zhan M., Zhong R., Shone S., Shone S., Shon
2604 GI------FTSNKRHGQD----GTKRHNSRRERASETNKAFDPSQRRQK 2642
                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000949; --
InterPro; IPR000949; --
InterPro; IPR001005; --
Pfam; PF00149; myb_DNA-binding; 1.
Pfam; PF01448; ELM2; 1.
SMART; SM01395; SANT; 1.
SEQUENCE 1963 AA; 207927 WW; 8F386DE56E66CB68 CRC64;
                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                          PRT; 1963 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 287:2185-2195(2000).
EMBL; AE003555; AAF50413.1; -.
FlyBase; FBgn0020427; Gug.
                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              CG6964 PROTEIN.
GUG OR CG6964.
                                       1807 DRE 1809
                                                                                  2643 KKE 2645
                                                                                                                                                                                        Q9VSK5
Q9VSK5;
                                                                                                                                                  RESULT
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g
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<pre>atch cal Similarity 19.9%; Score 550; DB 5; Length 1963; cal Similarity 19.9%; Pred: No. 1.5e-19; 486; Conservative 233; Mismatches 824; Indels 898; Gaps 110;</pre>	QRELQERMQSRVGQRGSGLSWSAARSEHEVSEIIDGLSEQENLEKQMRQLAV 394 	IPPMLYDADQORIKFINMNGLMADPMKVYKDRQVMNMWSEQEKETFREKFMQHPKNFGLI 454 	-ASFLERKTVAECVLYYYLFKKNENYKSLVRRSYRRGKSQQQQQQQQQQQQQQQQQDPMP 513 	RSSQEEKDEKEKEAEREEEEKPEVENDKEDLEKEKTDDTSGEDNDEKEAVASKGRKTAN 573   :     :     :     :     :       :	SQGRRKGRITRSMANBANSEBAITPQQSABLASMBLNBSSRWTBBE-METAKKGLLEHGR  :	NWSAIARNVGSKTVSQCKNFYFNYKKRONLDEILQQHKLKMEKERNARRKKKKAPAAASE 692  -  -  -  -  -  -  -  -  -  -  -  -  -	EAAFPPVVEDEEMEASGVSGNEEEMVEEAEALHASGNEVPRGECSGPATVNNSSDT 748 	ESIPSPHTEAAKDTGONGPKPPATLGADGPPGPPTPRTSRAPIEPTPASEATGAPTP 808	PPAPPSPSAPPFVVPK-EEKEEETAAAPPVEBGEEQKPPAAEELAVDTGKAEE 860	PVKSECTEBAEEGPAKGKDAEA-AEATAEGALKAEKKEGGSGRATTAKSSGAPQDSDSS- 918   :: :		ANASPQKPLDLKQLKQRAAAIPPIQVTKVHEPPREDAAPTK-PAPPAPPPPQN 1004    : ::	LQPESDAPQQPGSSPRGKSRSPAPPADKEAFAAEAQKLPGDPPCWTSGLPFPVPPREVIK 1064 ::	ASPHAPDPSAFSYAPPGHPLPLGLHDTARPVLPRPPTISNPPPLISSAKHPSVLERQI 1122	GAISQGMSVQLHVPYSE-HAKAPVGPVTMGLPLPMDPKKLAPFSGVKQEQLSPRGQAGPP	BSLGVPTAQEASVLRGTALGSVPGGSITKGIPSTRVPSDSAITYRGSITHGTPADVLX	KGTITRIIGEDSPSRLDRGREDSLPKGHVIYEGKKG	PPHETAAPKRTYDMMEGRVGRAISSASIEGIMGRAIPER 1339	
fatch ocal Sim 3 486;																			
Query Match Best Local Matches 48	Oy 343 Db 20	Qy 395 Db 79	Oy 455 Db 129	Oy 514 Db 185	Qy 574 Db 207	Qy 633 Db 244	Oy 693 Db 273	Qy 749 Db 328	Qy 809 Db 376	Qy 861 Db 429	Qy 919 Db 477	Oy 953 Db 537	Qy 1005 Db 583	Qy 1065	7	7	7	Db 725 Qv 1300	
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qq	DD 746AAAAGKYDMKYMMEQQGKYNVELSAAH	: QPPSKPGYQDSLKIPDIKPG 792
۶۵ ج	1340HSPHHLKEQHHIRGSITQGIPRSYVEAQEDY	PPPSRDLTEAY 13
3	261	SZS ÖÖDERÖKENIN 8ZZ
Oy Dp	1398 KTQALGPLKLKPAHEGLVATVKEAGRSIHE :	IPREELRHTPELPLAPRPLKEG- 1449 
δy	1450SITQGTPLKYD	TGASTTGSKKHDVRSLIGSPGRTFPPVHPLDVMADARALER 1501
a a	DD 873 PLAAKYGPPQDLKYPMPPVSQAGPADVKPYGGENLIKSSPYGPPFSPIDA	
δλ	1502 ACYEE	SPLTYEDHGAPFAGHLPRG 1557
q	924SARSTPG	QDSQGSNSNSQPPSMPPQPQQFQSPHPSPHMPSPAGGGLPPGMHPQ 976
δ	1558	PRLQEGSLSSSKASQDRKLTSTPRE 1591
QQ	Db 977 NLIHGPPPGAAGGSGPQPPPPTSLHQPTPTSAGPPSLQHGLHPGHQHSQLSVAS	LOHGLHPGHQHSQLSVASSIPPS 1036
οy	1592 IAKSPHSTVPEHHPHP-ISPYEHLLRGV	SGVDLYRSHIPLAFDPTSIPRGIPLDAAAA · 1648 
g G	Db 1037 SIGIPPTLSTMAPSHMHPHLHPHAH-LQGL	-HRP 1068
δ <del>δ</del>	1649 YYLPRHLAPNPTYPHLYPP	
3	TOOS UDDEFSMAFAREDSLOGAR	MANAGERAGE TIT
δ,	1709 MLRGLSPRES	SLALNYAAGPRGIIDLSQVPHLPVL 1743
q	Db 1119 TVRTPSPAQQPPRSMHDPQSSREPPTSQPSTTMAGSSGPGG	GPGG-PPPQQSPHAHRTSPLPGL 1177
ΟŊ	1744 VPPTPGTPATAMDRLAYLPTA	PQPFSSRHSSSPLSPGG 1781
qq	Db 1178 AGSGPPPGLIGHPWAIHPHLAHLPPCHPAHAALAHPGHHLLSHSIAGLGPGGCPIALLA	GHHLLSHSIAGLGPGGPIALLA 1237
οy	1782THLT	KPTTTSSSERERDRDRERDRDREREKSILTS 1817
qq	Db 1238 GPGGLGGIPESALSRRTPPSHLPHSHASSAPLTAHSVA	ASMTSTSMSLT 1285
οy	Qy 1818 TTTVEHAPIWRPGTEQSSGSSGSSGGGGG	-SSSRPASHSHAH 1858
qq	1286 TSTVPSSAFSRASPSVQISSSGGGPSGPGS	VGPGGMPNSSAAAAAAAAHRAASPASSVS 1345
ΟŊ	1859QHSPISPRTQDALQQRPSVLHNTGMKGIITAV	EPSKPTVLRSTSTSSPVRPAATFP 1914
qq	1346 SLSRQSPLHPVPQSPLSHHPSSSALSAAAAAV	AERDRHALMRQQSPHMTPP 1396
οy	Oy 1915 PATHCPL-GGTLDGVYPTLMEPVLLPKEAPRVAR	APRVAR-PERPRADTGHAFLAKP 1963
QQ	DD 1397 PVSNASLMASPLSKMYAPQPGQRGLGTSPPPHLRPGASPPVIRHPQMPL	SPPVIRHPOMPL 1445
δŏ	1964 PARSGLEPASSPSKGSE	202
qq	Db 1446PLPLIAPGGGIPQIGVHPGQSPYPH	SPYPHPLLHPSVFYSPHH 1483
οy	2024 EKTQSKPFSIQELELRSLGYHGSSY	SPEGVEPVSPVSSPSLTHDKGLPKHLEELDKSHLE 2083
qq	Db 1484 HPFNSPYGYAPYGP	GFPAYMKP 1505
δλ	2084 GELRPKQPGPVKLGG-EAAHLPHLRPLP	ESQPSSSPLLQTAPGVKGHQRVVTLAQ 2137
QQ	Db 1506PPQPGQLDPAAVMAAHHAGLQGPPPQQMRQDEQNAAAAAAAAAAAAAAAAAAA	NAAAAAAQAAAEKQHQAAAAAA 1561
Qy	2138 HISEVITQDY: :	218
g G	15	PGMGGPGTPTGLPPGAYPGSH 1615
ΟŸ	2184YLPPDHGAPARGSPHS	EGGKRSPEPNKTSVLGGGEDGIEPV 2225 : : : : : : : :

1616 MPGYPQGPPHGSPFAPQDGQPHGLKPTSHMDALRAHAANSAGMGGGHHPTEPLPIDIE. 1675 2226SPPEGMTEPGHSRAAVYPLLYRDGEOFFBGRMGSKGDGNT 2265
PDPEPEIPSPTHNIPRGPSPEAKPDDTECHRSQSAIFVRIDRGDYRSCTR 172
2266 SQPPAFFSKLTESNSAMVKSKKQEINKKLNTHNRNEPEYNISQPGTEIFNMPAITGTGLM 2325   1 :
OLSEYARPHVAFSPV
2372PAAMPITAADGR 2389
-  -  -  -  -  -  -  -  -  -  -  -
0 SDHTLTSPGGGGRAKVSGRPSSRKAKSPAPGLASGDRPPSV 243
1875 SQMERERLGIPPPHHVGLDPGEHMVRMPQPPEAGFQLPPNV 1915
10 5875 PRELIMINARY: PRT: 2157 AA.
10, Created) 10, Last sequence up
7
nomo Saptens (numan). Makaryota, Metasoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
[1] SEQUENCE FROM N.A. Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A., Abhasi N. Dickhoff B. Torets C. Madan A. Dors M. Vonne T.
x class
(FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ARIZ9/75; AAD18086.1; SEQUENCE 2157 AA; 228869 MW; 21B817F5B699B0DB CRC64;
Query Match '4.1%; Score 546.5; DB 4; Length 2157; Best Local Similarity 20.4%; Pred. No. 2.5e-19; Matches 514; Conservative 207; Mismatches 871; Indels 927; Gaps 114;
474 KRNENYKSLVRRSYRRRGKSQQQQQQQQQQQQQQQQQPMPRSSQEEKDEKEKEAE 530 
70 KGNDPNVSLVPKDGTGWASKQEQSDPKSSDASTAQPPESQPLPASQTPAS 119
531 KEEERPEVENDKEDLLKEKTDDISGEDNDEKEAVASKGRKTANSQGRRKGRITRSMANE- 589
120 NOPKRPPAAPENTPLVPSGVKSWAQASVTHGAHGDGGRASSLLSRFSREEF 170
590ANSEBAITPQOSAELASMELNESSRWTEEEMETAKKGLLEHGR 632   ::
NWSA
: 230 DPRGGLQPSGPPQFPPYRGMMPPFMYPPYLPFPPPYGPQGPYRYPTPDGPSRFPRVAGPR 289
637IARMVGSKTVSQCKNF-YFNYKRQNLDEILQQHKLKMEKERNARR 681
290 GSGPPMRLVEPVGRPSILKEDNIKEFDQLDQENDDGWAGAHEEVDYTEKLKFSDEEDGRD 349
682 KKKKAPAAASEEAAFPPVVEDEEMEASGVSGNEEEMVEEAEALHASGNEVPRG 734

ф	350	SDEEGAEGHRDSQSASGEERPPEADGKKGNSPNSEPPT 387
Oy	735	PATL
QQ	388	FKTAWAETSRPPETEPGPPAPKPPLPPPHRGPAGNWGPPGDYPDRGGPPCKPPAPE 443
Qy	787	**************************************
QQ	444	
Οy	802	ATGAPTPPPAPDSPSAPPPVVPKEEKEEETAAAPPVEEGEEQKPPAAEELAVDTGKAEEP 861
οqα	504	LKAEPAAPPAAPSTPAPPAVPKELPAPPAPP
Qy	862	VKSECTEEAEEGPAKGKDAEAAEATAEGALKAEKKEGGSGRATTAKSSGAPQDSDSSATC 921
qq	537	ASAPTPEKEPEEPAQAPPAQSTPTPGVAAAPTLVSGGSTSSTSSGSF 584
δλ	922	SADEVDEAEGGDKNRLLSPRPSLLTPTGDPRANASPQKPLD 962
qq	585	EASPVEPQLPSKEGPEPPEEVPPPTTPPVPKVEPKGDGIGPTRQPPSQGLGYPKYQKSLP 644
δλ	963	LKQLKQRAAAIPPIQVTKVHEPPREDAAPTKPAPPAPPPPQNLQPESDAPQQPGSSPRGK 1022
QQ	645	PRFQRQQQEQLLKQQQQHQWQQHQQGSAPPTPVPPSPPQPVTL-GAVPAPQAP 696
Qy	1023	SRSPADPADKEAFAAEAQKLPGDPPCWTSGLPFPVPPREVIKASPHAPDPSAFSYAPPGH 1082
qq	697	PPPPKALYPGALGRPPPMPPMNFDPRWMIPPYVD 731
Qy	1083	PLPLGLHDTARPVLPRPPTISNPPPLISSAKHPSVLERQIGAISQGMSVQLHVPYSEHAK 1142
QQ	732	PRELLOGERPELDFYPPGVHPSGLVPRERSDSGGSSSEPFDRHAP 774
Qy	1143	APVGPVTMGLPLPMDPKKLAPFSGVKQEQLSPRGQAGPPESLGVPTAQEASVL 1195
qq	775	:   :   :
Qy	1196	RGTALGSVPGGSITKGIPSTRVPSDSALTYRGSITHGTPADVLYKGTITRI-IGEDSPSR 1254
QQ	822	RSETPPVPPPPPYLASYPGFPENGAPGPPISRFPLEEPGPRP 863
δy	1255	LDRGREDSLPKGHVIYEGKKGHVLSYEGGMSVTQCSKEDGRSSSGPPHETAAPKRTYDMM 1314
QO	864	LPWPPGSDEVAKIQTPPPKKEPPKEETAQLT 894
ò	1315	EGRVGRAISSASIEGLMGRAIPPERHSPHHLKEQHHIRGSITQGIPRSYVEAQEDYLRRE 1374
qq	895	GPEAGRKPARGVGSGGQGPPPRRESRIETRWGPRPGSSRRGIPP 939
δλ	1375	RDLTEA
QQ	940	EEPGAPPRRAGPIKKPPPPPTKVEELPPKPLEQGD 973
Qy	1427	EIPREELRHTPELPLAPRPLK 1467
qq	974	FI   1   1   1   1   1   1   1   1   1
δŏ	1468	SKKHDVRSLIGSPGRIFPPVHPLDVMADARALERACYEESLKSRPGTASSSG 1519
QQ	1025	GRGRGEYFARGRGFRGTYGGRGRGARSREFRSYRE-FRGDDGRGGGTG 1071
QY	1520	GSIARGAPVIVPELGKPRQSPLTYEDHGAPFAGHLPRGSPVTMREPTPRLQ 1570
qq	1072	GPNHPPAPRGRIASETRSEGSEYEEIPKRRQ 1103
οy	1571	EGSLSSSKASQDRKLTSTPREIAKSPHSTVPEHHPHPISPYEHLLRGVSGVDL 1623
qq	1104	RGSETGSETHESDLAPSDKEAPTPKEGTLTQVPLAPPPPGAPPSPAPARFTARG 1157
ΟŊ	1624	YRSHIPLAEDPTSIPRGIPLDAAAAYIPRHLAPNPTYPHLYPP 1667
đ	1158	GRVFTPRGVPSRRGRGGGRPPPQVCPGWSPPAKSLAPKKPPTGPLPPSKEPLK 1210

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1689 GSSPLNAVPCEGPPGSEPPRRPPPAPHDGDRKELPREQPLP-------PGPIGT 1735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2183
1668 -YLIRGYPDTAALENRQTIINDYITSQQMHHNTATAMAQRADMLRGLSPRESSLAL---N 1723
                                   1211 EKLIPGPLSPVARGGSNGGSNVGMEDGERPRRRRHGRAQQQDK----PPRFRRLKQEREN 1266
                                                                                                            AARGSEGKPSLT----LPASAP----APEEA---LTTVTVAPAPRRAAKSPDLSNQNSD 1315
                                                                                                                                                                                      1316 QANEEWETASESSDFTSERRGDKEAPPPVLLTPKAVGTPGGGGGGAVPGISAMSRGDLSQ 1375
                                                                                                                                                                                                                                                                                                                                                                                                                  1483 LSSRQGSVTAPGGH------PR-HKPGPPQAPQGPS--PRP 1515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1633 EPLSPFEDVAGTEMSQSDSGVDLSGDSQVSSGPCSQRSSP----DGGLKGAAEGPPKRPG 1688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1845 SSQISGGAMDSQLHPNSGGFRPGTPSLHPYRSQPLYLPPGPAPPSALLSGVALKGGFLDF 1904
                                                                                                                                                                                                                                                           1376 RAKDLSKRSFSSORPGMERONRRPGPGGKAGSSGSSSGGGGGGGGGGGGTGPGRGDKRSWPS 1435
                                                                                                                                                                                                                                                                                                    --SSSRPASHSHAHQHSPISPRTQDALQQRPSVLHNTGMKGIITAVEPSKPTVLRSTSTS 1904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1736 ER----SQH-----TDRGTEPGPIRPS-HRPGPPVQF-GTSDKDSDLRLVVGDSLKAEKE 1784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2211 KTSVLGGGED------GIEPVSP-----PEGMTEPGHSRSAV-YPLLYRDG 2249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1785 LTASVTEAIPVSRDWELLPSAAASAEPQSKNLDSGHCVPEPSSSGQRLYPEVFYGSAGPS 1844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPFPYNPLI--MRLQAGVMASPPP-----PGLPAGSGP---LAGPHHAWDEEP 2502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :| |:| :| :| :| 1573 EESLPPPHSSGFLGSKPEGPQAESRDIGTEALTPHIWNRLHTATSRKSYRPSSMEPWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----LEELDKSHLEGELRPKQPGPVKLGGEAAHLPHLRPLPESQPSSSPLLQTAPGVKGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------YLPPPDHGAPARG-----SPHSEGGKRSPE-----PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2250 EQTEPSRMGSKSPGNTSQPPAFF-----SKLTESNSAMVKSKKQEINKKLNTHNRNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2302 PEYNISQPGTEIFNMPAITG--TGLMTYRSQAVQEHASTNMGLEAIIRKALMGKYDQWEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1724 YAAGPRGIIDLSQVPHLPVLVPPTPGTPATAMDRLAYLPTAPQPFSSRHSSSPLSPGGPT
                                                                                                                                                                                                                                                                                                                                                                             1905 SPVRPAATFPPATHCPLGGTLDGVYPTLMEPVLLPKEAPRVARPERPRADTGHAFLAKPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1965 AR-----SGLEPASSPSKGSEPRPLVPPVSG----HATIARTPAK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --NLAPHHAS-----PDPPAPPASASD-----PH----REKTQSKPFSIQELE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----LRSLGYHGSSYSPEGVE-----PVSPVSSPSLTHDKGL----PKH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2130 QRVVTLAQHISEVITQDYTRHHPQQLSAPLPAPLYSFPGASCPVLDLRRPPSDL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STMQATELGKLPAGGVLYPPPSFLYSPAFCPSPLPDTSLLQVRQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPPLSANAFNPLNASASLPAAMPITAADGRSDHTLTSPGGGGKAKVSGRPSSRKAKSPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---GDCNRRTPLTNRVWEDRPSSAGS
                                                                                                                                                                                                                           RDREREKSILTSTTTVEHAPIWRPGTEQSSGSSGSGGGG---------
                                                                                                                                                   1784 HLTKPTTTSS-----SERERDRDRE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLASGDRPPSVSSVHSE-----
                                                                                                                                                                                                                         1806 1
                                                                                                            1267
                                                                                                                                                                                                                                                                                                  1847
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
R.A. Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
R.A. Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
R.A. Adams M.D., Celniker S.E., Holt R.A., Evans G.A., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell W.D., Zhang Q., Chen L.X.
R.A. Brandon R.C., Balzel R.G., Change M., Pielifer B.D.,
R.A. Adams M.D., Colliker S.E., Richards S.E., Andelson C.R., Miklos G.L.G.,
R.A. Adams M.D., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Basaley E.M.,
Ballew R.M., Battler H., Cadieu E., Center A., Chandra I.,
R.A. Burtis R.C., Busam D.A., Bultler H., Cadieu E., Center A., Chandra I.,
R.A. Burtis R.C., Busam D.A., Bultler H., Cadieu E., Center A., Chandra I.,
R.A. Cawley S., Dahlke C., Devenport L.B., Davies P.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunk
R.A. Cabliellan A.E., Garg M.S., Gelbart W.M., Glasser K.,
A Gong F., Gorrell J.H., Gu Z., Kennistera S., Fleischmann W.,
R.A. Gong F., Gorrell J.H., Gu Z., Kenniston G.,
A Hortis N.L., Harvey D., Heilman T.J., Wel M.-H., Ibegwan C.,
A Liu X., Mattel B., Karift C., Karaitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Minmel B.E., Kodira C.D., Kraft C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Moshrefi A.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
R. Reinfert K., Reinfigton K., Sauders R., Shen B.,
Shiert K., Sendiger D., Simpson M., Strong R., Shier S., Shen E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Shang S., Yao O.A.,
Spier E., Spradling A.C., Stapleton M., Strong S., Yao O.A.,
Mullams S.M., Woodege T., Worley K.C., Wu D., Yang G., Zhao Q., Zhao Q., Zhao G., Zhao Drosophila melanogaster (Fruit fly). Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. NCBL\_TaxID=7227; 7297; BROMO; 1. 3080 AA; 338176 MW; 4602054387DE2C12 CRC64; Created)
Last sequence update)
Last annotation update) 3080 AA STRAIN-BERKELEY; MEDLINE=20196006; Pubmed=10731132; PROSITE; PS00455; AMP\_BINDING; 1. PROSITE; PS50014; BROMODOMAIN\_2; EMBL; AE003561; AAF50647.1; -. FlyBase; FBgn0035712; CG10115. Pfam; PF00439; bromodomain; 1. (TrEMBLrel. 13, C (TrEMBLrel. 13, I (TrEMBLrel. 16, I PRINTS; PR00503; BROMODOMAIN. PRELIMINARY; InterPro; IPR000873 InterPro; IPR001487 [1] SEQUENCE FROM N.A. CG10115 PROTEIN SM00297 01-MAR-2001 SECUENCE CG10115 **09VRY3**; Q9VRY3 ID Q9VRY3 SMART; RESULT 11 

Query Match
4.0%; Score 533; DB 5; Length 3080;
Best Local Similarity 18.6%; Pred. No. 1.8e-18;
Matches 561; Conservative 385; Mismatches 1041; Indels 1022; Gaps 138;

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<u>≿</u> g	60	OPORRRPSILSEFOPGNERSQELHLRPESHSYLPELGKSEMEFIESKRPRLEL 1   1   1   1   1   1   1   1   1   1
<u> </u>	113	AGSEDLTRDR
a	575	ATSIADLSLPSPVAHESETEQDEQVDQPAVVEAQPPALTSAMAPAANVKLPGRQTNNSLS 634
<b>≿</b> .	140	SLTGKL
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≿ g	17b	-MOKADELITWYGOLSKLEKKROGOLEEERARPPEPERFYVSPPPIESKHRSLVOIIYDEN 234   :     ::   :   ::   :
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ą	725	SSKAERISGAYSDKSGD-DFTETEEVLQIGMHKVLVYVKNH-RDAW 768
٠.	9 1	KQKFCQRYDQLMEALEKKVERIENNPRRRAKESKVREYYE
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≿ g	335	KQFPEIRKQRELQERMQSRVGQRGSGLSMSAARSEHEVSEIIDGLSEQENLEKQMRQLAV 394 ::
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<u></u>	395 861	1 PPMLINDLOQUIKETNEMINGLMADPMKVYKDRQVMNWMSDEKETFREKFWQHPKNFGLI 454  - PNLSYPAADSK
<u>⊁</u>	455	ASFLERKTVAECVLYYYLTKKNENYKSLVRRSYRRRGKSQQQQQQQQQQQQQQQQQQDPMP- 513
Q	899	SSABEDLSEIEAEAPQKAQKRKRKEKED-KRRKKTKSKADVETDDEDMEAEREPTPPPPP 957
<u>~</u>	514	RSSQEEKDEKEKEREAEKEEKPEVENDKEDLLKEKTD 551
ą	958	:  :                :
<b>₹</b>	552	
ð	1017	KKSSADSDPESDPSDSRESEDYSDDDHISLAKTKSLVKPTARTIAAQKKKSVPAESKVKM 1076
Ž.	580	GRITRSMANEANSEEAITPQQSAELASMELNESSRW 615
ą	1077	PTPVKRQVKGKGKGGRKAKDDSLD
λ	616	TEEEMETAKKGLLEHGRNWSAIARMVGSK
ð	1137	DEDEDEDSSRSRSMSPFKVDLHKKYSKSALNDDLSELLTTVKK 1179
<u>~</u>	299	QQHKLKMEKERNARRKKKKAPAAASEEAAFPPVV 700
ą	1180	VPTAETTKLSARHQDEADEERSSRESDGDFKSLSNSRGSSEERPPVAKKGKKAESSKK 1237
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ą	1238	EKEKKGRDKDRDREKDKEKSKDESPYLVAA
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ą	1298	YDVIKYRRSRAAFSGSSASNSLAPSEDSKSAITKSNRENRKASAKREKSPDAVENKRGRK 1357
Δī	784	TPPRRTSRAPIEPTPASEATGAPTPPPAPPSPSAPPPVVPKEEKEEETAAAPPVEEGE 841
ą	1358	SKDOKRSKESDKAEKSDKASKADTEKHSEKSKKKEEPPKVVEKAQREKSPAPVSALETIK 1417
>	842	EOKPPAAEELAVDTGKAEEPVKSECTEEAEEGPAKGKDAEAAEATAEGALKAEKKEGG 899

qa	1418 EPP	APTPIATSASGKVKEGPAKKEPKKRPDKQMPPPPKPADKSSEKG 1464
QY	900 SGRATTAK-	SSGAPQDSDSSATCSADEVDEAEGGDKNRLLSPRPSLLTPTGDPRANA 955
qq	1465 SGKKSSSKK	SGKKSSSKKAAQKAGQPQTNNNTNLEALDVETEQTLKDINRWLEHTPRFTEFSSASN 1521
QY	956 SPOK	PLDLKQLKQRAAAIPPIQVIKVHEPPREDAAPIKPAPPAPPPP 1002
qq	1522 SPSRYNLLD	:         SPSRYNLLDDFDSGIGSKLDADFRRPVALAAPKAELVPTKLA 1564
ΟY	1003 QNLQPESDA	QNLQPESDAPQQPGSSPRGKSRSPAPPADKEAFAABAQKLPGDPP 1047
qq	1565 EALNELVSE	EALNELVSEPKEAVSKSESESVAPTPSSVSSSCGTPPHSMHSGNSIGSTSAT 1616
QY	1048CWT	REVIKASPHAPDPSAF
qq	1617 AASSSNCSN	AASSSNCSNNSMPTPLPVAVTP-TPTPAPPPLLPTPKPKEPSTTQLILNPP- 1666
QY	1102 ISNPPP	LISSAKHPSVLERQIGAISQGMSVQLHVPYSEHAKAPVGPVTMGLPLPM 1156
qq	1667PPPHIK	PPPHIKQQLAKEAKRKSLKEKQAAQAAQAQQVKAKANVMRTI 1708
QY	1157 DPKKLAPFS	DPKKLAPFSGVKQEQLSPRGQAGPPESLGVPTAQEASVLRGTALGSVPGGSITKGIPSTR 1216
qq	1709	DRLQP-GKAKGNLLQNVVAVKSTE 1731
QY	1217 VPSDSAITY	VPSDSAITYRGSITHGTPADVLYKGTITRIIGEDSPSRLDRGREDSLPKGHVIYE 1271
qq	1732 EGGDSH	HAGVNPVTTKVKELKNALITETC-EGAP-KLSLGTVLKTQDFSLGKSLEEMS 1786
οy	1272 GKKGHVLSY	EGGMSVTQCSKEDGRSSSGPPHETAAPKRTYDMMEGRVGRAISSASIEGLM 1331
qq	1787 GKKD	
Qγ	1332 GRAIPPERH	GRAIPPERHSPHHLKEOHHIRGSITGGIPRSYVEAGEDYLRREAKLLKREGTPPPPPP 1389
qq	1807 SPPTTPNTE	:  :   :     :     :       :         :
Qy	1390 SRDLTEAYKT	TQALGPLKL-KPAHEGLVATVKEAGRSIHEIPREELRH 1435
qq	1864 SED-EEKQQ	SED-EEKQQTPVQDLQCDSKVAPPAHSPAGDNFSLPTVMRQRKPSTGSTNSERSSFSQ 1920
QY	1436 TPELPLAPR	TPELPLAPRALKEGSITQGTPLKYDTGASTTGSKKHDVRSLIGSPGRTFP 1485
q <sub>Q</sub>	1921 DPDSPRIAI	DPDSPRIAIDERYGSYAAGSYTSPIGASPIGASPIMVSPKPNDDMGKPASP 1971
δλ	1486 PVHPLDVMA	PVHPLDVMADARALERACYEE-SLKSRPGTASSSGGSIARGAPVIVPELGKPRQSPLTYE 1544
QQ	1972YPLN	GAIKVGFYQDTTTKSSPDKSCSPREMNSPYP 2006
δλ	1545 DHGAPFAGHL	LPRGSPVTMREPTPRLQEGSLSSKASQDRKLTST 1588
QQ	2007 QYSQH	-YSQHIYSSASSPNVSTPDMSGTSPYGGGNSYNPSGSEASKTPAYSSTSPLPIYDQ 2062
QY	1589PREIAK	PREIAKSPHSTVPEHHPHPISPYEHLLRGVSGVDLYRSHIPLAFDPTSIPRGIPLDA 1645
QQ	2063 YKQPRSQES	YKQPRSQESDYNSSMSPSTPNPHSPYQQPQSSPYTTPQQS 2102
δλ	1646 AAAYYLPRH	AAAYYLPRHLAPNPTYPHLYPPYLIRGYPDTAALENROTIINDYIISQQMHHNTATAMAQ 1705
QQ	2103 QSTHPSPYH	QSTHPSPYH-NQSPYHQQQHSPYHP-PAAQQQQQSSQPSHSPAHQQA- 2148
QY	1706 RADMLRGLS	RADMLRGLSPRESSLALMYAAGPRGIIDLSQVPHLPVLVP 1745
qq	2149LS	LSPMHSVESPASSAATQPPTPLAQSPAEQQHSPYQQPVLSPYQQPVGPPV 2201
QY	1746PTPG	-PTPGTPA-TAMDRLAYLPTAPQPFSSRHSSSPLSPGGPTHLTK 1787
qa	2202 VPPVQPSAG	VPPVQPSAGAQASTALGNNGYAPTHDSYQQLQQQQRSLYNPATLINPLSTAASSTASITK 2261
Qy	1788 p	TTTSSSERERDRDREREREREKSILTSTTVEHAPIWR 1828

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2011
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                                                                                                                                                                                                                                                                                                                            FAKDNSCOLQOQQQQQQQSP-----QVTTNKQQANQQTQQQPQQQSQQSQPHLTQLQTAL 2575
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2636 VAAAVSESSSNMMNLPST-AHQ------HHLSQT------HHLAAYNKPTPPPPQTYSN 2681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGASCPVLDLRRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEPNKTSVLGGGEDGIEPVS 2226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2320 TGTGLMTYRSQAVQEHASTNMGLEAIIRKALMGKYDQWEESPPLSANAFNPLNASASLPA 2379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2900 Q---TAADAAAISLKTSTGG-----MVPGSAFNFAPTPGTLGLYGDQAAAASSYLDQ- 2948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2438 DCNRRIPLINRVWEDRPSSAGSTPFPYNPLIMRLQAGVMASPPPPGLPAGSGPLAGPH-H 2496
                                                                                                                               -----PKYPTYAQYQSTNAAANAAAA------ADAVDN------LQQQQQKI 2401
 ---NPYYM------PPAPAHSGTAANPSGN 2974
                                                                                                                                                                                   ------PVSGH-----SPDP
                                                                                                                                                                                                                                                              2462 OQQQQQPTQNQTQSLLNKQQQMFNSFLGTMAFGKPIGNIAPDKAFEMYNRAAAMGFPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2741 QPQQQQQQQQQAPAVPP----AEVKAPAKRGRKKKAATIAAEAAAAKQQQQQQQQQ
                                --PGTEQSSGSSGGGGGSSSRPASHSHAHQHSPISPRTQDALQQRPSVL-HNTGMKG
                                                                                                IITAVEPSKPTVLRSTSTSSPVRPAATFPPATHCPLGGTLDGVYPTLMEPVLLPKEAPRV
                                                                                                                                                                                                                                                                                                                                                           DKGLPKHLEELDKSHLEGELRPKQPGPVKLGGEAAHLPH-----LRPLPESQPS----
                                                                                                                                                                                                                                                                                                                                                                                 SONYQQQQQQTQAQKLPQQQQQPPQQLNYQQQQAQINHNYTAQQQATAVPDKPPAAQST
                                                                                                                                                                                                                                                                                                                                                                                                                           -----SSPLLQTAPGVKGHQRVVTLAQHISEVITQDYTRHHPQQLSAPLPAP--LYSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-LMQSMLGYAGNYFDKTMPPAAHMYSASSSAASAYGNPAQQLPGNYVPGNNNPAHQQQQ
                                                                                                                                                                ---ERPRADTGHAFLAKPPARSGLEPASSPSKGSEPRPLVP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPEGMTEPGHSRSAVYPLLYRDGEQTEPSRMGSKSPGNT--SQPPAFFSKLTESN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SAMVKSKKQEINKKLNTHNRNE------PEYNISQPGTEIFNMPAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2380 AMPITAADGRSDHTLTSPGGGGKAKVSGRPSSRKAKSPAPGLAS -- GDRPPSVSSVHSEG
                                                                ----OQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ
                                                                                                                                                                                                                                                                                            2012 PAPPASASDPHREKTQSKPFSIQELELRSLGYHGSSYSPEGVEPVSPVSSPSLTH----
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Catarrhini; Hominidae; Homo.
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Last annotation update)
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Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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                                                                2322 QLQGTPQQQQLQGS-----
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                                                                                                                                                                                                                                                                  QPGNERSQELHIRPESHSYLPELG-KSEMEFIESK------RP-----RLELLPDP 116
                                                                                                                                                                                                                                                                                                                                                                         EDEEMEASGVSGNEEEMVEEAEALHASGNEVPRGECSGPATVNNSSDTESIPSPHTEAAK 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    821 VVPKEEKEEETAAAPPVEEGEEQKPPAAEELAVDTGKAEEPVKSECTEEAEEGPAKGKDA 880
                                                                                                                                                                                                                                                                                                                                                                                                                             LIQNMDRVDREITMVEQQISKLKKKQQQLEEEAAKPPEPEKPVSPPPIESKHRSLVQIIY 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                412 LPQSS-----SSESSPPSPQPTKVSRHASSSPESPKPA---PAPGSHREISSSPT 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKNRSHGRAKRDKSHSHTPSRRMGRSRSPATAKRGRSRSRTP-----TKRGHSR 507
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-----RTPSRHSCSGSSPPRVKSSTPPRQSPSRSSSPQPKVKAIISPRQRSHSG 932
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                                                                                                                                                                                                                                                                                                                                               117 LLRPSPLLA----TGQPAGSEDLTKDRSLTGKLEPVSPPSPPHTDPELELVPPRLSKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 DENRKKAEAAHRILEGLGPQVELPLYNQPSDTRQYHENIKINQAMRKKLILYFKRRNHAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRSPQWRRSRSAQRWGR-----SRSPQRRGRSR-----SPQRPGWSRSRNTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEKEKEAEKEEEKPEVENDKEDLLKEKTDDTSGEDNDEKEAVASKGRKTANSQGRRKGRI
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Obtaki S., Umeki K., Sawada Y.;
"Homo sapiens mRNA for RNA binding protein, complete cds.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: ABO16092; BAR83718.1; -.
InterPro; IPR002965; -.
PRINTS; PR01217; PRICHEXTENSN.
SEQUENCE 2752 AA; 299671 MM; 109C64F181097123 CRC64;
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                                                                                                                                                                                   1. 4.0%; Score 522.5; DB 4; Similarity 19.1%; Pred. No. 5.4e-18; 3; Conservative 314; Mismatches 1071;
                                                                                                                                                                                     Query Match
Best Local Simi
Matches 543;
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SILTSTITVEHAPIWRPGTEQSSGSSGSSGGGGGSSSR--PASHSHAHQHSPISPRTQDA 1870
                                                                                     1984 SRISPVIRRRSRSRISPVIRRRSRSRISPVIRRRSRSRIPPAIRRRSRSRIPLLPRKRSR 2043
                                                                                                                           1924
                                                                                                                                               2044 SRSPLAIRRRSRSRTPRTARGKRSLTRSPPAIRRRSASGSSSDRSRSATPPATRNHSGSR 2103
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2104 TPPVALNSSRMSCFSRPSMSPTPLDRCRSPGMLEPLGSSRTPMSVLQQAGGSMMDGPGPR 2163
                                                                                                                                                                                                                                                                       1945 VARPERPRADTGHA------FLAKPPARSGLEPASSPSKGSEPRPLVPPVSG 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SERTAPAANLASR-----IPAASAAAMNLASARTPAIPTAVNLADSRTPAAAAAMNLA 2271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----AAHLPHLRPLPESQPSSSPLL-----QTAP-GVKGHQRVVTLAQHISEVITQDY 2147
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
MASCENT POLYPEPTIDE-ASSOCIATED COMPLEX ALPHA POLYPEPTIDE (ALPHA-NAC, MUSCLE-SPECIFIC FORM GP220).
NACA.
Mus musculus (Mouse).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi:
Mammalia; Eutheria: Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                          1871 LQQRPSVLHNTGMKGIITA----VEPSKPTV-LRSTSTSSPVRPAATFPPATHCPLGGT
                                                                                                                                                                                                                                                                                                 2164 IPDHQRTSVPENHAQSRIALALTAISLGTARPPPSMSAAGLAARMSQVPAPVPLM----
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us-09-522-753-5.rspt

NCBI_TaxID=10090; [1] SEQUENCE FROM N.A. MEDILINE=96312450; bubmed=8698236;	Qy	1270 YE : 735 VQ
Yotov W.V., St.Arnaud R.; "Differential splicing-in of a proline-rich exon converts alphaNAC into a muscle-specific transcription factor."; Genes Dev. 10:1763:1772(1996)	Qy	1307 PK 
	۲۵.	1352 851 SP
	Qy	
220599 MW; 003646AA864DEBFD CRC64;	qq	911 AP
	Qy	1389 PS
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GPATVNNSSDIESIPSPHTEAAKDIGQNGPKPPATLGADGPPPGPPT 784	ý f	1440 PL 1031 KR
GEATETVPATEQELPQPQAETAVLPMSSALKVAAVGQPGPTPPSSLGPQQSPIVTAHQPS 62	λδ	
P-PRRISRAPIE 810  I	qq	1085 KE
	Qy	1525
KTSTS	qq	1145 IP
	Qy Dp	1583 RK :: 1188 KE
	Qy	1622 DL
PSTSLGCHLPLLHHSSVDSPIQPPGQSGLAV	qa :	1248 TA
T	25 A	1298
	Qy Db	1742 VL
PKGSNVALQPLVTQVPASQKTGLKEIPVSCIGATH 409		
-REDAAPTKPAPPAPPPQNLQPESDAPQQPGSSPRGKSRSPAPPADKEAFAAEAQK 1041	: 셤	1367
LPGDPPCWTSGLPF-PVPPREVIKASPHAPDPSAFSYAPPGHPLPLGLHDTARPVL 1096	දු දු	1852 AS : 1397 TT
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PIALKESPSSQSASSLEVLSEDTVTKKTTGGPAPVVRPAIAGVATTTSLRA 563	3 2	41 /C#1
HVPYSE-HAKAPVGPVTMGLPLPMDPKKLAPFSGVKQEQLSPRGQAGPPE 1182   :	5 A	
SLGVPTAQEASVLRGTALGSVPGGSITKGIPSTRVPSDSAITYRGSI 1229 . 	oy G	2021 PH 1 1557 PS
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679 RQGHPDASVTAKGTVVCLADSSLDTSVSASKGSALSGASSPLYPLEVSFLPEAGLA 734		CACT

δy d	1270	YEGKKGHVLSYEGGMSVTQCSKEDGRSSSGPPHETAA	1306
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g d	791	OSPEKUDPIMSDVTPTSPKKTSATAVPKDTSATLSLKSVPAVTS)	ט ע
Qy	1352	RGSITQGIPR	1361
ф С	851	SPPKAPVAPSNEATIVPTE1PTSLKNALAAATPKETLATSIPKVTSPSPQKTPKSVSLKG	910
Qy	1362	SYVEAQEDYLRREAKLLKRE	1388
đ	911	APAMTSKKATEIAASKDVSPSQFPKEVPLLQHVPPTSPPKSPVSDTLSGALTSPPPKGPP	970
Οy	1389	PSRDLTEAYKTQALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPEL	1439
QO	971	ATLAETPTYPKKSPKPAASKKTPATPSPEGVTAVPLEIPPCSKKAPKTAAPKESSATSSS	1030
Οy	1440	HDVRSL	1483
q	1031	KRAPKTAVSKEIPSKGVTAVPLEISLPLKETSKSATPGEKSASSPKRSPKTAGP	1084
Qy	1484	FPPVHPLDVMADARALERACYEESLKSRPGTASSSGGSIAR	1524
qq	1085	KETPPGGVTAVPPEISLPPKETPQNATPNESLAASSQKRSPKTSVPKETPPGGVTAMPLE	1144
Qy	1525	LIYEDHGAPF	1582
qq	1145	IPSAPQKAPKTAVPKQIP-TPEDAVTILAGSPLSPKKASKTAAP	1187
Οy	1583	RKLTSTPRBIAKSPHSTVPEHHPHPISPYEHLLRGVSGV	1621
qq	1188	:	1247
Qy	1622	DLYRSHIPLAFDPTSIPRGIPLDAAAAYYLPRHLAPNPTYPHLYPPYLIRGYPDTAALEN	1681
qa	1248	TAVPSEISPS-PPTPASKGVPV-TLTPKGAPNALAESPASPKKVPKTAAPEE	1297
Qy	1682	RQTIINDYITSQQMHHNTATAMAQRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLP	1741
qq	1298	TSTTPSPQKIPKVAGPKEAS	1317
Oy	1742	VLVPPTPGTPATAMDRLAYLPTAPQPFSSRHSSSPLSPGGPTHLTKPTTT	1791
qq	1318	-ATPPSKKTPKTAVPKETSAPSEGVTAVPLEIPPSPRKAPKTAAPKETPA	1366
Qy	1792	SSSERERDRDREREREKSILTSTTTVEHAPIWRPGTEQSSGSSGGGGGSSSRP	1851
qq	1367	PSPEGGTTAPVQIPPSPRKGSKRAGSKETP	1396
Qγ	1852	ASHSHAHOHSPISPRTODALQORPSVLHNTGMKGIITAVEPSKPTVLRSTSTSSP	1906
qa	1397	TPSPEGVTAAPLEIPISSKKTSKMASPKETLVTPSSKKLSQTVGPKETSLEGATAVPLE	1456
Qy	1907	VRPAATFPPATHCPLGGTLDGVYPTLMEPVLLPKEAPRVARPERPRADTGHAFLAK	1962
qq	1457	I I I I I I I I I I I I I I I I I I I	1510
δλ	1963	ARSGLEPASSPSKGSEPRPLVPPVSGHATIARTPAKNLAPHHASPDPPAPPASASI	2020
qq	1511		1556
δy	2021	PHREKTQSKPFSIQELELRSLGYHGSSYSPEGVEPVSPVSSPSLTHDKGLPKHLEELDKS	2080
qq	1557	PSSHKKTSKTIELKEAPATLPP-SPTKSPKIPSSKRAPR	1594
Óγ	2081	HLEGELRPROPGPVKLGGEAAHLPHLRPLPES-OPSSSPLLQTAPGVKGHQRVVTLAQHI	2139
qq	1595	EPPASPSIKPVTTSLAQTAPPSLQKAPS	1627

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R.A. Adams M.D., Celniker S.E., Holf R.A,
R.A. Adams M.D., Celniker S.E., Holf W., Hoskins R.A., Galle R.F.,
R.A. Gocayer S.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
B. Sutton G.G., Wortunan J.R., Blazej R.G., Champe M., Pfeiffer B.D.,
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R.A. Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
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R.A. Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
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R. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A. Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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R. Borkin D., Harvey D., Heinan T.J., Hernandez J.R., Harris M.,
Harris N.L., Harvey D., Heinan T.J., Hernandez J.R., Houck J.,
A. Harris N.L., Harvey D., Heinan T.J., Mein M.-H., Ibegwam C.,
A. Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Alul X., Mattei B., McIntosh T.C., Morled D.,
A. Murmel B.E., McIntosh T.C., Morled D.,
A. Murkulov G., Milshina N.V., Mobarry C., Morled D.,
A. Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.E.,
A. Nelson D.R., Nixon K., Nusskern D.R., Pacieb J.M.,
                               -----TIIPKENLAAPAVLPVSSKSPAAPARASASLSPATAAPQTAPKEATIIPSCK 1679
                                                                                           1680 KAAATETPIETSTAPSLEGAPKETSETSVSKVLMSSPPKKASSSKRASTLPATTLPSLKE 1739
                                                                                                                                                                                                                                                                                            : | | : : | | | : --AVALAPQTVPVEKDŢSKAIETLLVSPAKGSDCLHSPKGPVGSQVATPLAAFŢSDKVPP 1892
                                                                 2173 VLDLRRPPSDLYLPPPDHGAPARGSPHS------EGGKRS-----PEPNK 2211
                                                                                                                                  2212 TSVL-----GGGEDGIEPVSP--PEGMTEPGHSRSAVYPLLYRDGEQTEPSRMGSKSPG 2263
                                                                                                                                                                                                                             ----PTARTEMLAAPAPESALAITAPIQKSPGANSNSASSPKCPDPSSKKDTKGLPS--- 1834
                                                                                                                                                                                                                                                                                                                                                                        1893 EAVSASV-APKPAPAA----SLTLAPSP----VAPLPPKOPLLESAPG--SVLES 1936
                                                                                                                                                                                                    2264 NTSQPPAFFSKLT--ESNSAMVKSKKQEINKKLNTHNRNEPEYNISQPGTEIFNMPAITG 2321
                                                                                                                                                                                                                                                                                                                                       ---SASLPAAMPITAADGRSDHTLT---SPGGGGKAKVSGRPSSRKAKSPAPGLASGDRP 2427
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Last sequence update)
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2140 SEVITQDYTRHHPQQLSAPLPAPLYS-FPGA-
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
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NCBI_TaxID=7227
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Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
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R. Enbase, Republoocie, CG11122. 136; 199 FQHLSEQHADKY---FACQPCRLR-----FQDADHLLGHQRQQHSLHHPEDGHATKPGL 249 432 464 521 Gaps 343 QRELQERMQ--SRVGQRG-SGLSM---SAARSEHEVSEIIDGLSEQENLEKQ--MRQLAV 394 581 642 YATHYEVVGRELLAGNLLRHLFIPKRALGRFAAASNCIRWPQIAPAATVQQPKQEQVQPE 701 EETRSSASSRSSYEVSTPTPLSALEQQQPSPASGSGNASSSSSCSPSSSSASTLLSTATR 761 ---SQEEK 520 95 42 YQHHSRDYASHLSPGSIIQPQRRRPSLLSEFQP----GNERSQ-ELHLRPESHSYLPEL 250 MGADEPVLFRLGLTQNRLPSHRNRNQRKEEEPPPLATPS------SKSRSSS ---ELPLYNQPSDT----RQYHENIKINQAMRKKLIL----GKSE----MEFIESKRP-----RLELLPDPLLRPSPLLATGQPAGSEDLTKDRSLT GKLEPVSPPSPPHTDPELELVPPRLSKEELIQNMDRVDREITMVEQQISKLKKKQQQLEE -----RAATQRQQNQHQHQQSQSHQQ 203 EAAKPPEP-EKPVSPPPI-----ESKHRSLVQIIYDENRKK---AEAAHRILEGLG GRLFTSSSTSTTSATSSSASHKSDLIMLHGPSQLGPGGASYPTLLTADQFGGTGELLPLA 283 YFKRRNHARKQWKQKFCQRYDQLMEALEKKVERIENNPRRRAKESKVREYYEKQFPEIRK KFRRRPHTKHSWKWKW-------DYVKKFTLINE 395 I-----PPMLYDADQQR-IKFINM---NGLMADP-----MKVYKDRQVMNWW-----CVLYYYLTKKNENYKSLVRRSY---RRRGK-------SQQQQQQQQQQQQ Mismatches 1037; Indels 1112; Length 3536; Pfam: PF00096; Zf-CZH2; S.
PRINTS: PR01217; PRCHEXTENSN.
PROSITE: PS00028; ZINC\_FINGER\_CZH2; 4.
DNA-binding; Metal-binding; Zinc-finger.
SEQUENCE 3536 AA; 384634 MW; E16091990FBF9EEE CRC64; 3.9%; Score 519; DB 5; 19.0%; Pred. No. 1.1e-17; ------QQQQPMPRS-----Conservative 364; InterPro; IPR000822; InterPro; IPR002965; Similarity 250 PQV---------Best Local Sim Matches 589; Query Match 143 296 378 438 702 96 522 433 582 505 516

SSTSSAPSSCIKCGRKCSGLMDLYRHMLDCSGDYVWSLAKKRK 821	KEKEAEKEEE-KPEVENDKEDLLKEKTDDTSGEDNDEKEAVAS 566	YRYYCGTKKRRAFSKKLKQLSARKEKLEVEVEEGTGDGDGDAEVDGDGEAEAEGEESVS 881	KGRKTANSQGRRKGRITRSMANEANSEEAITPQQSAELASMELN 610 	GRNWSAIARWGSKTVSQCKNFYFNYKKRQNLDE  :  :    :            LRTTRSRSRSSVVATGSSAAVAAQQRSRRKQKQQQOK	ILQOHKLKMEKERNARRKKKKAPAAASEEAAFPPVVEDEEMEASGVSGNEEEMVEEAEAL 724    : :: :  ::   :   :  QQQQKQQCKKQEQRALEKVKSPPEPPAAVESDQMA 1038		841	EQKPPAAEELAVDTGKAEEPVKSECTEBAEEGPAKGKDAEAAEAT 886 	AEGALKAEKKEGGSGRATTAKSSGAPODSDSSATCSADEVDEAEGGDKN 935 :  -     -    :    :   PQPVDHQSPAAAVVAEKERVQPKTPKRKAVSRRIIKMDATPETLAEPIQER 1235	SPRPSLLTPTGDPRANASPQKPLDLKQLKQRAAAIPPIQVTKVHEPPREDA 989 	APTKPAPPPAPPPPQNLQPESDAPQQPGSSPRGKSRSPAPPADKE 1033 	KLPGDPPCWISGLPFPVPPREVIKASPHAPDPSAFSYAPPGHP 1083 	LPLGLHDTARPVLPRPPTISNPPPLISSAKHFSVLERQIGAISQ 1127 : : ::	-GMSVQLHVPXSEHAKAPVGPVTMGLPLPMDPKKLAPFSGVKQEQLSP 1174   : :  :  :  :  :  SGTTGDPGLVGLQHHRAGGMPARRQTICGFEARNLIGLDMEMEPLDLSKKSSRKPSPVPP 1512	RGQAGPPESLGVPTAQEASVLRGTALGSVPGGSITKGIPS 1214	TRVPSDSAITYRGSITHGTPADVLYKGTITRIIGEDSPSRLDRGREDSLPKGHVIYEGKK 1274	GHVLSYEGGMSVTQCSKEDGRSSSGPPHETAAPKRTYDMMEGRVGRAISSASIEGLMGRA 1334	IPPERHSPHHLKEQHHIRGSITQGIPRSYVEAQEDYLRREAKLLKREGTPPPPPFSRDLT 1394	EAYKTQALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGSİT 1452
2 ISMSNSTCTSSAATTTVSSTSSA					-					RLL		AFAAEAQ       A	44 IV					ıo <del>⊲</del>	10 10
163	521	822	567	611	665	725	782	842	987 1185	936	990	1034	1084	1128	1175	1215	1275	1335	1395
QQ	Qy	qq	QY Db	Qy Dp	Qy Dp	8 8	Qy	QY Dp	Oy Dp	Qy Db	çy G	Qy Dp	Oy Db	Qy Dp	Qy	QY Db	Qy Db	ζς Q	ò f

Qy Dp	1453 QC 1764	OGTPLKYDTGASTTGSKKHDVRSLIGSPGRTFPPVHPLDVMADARALERACYEES 1	507
oy da	1508 LE	LKSRPGTASSSGGSTARGAPVIV-PELGKPROSPLTYEDHGAPFAGHLPRGSPVTMREPT 1 :	566
δ		SSLSSSKASQDRKLTSTPREIAKSPHSTVPEHHPHPISPYEHLLRGVSGVDLYRS	
QQ Op	1837 TS	: PDPVP 1	874
Οy	1627 н	TYPHLYPPYLIRGYPDTAALENR	1682
q	1875 NI	NLPQAETSVPAPVEVISVAPAVLPLPTRTATPPPTTMAETNC 1	918
Qy	1683 07	AMAQRADMLRGLSPRESSLALNYAAGPRGIIDLSC 	742
qq	1919 S	SSLMEEHSSNLNNNTSSGFHSLAQ-SEQPI 1	947
Qy	1743 LV	LVPPTPGTPATAMDRLAYLPTAPQPFSSRHSSSPLSPGGPTHLTKPTTTSSSERERDRDR 1	802
qa	1948 PJ	PTAATTAEEAPPVKEDEELPAKKKQRRRRKNELAAIVADQLLESFKIDNARRDNLKKL 2	2002
ογ	1803 EF	ERDRDREREKSILTSTTTVEHAPIWRPGTEQSSGSSGSGGGGGSSSRPASHAHQHSP 1.	1862
qq	2006 EN	ENLAYEKSEDLLLTGMLIMPSTKRNAALGPSSAAAAKLAKKEAADTVAESP 2	2056
ΟŊ	1863 IS	ISPRTQDALQQRBSVLHNTGMKGIITAVEPSKPTVLRSTSTSSPVRPAATFPPAT 1	917
qq	2057 AN		2105
δλ	1918 нс	HCPLGGTLDGVYPTLMEPVLLPKEAPRVARPERPRADTGHAFLAKPPARSGLEPASSPSK 1	977
ф	2106		2146
δλ	1978 GS	SGHATIARTPAKNLAPHHASP	2009
Q	2147 VP	VAREQQLTRQQQSKLDKQEQLPPAATFSRDPRLNKNIHKEQADHKAAPKEQSATATT 2:	2203
Qy	2010		2016
qq	2204 NE	NENPEEDDNYLTEIAKNVNEKIMSATTNEDFEFAHDEFDGEGDPDQDQDQDQDKYYRPPT 2:	263
Οy	2017 \$	SASDPH	2022
qq	2264 SN	 SMSVRSAPNI.NDEHSNFGSMCDDNTNTEVMDMDLDDEMSVYTSYSQDLGRGGRGRRRRRR 2	2323
δy	2023	SEKTQSKPFSIQELELRSLGYHGSSYSPEGVEPV 2	2056
QΩ	2324 RS	RSVLLTRRPKKRTQRSELDAEKFGCKLCGKSFFTATSLSKHNMTLAHVSKVSAQEYLQSQ 2	2383
οy	2057 SE		2103
QQ	2384 TP	TAPSSPQDGHDLENKRERQAETMLQHQEEQPAAAQQQMRASVLMVPAQMAHQER 2.	437
δλ	2104 PH	PHLRPLPESQPSSSPLLQTAPGVKGHQRVVTLAQHISEVITQDYTRHHPQQLS 21	156
qq	2438 EF	:	497
Qy	2157	APLPAPLYSFPGASCPVLDLRRPPSDLYLPPPDHGA-PARGSPHSEGGKRSPE 2'	208
qq	2498 PT	PTAPTASRININPDERLEYECCNILKSAETPRPHPGGGAGPAPTSVIVTAGRKQPP 2:	553
Qy		EGMTEPGHSRSAVYPLLYRDGEQTEPSRMGSKSPGNTSOP	2268
<b>Q</b>	2554 PE	PPASPSPSRSSLPPPASPSPSLPPPASPSLSLPPPASPSPSPSPPP 20	2601
δ d	2269 PP	PAFFSKLTESNSAMVKSKKQEINKKLNTHNRNEDEYNI-SQPG-TEIF-NMPAITGTGLM 2:    -  -  -  -  -  -  -  -  -  -  -  -  -	2325

οy	2326	TYRSQAVQEHASTNMGLEAIIRKALMGKYDQWEESPPLSANAFNPLNASASLPA 2379	
q	2644	::    :: :  THININELSPSYSAVSQFSATTTSRFKTKAAMKGYENVNLQM 268	<u> </u>
٥y	2380		8 t
qq	2684	DMLELAKSGRGVCKLIELADIALGSEKPGGEFLPHLPPAPAAPTVT 2729	<u> </u>
à g	2432	SVHSEGDCNRTTPLTNRVWEDRPSSAGS-TPFPYNDLIMRLQAG 2474	S 컴 
3	9	SE FFYNGGIFIFI FFFFFFFFFYNGEMEKKKOSTSSNIIMHASIINAAAG	8
g S	2475	VAMSSPPPFGLPAGSGPLAGPHHAWDEEPKPLLCSQYET 2512   1 : 1	់ ដ
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10.2	0921R1	R1 PRELIMINARY; PRT; 2157 AA.	8
222	01-M	QJAIKI; QJAMY-1999 (TrEMBLrel. 10, Created) 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)	
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နှင့် လ	Mus n Eukar	Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	ă 
888	Mamm	Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (NEI_TaxID=10090;	<i>8</i>
R R P	SEQUE	1  SEQUENCE FROM N.A.	<u> </u>
2	Rower	n L., Qin S., Madan A., Abbasi N., James R., Dickhoff R.,	S .
<b>₹</b> ₽	Shaf "Sequ	Shaffer T., Ratcliffe A., Loretz C., Lasky S., Hood L.; "Sequence of the mouse major histocompatibility class III region.";	전 
Z K	EMBL;	Submitted (NOV-1998) to the EMBL/Genbank/DDBJ databases. EMBL; AF109719; AAC82480.1;	<i>&amp;</i> 
S	SEQUI	ENCE 2157 AA; 229073 MW; 35B21F6B7C971F40 CRC64;	<u>~</u>
000	ery Ma	3.98;	<i>3</i> 1
W	Matches 506	. Conservat	<u> </u>
ογ	474	KKNENYKSLVRRSYRRRGKSODOQQQQQQQQQQQQQQQPMPRSSQEEKDEKEKEKER    :	
g	70	KGNDPNVSLVPKDGTGWASKQEQSDPKSSDASTAQPPES	
δ	531	KEEEKPEVENDKEDLIKEKTDDISGEDNDEKEAVASKGRKTANSQGRRKGRITKSMANEA 590	· ·
g	129	-PENTPSVPSGVKSWAQASVTHGAHGDGGRASNLLSRFSREEFPTLQAAG 177	- č
οy	591		S 2
a	178	DQDKAAKERESAEQSSGPGPSLRPQNSTTWRDGGGRGPDDLE-GPDSKLHHGHDPRGGLQ 236	
ογ	637	939	S 7
QQ	237	PSGPPQFPPYRGMMPPFMYPPYLPFPPPYGPQGPYRYPTPDGPSRFPRVAGPRGSGPPMR 296	<u> </u>
ογ	637	IARMVGSKTVSQCKNF-YFNYKKRONLDEILQQHKLKMEKERNARRKKKKAPA 688	- 
qq	297	VEPVGRPSILKEDNLKEFDQLDQENDGWAGAHEEVDYTEKLKFSDEEDGR 348	
Οý	689	AASEEAAFPP	S 6
g	349		
δ	747	DTESIPSPHTEAAKDTGONGPKPPATLGADGPPPGPPTPP 786	
g	396		<u> </u>
δy	787	RRTSRAPITP 808	<del>-</del>

qq	446 7	:	ñ
Oγ	809	EEGEEOKPPAAE 84	6
QQ	206	PAAPPVTPAAPALPPVVPKEIPAAPALPPTPTPEKEPEEPAQAPPVQAAPSPG 560	0
δy	850 1	ELAVDTGKAE-EPVKSECTEEAEEGPAKGKDAEAAEATAEGALKAE 894	4
qq	561	VAPVPTLVSGGGCTANSNSSGSFEASPVEPQLPSKEGPEPPEEVPPPTTPPAPKME 616	بو
ΟŊ	895	KKEGGSGRATTAKSSGAPQDSDSSATCSADEVDEAEGGDKNRLLSPRPSLLTPTGDPRAN 954	4
q	617	PKGDGVGSTRQPPSQGPRFQ 647	7
ΟŊ	955 #	AAAIPPIQVT	14
g	648 F	RQQQEQL-LKQQQQQQQWQQQQQGTAPPAPVPPSPPQPVTL-GAVPAPQA 695	Ŋ
δy	1015 F	ADKEAFAAEAQKLPGDPPCWTSGLPFP	74
ДQ	969		m
δλ	1075 E	FSYAPPGHPLPLGLHDTARPVLPRPPTISNPPPLISSAKHPSVLERQIGAISQGMSV 113	31
qq	724 N	MMIPPYUDPRLLQGRPPLDFYPPGVHPSGLVPRERSDSGGSSSEPF 769	ō
δy	1132 (	QLHVPYSEHAKAPVGPVTMGLPLPMDPKKLAPFSGVKQEQLSPRGQAGPPESL 118	84
<del>Q</del>	770 E	ERHAPPLLRERGIPPVDPKLAWVGDVFTITPIDPRPLISPLRQAADEEE- 818	80
οy	1185	GVPTAQEASVLRGTALGSVPGGSITKGIPSTRVPSDSAITYRGSITHGTPADVLYKGTIT 124	44
QQ	819		2
δλ	1245 F	RIIGEDSPSRLDRGREDSLPKGHVIYEGKKGHVLSYEGGMSVTQCSKEDG 129	94
qq	853 F	RFPLEESAPPGPRPLPWPPGNDEAAKMQAPPPKKEPSKEEPPQLSGPEAGRKPA 906	و
δλ	1295 F	RSSSGPPHETAAPKRTYDMMEGRVGRAISSASIEGLMGRAIPPERHSPHHLKEQHHIRGS 135.	54
qq	907 F	RGGGGPPPPRRENRTETRWGPRPGSCRRGIPPEE940	0
δλ	1355 1	ITQGIPRSYVEAQEDYLRREAKLLKREGIPPPPPPSRDLTEAYKTQALGPLKLKPAHEGL 141	14
Dp	941		80
δλ	1415 \	-LKYDTGASTTG 14	29
qq	- 696	EQGDETPKVPKPDALKTAKGKVGPKETPPGGNLSPAPRLRRDYSYERVGPTSCRG 102	23
οy	1468 -	SKKHDVRSLIGSPGRTFPPVHPLDVMADARALERACYEESLKSRPGTASSSGG 152	20
QQ	1024 F	RGRGEYFARGRGFRGTYGGRGRGARSREFRSYRE-FRGDDGRGGGSGG 107	20
δλ	1521	SIARGAPVIVPELGKPRQSPLTYEDHGAPFAGHLPRGSPVTMREPTPRLQEGSLSS 157	92
qq	1071	TNHPSAPRGRIASETRSEGSEYEEIPKRRQRGSETG 110	07
Qy	1577	SKASQDRKLTSTPREIAKSPHSTVPEHHPHPISPYEHLLRGVSGVDLYRSHIPLA 163	31
qq	1108		41
δλ	1632 E	FDPTSIPRGIPLDAAAAYYLPRHLAPNPTYPHLYPPYLIRGYPDTAALE 168	80
qa	1142 #	APPSPAPARFSTARGGRVFTPRGVPSRRGRGGRPPPVCSGWSPPAKSLVPKKPPTGPLP 1201	01
δy	1681 N	NRQIIINDYIISQQMHHNTATAMAQRADMLRGLSPRESSLAL 172 :: : : ::	22
Q	1202 E	QODKPPRFRRLKQ 12	57
δλ	1723 -	NYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAMDRLAYLPTAPQPFSSRHSSSPLSP 177	79

-LTAATVPPPRRTAAKSPDLSN 1307	1803	ANAGGAGPGISAMSRG 1367	GSS 1848 	GIITAVEPSKPTVLRS 1900	: SNPAGIQQ 1474	VARPERP-RADIGHAF 1959	-PRPKPGPPQAPQGSSPRPPTRYD 1515	PHHASPDPPAPASAS 2019		SPSLTHDKGLPKHLEE 2076	GTEALTPHI 1606	ESQPS 2115	SQSDSGVDLSGDSQVS 1658	APLPAPLYSFPGASCP 2172	-AEGPPKRPGGPSPLNAVPGESAS 1698	-GSPHSEGGKRSPEPNKISVLGGGE 2219	DRGPEPGP 1748	-HSRSAVYPLLYRDGE 2250	AVP-ISRDWELLPSAS 1805	SKKQEINKKLNTHNRN 2300	SGGAPIDSQLH 1858	IIRKALMGKYDQWEE- 2359	:     :: : LSGVALKGQFLDFSAL 1907	-LNASASLPAAMPITAADGRSDH 2392	: SPSDFYS 1958	VHSEGDCNRRTPLTNR 2448	1999	SGPLAGP 2494	 RVLPSPARPFAPSLGR 2047		
ERENAARGADGLTAASTPGPEETLTAATV	GGPTHLTKPTTTSSSERERDRDRE	QNSDQANEEWETASESSDFASERRGDKETPPAALMTSKAVGTPGANAGGAGPGISAMSRG	RDRDREREKSILISTTTVEHAPIWRPGTEQSSGSSGSSGGGGGSS   ::	SRPASHSHAHQHSPISPRTQDALQQRPSVLHNTGMK	SWPSPKNRSRPPEERPPGLPLPPPPSSSAVFRLDQVIHSNPAGIQQ	TSTSSPVRPAATFPPATHCPLGGTLDGVYPTLMEPVLLPKEAPRVARPERP-RADTGHAF	ALAQLSSRQGNVTAPGGHPRPKPGPPQAPQ	LAKPPARSGLEPASSPSKGSEPRPLVPPVSGHATIARTPAKNLAPHHASPDPPAPPASAS	RGVGG	DPHREKTQSKPFSIQELELRSLGYHGSSYSPEGVEPVSPVSSPSLTHDKGLPKHLEE	-KRERPPRKPELLQEETVPASHSSGFLGSKPEVPGPQEESRDSG	LDKSHLEGELRPKQPGPVKLGGEAAHLPHLRPLP	WNRLHTATSRKSYQPGSIEPWMEPLSPFEDVAGTEMSQSDSGVDLSGDSQVS	SSPLLQ-TAPGVKGHQRVVTLAQHISEVITQDYTRHHPQQLSAPLPAPLYSFPGASCP	S	VLDLRRPPSDLYLPPPDHGAPARGSPHSEGG	GSEPSEPPRRRPPASHEGERKELPREQPLPPGPIGTERSQRTDRGPEPGP-	DGIEPVSPPEGMTEPGHSRSA		-QTEPSRMGSKSP-GNTSQPPAFFSKLTESNSAWVKSKKQEINKKLNTHNRN	TSAEPQPKSLGSGQCVPEPSPSGQRPYPEVFYGSPGPPNSQVSGGAPIDSQLH	EPEYNISQPGTEIFNMPAITGTGLMTYRSQAVQEHASTNMGLEAIIRKALMGKYDQWEE		SPPLSANAFNP	QATELGKLPAGGVLYPPPSFLYSAAFCPSPLPDPPLLQVRQDLPSP-	TLTSPGGGGKAKVSGRPSSRKAKSPAPGLASGDRPPSVSSVHSEGDCNRRTPLTNR	TPLQPGGQSGFLPSGAPAQQMLLPVVDSQLPVVNFGSLPPA	VWEDRPSSAGSTPFPYNPLIMRLOAGVMASPPPPGLPAGS-	PPPAPPPLSLLPVGPALQPPNLAVRPPPAPAARVLPSPARPFAPSLGR	HHAWDEEPKPLLCSQYETLSDS 2516	AELHPVELKPFQDYRKLSSN 2067
1258 E	1780 G	1308 0	1804 - 1368 D	1849 -	1428 SI	1901 T	1475 Ai	1960 L	1516 -	2020 DI	1555 -1	2077 LI	1607 W	2116 S	1659 Š	2173 VJ	1699 G	2220 DC	1749 -	2251	1806 T	2301 E	1859 -1	2360	1908 Q	2393 TI	1959 TI	2449 VA	2000	2495 HI	2048 AI
qq	ΟŸ	qq	δ q	οy	Op Op	ογ	QQ	οy	qq	οy	qq	δy	qa	Qy	q	δŏ	q	οy	qq	QY	QQ	οy	qq	οy	qq	δy	qq	δ	qq	δy	q

Search completed: September 8, 2001, 14:38:43 Job time: 4750 sec

09jltl rattus norv 09jks6 rattus norv

Q9VID9 Q9VH10 Q9JLT1 Q9JKS6 Q9JKS6

99 ОНА В 09W3Z0

Q9vid9 drosophila Q9vh10 drosophila

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1394 SGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVKAGETVRSRHTSVVS 1453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butharia; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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SEQUENCE 1047 AA; 113817 MW; B5A1EDE938B7222A CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 113.8 KDA PROTEIN (FRAGMENT).
HOMO sapiens (Human).
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09dm1 drosophila
09vc3 drosophila
09y6v0 homo sapien
09y6v0 homo sapien
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09gyx6 mus musculu
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Copyright (c) 1993 - 2000 Comp
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    protein search, using sw model

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ALIGNMENTS

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Gaps

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090435 caenorhabdi 043161 homo sapien 09upa5 homo sapien 0903y8 caenorhabdi

Q9UPA5 Q9N3Y8 Q9PU36

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094c00 drosophila 094ba8 homo saplen 0917u4 drosophila 0917u4 drosophila 09165 homo saplen 09163 drosophila 017490 caenorhabdi 0917343 caenorhabdi 0917343 caenorhabdi 0917343 drosophila 094736 drosophila 094736 drosophila 094736 drosophila 094736 drosophila 094736 drosophila

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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_Tax_D=7227;
                                                                                                                                                                                                                                                                                                                   DVIITRQIASDKDARERGSQSSDSSSSLSSHRYETPSDAIEVISPASSPAPPQEKLQTYQ
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PRINTS; PRO0308; ANTIFREEZEI.
PROSTIE; PSO0687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
SMART; ANOU395; SANT; 1.
SEQUENCE 3469 AA; 364115 MW; 6284E14C5C247CD9
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ογ	1540 PVV	PVVSHSPEDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPS 1599
qq	2408 PPQ	PPQQSSPQAPPPQGYGVGVSSPYARSPFAGVVE 2440
δý	1600 QYQ	QYQLYAMENTRQTILNDYITSQQMQVNLRPDVARGL
qq	2441 QPQ	2VLSTRQIVMHDYITSQQMQQQQQQQQQQQQRNMSRGSSASGGGGGGGSDKES 2497
δy	1636 -SP	PATRGIIDLTNMPPTIL
QQ	2498 PSP	PSPRNSVGSASGFAYGGDKESAPRGRPEYSSRASPADHVNSTPSPHRTPPPQR 2550
δλ	1678 ITYI	1722
QQ	2551 QGV	QGVIQRHNTGSKPPSPAAPPPSRMHMPPYQYAPSGHDALASFVDVAVQQPQLPVPS 2606
δλ	1723 ERE	ERERERIAAASSDLYLRPG-SEQPGR-PGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNG 1780
С	2607 QKD	QKDDKLPHAVVG 2641
δλ	1781 TSV	SVITPLDPTAQLRIMPLPAGGPSISQGLPASRYNTAADALAALVDAAASAPQMDV 1836
qq	2642V	VAQPPPPTAHHDQRYRDLTLHHHHHTLVQQQIAQQQHYRSLNVAAQVDMQRQMDQ 2696
δy	1837 SK-	TKESKHEAARLEBNLRSRSAAVSEQQQLEQKTLEVEK 1875
₽ 2	2697 AKR	AKRVMRHQQHQVQQQQQQQQQQHNHALERDREMQERMRERDRERERERERERERER 2756
δλ	1876	SAPPSGKPQPHSS 1897
q	2757 ERE	EREREREREREREQDRARRYVAEEREHDSRRMERMFAGNYVTGSGGAGGGGPSPGQFLRAS 2816
δλ	1898 VVY	VVYSEAGKDKGPPPKSRYEEELRIRGKITITAANFIDVIIIRQIASDKDA 1947
qq	2817 V	PETGPPRSIPDRERESYYRQAHGGPAPEDTPGQLSAQSLIDAIIKHEINRSNDATAG 2874
δλ	1948R	RE
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qq	2930 LTA	LTAENNGKPSSSGSPSVINIDLDQERISAAAAAVAQQQQQQAPPPSQSSQSKSVH 2985
Οý	2028 -00	-QQLPPSSQAEGMGQVPRTHRLITLADHICQIITQDFARNQVSSQTPQ-QPPTSTFQN 2083
qq	2986 GQL	RTPTSQSGGSAPSPQQIHTKSITFGELTDSIITSDYGTNPHLRPPYMAYLQ 3039
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RA Adams M.D., Celniker S.E., Hichards S., Ashburner M., Hendelerson S.N.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Hendelerson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Adril J.F., Agdoryan A., An H.-J., Andrews-Pfannkoch C., Baddwin D.,
RA Adril J.F., Doyle C., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Basun R.N., Basun A., Baxendale J., Brokstein D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein D., Bolshakov S.,
RA Borkova D., Botchan M.R., Buuler H., Cadieu E., Center A., Chandra I.,
RA Buttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Dietz S.M.,
RA Gerblos B., Delcher A., Dubre C., Davelport I. B., Duvies P.
RA Grodek R., Gong E.E., Downes M., Dugan-Roccha S., Dunkov B.C., Dunn P.,
RA Harris N.L., Harvey D. L.E., Downes M., Dugan-Roccha S., Dunkov B.C., Dunn P.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Jalali M., Kalubh F., Karpen G.H., Ke Z., Kennison J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Mannal B.E., Molitch N.Y., Mobarry C., Morris J., Moshrefi A.,
RA Marking W., Murphy B., Murphy L., Murshkern D.R., Pacleb J.M.,
RA Methory G., Milshina N.Y., Mobarry C., Morris J., Moshrefi R.,
Rainer E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Mang Z.-Y., Wassarman D.A., Wenlastock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Weilliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
R. Fe J., Yang R. Fe J., Rayer E., Sand F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhao G., Zhang G., Zhang G., Zhao G., Zhao G., Zhao G., Zhang G., Zhao G., Zhao G., Zhao G., Zhang G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao 
---ISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGGDSDMAAAQPGTEIFNLPAVTTS 2244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3292 TPNQYEVVDASG--RRSAGSGSVSVSGANSHHSPYHPPAAAYAPSTYAFPYSALNVPG 3349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                          3235 V---EVRTEDEVTADMVAHSHAAVHAAHVAHAAHVAHAAAMELQHRSKEPPPPEISVSRK
                                                                   GRNIIRMP-----QAVSPRKFNHEMMLHHVMGTTGAGGEAGQFFLPSRVVLPEQRGTPS
                                                                                                                                                   GSVSSRGHSFADPASNLG---LEDIIRKALMGSFDDKVEDHGVVMSQPMGVVPGTANTSV
                                                                                                                                                                                                                              -----GYGKNRT
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Last annotation update)
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SMR OR CG4013.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 QLEEEA--AKPPEPEKPVS-----PPPVEQKHRS--IVQIIYDENRKKAEEAHKIFE-- 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GLGPKVELPLYNQPSDTKVYHENIKTNQ-VMRKKLILFFKRRNHARKQREQK 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PMKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNFGLIASYLERKSVPDCVLYYYLTKKNEN 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                    556 ANANNMHLPPH-----PQQQHQQQQQQQQQQQQHQAHQQQHQRSSPAQVQQQQQQQMNSSR 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  657 QPVVSSMSTVVSQPVGTVTVTTAGLSAS------HSGSSGNVAAGLGTGNTGSA 704
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      S., Zhu X., Smith H.O
                                                                                                                                                                                                                                                                                                                                                                                                               AFSTEQSRYPPHSVQYTFPNTRHQQEFAVPDYRSSHLEVSQASQLLQQQQQQCLRRRPSL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  610 QSH----NDMCRQVVT-----TPMGMQLKVETLPQQQQKQQQHQQQQQQQQGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---VSAAVLPLVHPL-----PEGLRASADAKKDPAFGGKHEAPSSPI-SGQPCGDDQNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S------PSKLS-----KEELIQSMDRVDREIAKVEQQILKLKKKQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  765 SLMEEAALAKEQRAAKELNDNNNDQEPMVELSWRSQMLAEKIYAANRKTAQAQHSMLQNA
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                                                                                                                                                                                                                                                                                                                                                                         Indels 1287;
                                                                                                                                                                                                                                                                                                                               Length 3502;
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SE 3502 AA; 369068 MW; 74C8004F9DA8F8D9 CRC64;
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Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
EMBL, AE003490; AAF48196.1; -.
FlyBase; FugnO012430; Smr.
InterPro; IPRO01005; -.
InterPro; IPRO01005; -.
PRAM: PF00249; Myb_DMA-binding; 1.
PRINTS; PRO0369; ANINEREEZEI.
PRINTS; PRO0369; ANINEREEZEI.
PROSTIE; PS00687; ALDBHYDE_DEHYDR_GLU; 1.
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les 649; Conserv
                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                 Query Match
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a	2311	TVPSLAAPSSYLYPTRSVKTIGGGGVVPGVLP-GVPGSALYLQPVPVPVPISISGQG 2366
οy	1300	TPRATTESFEDGLKYPKQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHEIP 1355
qq	2367	QLPPRAGQPPPAQPP
δλ	1356	
QQ	2393	LSPQQAHHLHPSHGHSPSQQQQQQQQQQQQQQAAAQQQQLLVKSGSITHGTPANS 2449
o t	39	RGMPPLEIVPENIKVVERGKYEDVKAGETVRSR 144
a d	4.5	~
yo g	1448	HTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTSDVTI 1507    -  -  -  -  -  -  -  -  -  -  -  -  -
ì	7 7 0	CONTRACTOR TO THE
3 8	2545	
δŏ	1568	PTPGYPSQYQLYAME
ф	2567	:
Qy	1624	QVNLRPDVARGLSPREQ
qq	2605	QQQQQQQQQRINMSRGSSASGGGGGGGGDKESPSPRNSVGSASGFAYGGDKESAPRGRPE 2664
δŏ	1646	
q	2665	YSSRASPADHVNSGHDALASFVDVAVQQPQLPVPSQKDDKSPGPSTAPGQVPGSG 2719
Qy	1686	ITFPPRPYNSASMSPGHPTHLAAAASAERERERERERERERERIAAASSDLYLRPGSEQP 1745
QQ	2720	PPLGPSPLGVAQP 2738
οy	1746	RIMPLE
qq	2739	PPPTAHHDQRYRDLTLHHHHHTLVQQQIAQQQHYRSLNVAAQVDWQRQM 2787
Qγ	1805	ISQGLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAA 1859
qa	2788	DQAKRVMRHQQHQVQQQQQQQQQHNHALERDREMQERMRERDRE 2833
δλ	1860	VSEQQQLEQKTLEVEKSS 1885
QQ	2834	REREREREGREREREREREREREREREGDRARRYVAEEREHDSRRMERMFAGNVVTGSG 2893
Qy	1886	AFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFID 1934
qq	2894	GAGGGGPSPGQFLRASVPETGPPRSIPDRERESYYRQAHGGPAPEDTPGQLSAQSLID 2951
δλ	1935	VIITRQIASDKDARERGSQSSDSSSSLSSHRYETPSDAIEVI 1976
qq	2952	AIIKHEINRSNDATAGPGREFPRPSFVHAPLPPRGSGSGGGTGTRSSPANVLHPM 3006
. 0y	1977	SPASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGP 2013
QQ	3007	YLRDLRQPLDGGAGSMLTAENNGKPSSGGSPSVINIDLDQERISAAAAAVAQQQQQQAP 3066
Qy	2014	LHHYRPQQESPSPQQQLPPSSQAEGMGQVPRTHRLITLADHICQIITQDFARNQV 2068
Q	3067	PPSQSSQSRSVHGQLRTPTSQAGGSAPSPQQIHTKSITFGELTDSIITSDYGTN 3120
δλ	2069	SSQTPQ-QPPTSTFQNSPSALVSTPVRTKTSNRYSPESQAQSVHHQRPGSRVSPENLVDK 2127
QQ	3121	PHLRPPYMAYLQETQSIL-PPDRWK-QNRRMQQKAEEAKHSQQQQQQHQQ 3170
οy	2128	SRGSRPGKSPERSHVSSEPYEPISPPQVPVVHEKQDSLLLLSQRGAEPAEQRNDARSP 2185
<b>q</b>	3171	оннаооооооооннаооннромрстсясаярссясося

δλ	2186 GSISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGGGDSDMAA 2228	Q
qq		qa
Qy	2229 AQPGTEIFNLPAVTTSGSVSSRGHSFADPASNLGLEDIIRKALMGSFDDKVEDHGVV 2285	δŏ
QQ	3269 FLPSRVVLPEQRGTPSGGGGAPGAGGPGSGGGATTIEKYVKTRIAEVMRDDI 3320	අධ
ογ	2286 MSQPMGVVPGTANTSVVTSGETRREEGDPSPHSGGVCKPKLISKSNS 2332	- Oy
QQ	3321GYGKNRTVEVRTEDEVTADMVAHSHAAVHAAHAAHVAHAAAMELQ 3368	<b>q</b> a
Οy	2333 RKSKSPIPGGGYLGTERPSSVSSVHSEGDYHRQTPGWAWEDR2374	ζο
qq	3369 HRSKEPPPPEISVSRKTPNQYEVVDASGDQAVAPPGAFAKARAAHALSELGAVGGGVSLV 3428	qa
ογ	2375	, o
qq	3429 VGGGSGGIAGGPGGVSVGVPGGGGPGGGGGGGGHNSSSSQASAAVAAAV 3480	qa
Οy	2409 NQAAPHQQNRIWEREPAPLLSAQYETLSDSD 2439	Qy
QQ	3481 AAASESKPLILSKYDALSDED 3502	qa
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076891	894	අ <sub>ධ</sub>
S S E	1100 (TATEMENT OF CAMPAND OF CAMP	Qy
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E N	EG: 49E4.1 PROTEIN. FITTACH OR FG: 40E4 1 OP CG: 3064	Qy
So	Drosophila melanogaster (Fruit fly). Fibaronia Melanogaster Arthrophysia Dowanoda, Incorta.	qu
888	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ebhydroidea; Drosophilidae: Drosophila	40
N O	NCBI_TaxID=7227; [1]	qa
RA	SEQUENCE FROM N.A. Papagiannakis G., Spanos L., Siden-Kiamos I., Louis C.;	Oy
RT RL	quencing the distal X chromosome of Drosophila mel mitted (JUL-1998) to the EMBL/GenBank/DDBJ databas	qa
RP	[2] SEQUENCE FROM N.A.	Qy
R.R.		qu
<u>0</u>	EMBL; AL031128; CAA20006.1; FlyBase; FBgn0025392; futsch.	δō
ÖS	5327 AA;	qq
õä	Query Match 4.6%; Score 584.5; DB 5; Length 5327;	Oy 40
Ä	8; Conservative 412; Mis	90 .c
δλ	53 ASQLLQQQQQQLRRRPSLLSEFHPGSDRPQERRTSYEPFHPGP-SPVDHDSLESKR 108	δο <i>Έ</i>
qq	750 ATGATQATQKKPISRRPRGVSPSKRAPAPGSPVKQAKPKAADLKK 794	- i
ر د د	109 PRLEQVSDSHFQRVSAAVLPLVHPLPEGLRASADAKK	경 옵·
3 8		Qy
S 8	140	q <sub>Q</sub>
Qy		QY OY
qq	KKSAEEEIEAAIAKVEAAERKARLEGASARODESELD	qa

QY         225           DD         225           QY         273           DD         1030           QY         295           DD         1145           QY         356           DD         1205           QY         456           QY         456           QY         456           QY         516           QY         516	PPPVEQKHRSIVQIIY
Db         1264           Qy         564           Db         1323           Qy         622           Db         1381	ATTVITQËNQËDIAMËQVKDKËBHËQKIËSGIITË REQATPRGRKTANSQGRR-KGRITRSMIDEAAA :
QQ     678       DD     1423       QQ     722       DD     1474       QQ     774       DD     1534	LLQQHKQKTSRKPREERDVSQCESVASTVSAQEDEDIEASNEEE 721
Qy     832       Db     1585       Qy     889       Db     1639       Qy     949       Db     1674	HASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCSADED 888  :: :
Oy 1007 Db 1725 Oy 1067 Db 1772 Oy 1102 Oy 11832	LQPAPHQLITNLPEGVRLPTTRPTRPPPPLIPSSKTTVASERPSFIMGGSISQGTPGTYL 1066

517; DB 4; Length 3261; No. 3.1e-19; smatches 1038; Indels 816; Gaps 129; | | | : ||:|| : DEGDKTTSRRVSVADSIKDEKSLLVSQEASR 3010 SPMVKSKKQEIFRKLNS-----SGGGDSD 2225 DPASNLGLEDIIRKALMGSFDDKVEDHGVV 2285 ::|:||||||||:|: ---MDKADKSKEPSR--PESVAESIKHENT 2890 PGSRVS-PENLV----DKSRGSR-----PG 2134 TESVKDGKSPVASKEASRPASVAENAKDSA 3064 -----PSPHSGGVCKPKLISKSNSRK--- 2334 HRQTPGWAWEDRPSSTGSTQFPYNPLTMRM 2392 -----VPVVHE-KQDSLLLLSQRGAE 2174 RKNYCSLRDETPERKSGQEKSHSVNTEEKI 756 PLVHPLPEGLRASADAKKDPAFGGKHEAPS 157 -----PPVEQK------HRSIVQII 239 LSEFHPGSDRPQERRTSYEPFHPGPSP--- 98 lata; Vertebrata; Euteleostomi; crhini; Hominidae; Homo. IWEREPAPLLSAQYET 2434 inBank/DDBJ databases. BB6A645DD9B6BC CRC64; equence update) 3261 AA.

:	YDENRKKAEEAHKIFEGLGPKVELPLYNQPSDTKVYHENIKTUQVMFK 287    : :	KLILFFKRRNHARKQREQKICQRYDQLMEAWEKKVDRIENNPRRAKESKTREYYEKQFP 347 	EIRKQREQOERFORVGORGAGLSATIARSEHEISEIIDGLSEQEN 392 	NEKOMRQLSVIPPWMFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHE 444	SKR   : SKQTSE		ENTKEKDKIDGTABETEEREQATPRGRKTANSQGRRKGRITRSMTNEAAAAAAAATE 605     :	EPPPP	651	695	HPEPSLPLSRTRRRNVRSVYATMGDHENRSPVKEPVEQPR	ASNEEENPEDSEVEAVKPSEDSPENAT 742                     1 VTRKRLERELQEAAAVPTTPRGRPPKTRRRADEEEENEAKEPAETLKPPEGWRSPRSQK 1585	SRGNTEPAVELEPTTETAPSTSPSLAVFSTKPAEDESVETQVNDSISA 790 :	ETABOMDVDQQEHSAEEGSVCDPPPATKADSVDVEVRVPENHASKVEGDNTKER 844    :	-DLDRASEKVEPRDEDLVVAQQINAQRPE-PQSDNDSSATCSADE-DVDGEP 893 	ERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQL 930  :::	-HRAAVIPPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEQRQRQEQI 983        :	DLECRSSTSPCGTSKSPNREWEVLQPAPHQLITNLPEGVRLPTTRPTRPPPPLI 1037   :
:       SEDSERTGGSPSVRHGSFHEDEDP	YDENRKKAEEAHKIFEGLG    : ::  :   YDSSRREQMADMA			NEKQMRQLSVIP 			ENTKEKDKIDGTAEETEEREQATPI : :     LKTPPSVGPPSVTVYLESAPS	EPPPPLPP	- PPEPISTEPVETSRWTEEEMEVAK		VSQCESVASTVSAQEDEDIE :   :     :   :   KMEAEKITRTASKNSAADLEHPEP	VTRKRLERELQEAAAVPTTPRRGRI	SENGNTEPAVELEI :       : TAAGGGPQGKKGKNEPKVDATRPE	ETAEQMDVDQQEHSAEEGSVCDPPI 	-DLDRASEKVEPRDEDI 	ERQRMFPMDSKPSL  :::   EXEDVSASGPSPEATQLAKQMELEC	QHRAAVIPPMVSCTPCNIPIGTPVSGY 	DLECRSSTSPCGTSKSPNREWEVLK
849	240	288	348	393	445	499	546 1228	606	614	652	696	716	743	791 1646	845 1688	894	931 1806	984
QQ	Oy Op	Qy Dp	Qy Dp	Qy	Qy	Oy Dp	Oy.	Qy Db	δλ Dp	03 P	Oy Db	ð a	δ q	S G	Oy Dp	Qy	Oy Dp	ò

qq	Db 1843 DLQPPAGAQALQPSEEGMETDEAVSGILETEAATESSRPPVNAPD	- 1887
ογ	1038 PSSKTTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQETPKPSVGS	E 1095
qq	1888 PSAGPTDTKEARGNSSETSHSVP	: K 1927
δλ	1096	G 1142
q	DD 1928 GRQKTTRSRRKRNTNKKVVAPVESHVPESNOAQGESPAANEGTTVQHPEAPQEEKQS	S 1984
ò q	QY 1143 SITRGTPTSKISVESIPSLRGSITQGTPALPQTGIPTEALVKGSISRMPIEDSSPE	E 1198
Οy	1199 KGREEAASKGHVIYEGKSGHILSYDNIKNAREGTRSPRTAHEISLKRE	
qq	Db 2038 DEEPQARFRVHSIIESDPVTPPSDPSIPIPTLPSVTAAKLSPPVASGGIPHQSPPTK	K 2094
Qy	1254 IKQGMSMRESPVSAPLEG	E 1306
qq	2095	T 2149
oy e	QY 1307 SFEDGLKYPKQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHEIPRQDILJQE	E 1363 A 2202
Οy	1364	
đ	Db 2203 DKEKVAPVIAPKITSVISR-MPVSIDLENSQKITLAKPAPQTLTGLVSALTGLVNVSL	: L 2259
δý	Qy 1423 VPEN-IKVVERGKYEDVKAGETVRSRHTSVVSSGP-SVLRSTLHEAPKAQLSPGIYDD	D 1478
qq	2260 VPVNALKGPVKGSVTTLK	P 2300
δλ	1479	1523
QQ	Db 2301 VNVLTTPVNATVGTVNAAPGTVNAAASAVNATASAVTVTAGAVTAASGGVTATTGTVTMA	A 2360
Οy	1524	L 1564
qq	2361 GAVIAPSTKCKQRASANENSRF	S 2417
οy	1565PTQLDPAMP	L 1603
qq	Db 2418 GQKTEGPQRISAKISQIPPASAMDIEFQQSVSKSQVKPDSVTASQPPSKG-PQAPAG	G 2473
Oy	1604 YAMENTROTILNDYITSQQ	1651
QQ	2474 YANVATHSTIVLTAQTYNASPVISSVKADRPS	V 2528
οy	1652	T 1704
අ	2529 LTQGINTPPVLVHNQ	P 2585
οy	QY 1705 HLAAAASAERERERERERERERERIAAASSDLYLRPGSEQPGRPGSHGYVRSPSPSV	V 1761
οp	2586 ALPSKLPTEVNHVPSGPSIP	- 2640
Qy	1762 RIQETMLQQRPSVFQGINGTSVITPLDPTAQLRIMP	1812
qq	2641	v 2695
δλ	1813	E 1872
qq	Db 2696 RMNTPTLPSITYSIRPEALHSPRAPLQPQQ	2725
οy	QY 1873 VEKRSVQCLYTSSAFPSGKPQPHSSVVXSBAGKDKGPPPKSRYEEELRTRGKTTITAANF	F 1932
qq	2726	V 2770
Qy	QY 1933 IDVIITRQIASDKDARERGSQSSDSSSSLSSHRYETPSDAIEVISPASSP	- 1982
QQ	Db 2771 OSEVLVMOSEYRLHPYTVPRDVRIMVHPHVTAVSEOPRAADG	G 2812

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Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
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A bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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A botsier C., Gabrielian A.E., Garraz C., Ferriers S., Ferischmann W.,
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Merkulov G. Milshina N.V., Wobarry C., Morris J., Mosherson D.,
Merkulov G. Milshina N.V., Wobarry C., Morris J., Mosherson D.,
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Merkulov G. Milshina N.V., Wobarry C., Morris J., Mosherson D.,
Merkulov G. Milshina N.V., Mosherson D.,
Merkulov G., Milshina N.V., Mosherson D.,
Merkulov G
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                                                                                                                                                                                                                                                                                                                                                                                                                SSVGLPSRTKTAAQGPPPEGEPLQPPQPVQSTQPAQPAPPCPPSQL-----GQPGQPPS 2979
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Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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---APPQEKLQTYQP--EVVKANQAENDPTR-----QYEGPLHHYRPQQESPSPQQQLPP
                                                                              2813 VVKVPPASK-APQQPGKEAAKTPDAKAAPTPTPAPVPVPVPLPAPAPAPHGEARILTVTP
                                                                                                                                                            SSQAEGMGOVPRTHRLITLADHICQII-----TQDFARNQVSSQTPQQPPTSTFQNSPS
                                                                                                                                                                                                                                          SNOLOGLPLTPP-----VVVTHGVQIVHSSGELFOEYRYGDIRTYHPPAQLTHT-OFPAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2980 SKMPQVSQEAKGTQTGVEQPRLPAGP-----ANRPPEPHTQVQRAQAETGPTSFPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2185 PGSISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGGGDSDMAAAQPGTEIFNLPAVTTS
                                                                                                                                                                                                                                                                                                                                      ALVSTPVRTKTSNR-----YSPESQAQSVHHQRPGSRVSPENLVDKSRGSRPG----
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Last sequence update)
Last annotation update)
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01-MAY-2000
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972; Gaps 124;
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|165 ALNDDLSELLTTVKKVPTAETTKLSARHQDEADEERSSRESDGDFKSLSNSRGSSEERPP 1224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKESKTREYYEKOFPEIRKOREQOERFORVGORGAGLSATIARSEHEISEIIDGLSEQEN 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----IYDENRKKA-EEAHKIFEGLGPKVELPLYNQPSDTKVYHENIKTNQVMRKKLIL 291
Sun E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 520; Conservative 392; Mismatches 1010; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            338176 MW; 4602054387DE2C12 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.0%; Score 507; DB 5; 18.0%; Pred. No. 1e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0503; BROMDOMAIN.
PROSITE; PS00455; AMP_BINDING; 1.
PROSITE; PS00455; AMP_BINDING; 1.
SMART; SM00297; BROMO; 1.
SEQUENCE 3080 AA, 338176 WW;
                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001487; -
Pfam; PF00439; bromodomain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Qy	635	VAKKGLVEHGRNWAAIAKMVGTKSEAQCKNFYENYKRHNLDNLLQQHKQKT-SRKPREE 693 	
o dy	694	RDVSQCESVASTVSAQED	
oy Db	729	EAVKPSEDSPENATSRCHTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVETOVN 785 	
Oy Dp	786	DSISAETAEQMDVDQQEHSAEEGSVCDPPPATKADSVDVEVRVPENHASKVEGDNTK 842   : :         :       :       SKKKEEPPRVVEKAQREKSPAPVSALETIKEPPAPTPIATSASGKVKEGPAKK-EPKKRP 1446	
Qy Db	843	ERDLBRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDV 889 :::         :       : : DKQMPPPRPADKSSEKGSGKKSSSKRAAQRAGQPQTNNNTNLEALDVETEQTLKDI 1503	
Oy Dp	890 1504	DGEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVIP 938 :	
Oy Dp	939	PMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEQRQROEQIDLECRSSTSP 993	
oy G	994	CGTSKSPNREWEVLQPAPH	
Qy Db	1030	TRPPPPLIPSSKTTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQETPK-PSVGSISL 1088	
oy ob	1089	GLPRQOESAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVRGTAGAIQEGSI 1144	
Q Q	1145	TRGTPTSKISVESIPSLRGS-ITQGTPALPQTGIPTEALVKGS 1186 ::: :  :   :     :     :	
Qy Db	1187	ISRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIKNAREGTRSPR 1236   :	
OY Db	1237	TAHEISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSI 1296	
Q D	1297	MQ-GTPRATTESFEDGLKYPKQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHEIP 1355       : :   : :	
o d	1356	RODILTQESRKTPEVVQSTRPI1EGSISQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSR 1415 	
OY Db	1416	LEIVPENIKVVERGKYEDVRAGETVRSRHTSVVSSGPS 145	
Οÿ	1458	VLRSTLHEAPKAQLSPGIYDDTS	
qq	2000	EMNSPYPQYSQHIYSSASSPNVSTPDMSGTSPYGGGNSYNPSGSEASKTPAYSST 2054	
ço q	1487	SYQNTMSRGSPMMNRTSDVIIPPNKSTNHERKSTLIPTQRESIPAKSPVPGVD 1539  :	
ογ			

qq	
Qy	1597 YPSOYQLYAMENTROTILNDYITSQOMQVNLRPDVARGLSPREQPLGLPYPATRGI 1652
QQ	2171 AQSPAEQQHSPYQQPVLSPYQQPQQQQQQPPVVPPVQPSAGAQASTA 2216
ογ	1653 IDLTNMPPTILVPHPGGTSTPPMDRITYIPGTOITFPPRPXN-SASM 1698
qq	
δō	9 SPGHPTHLAAAASAERERERERE KERERERIAAASSDLYLRPGSEQ 974
2 2	22/3 LPESTITITYNGAAQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ
2 2	
ò	6 TMLQORPSVFOGTNGTSVITPLDPTAQLRIMPLPAGGPSISOGLPASRYNTAAD
셤	:     :     :
ογ	1820 ALAALVDAAASAPQMDVSKTKESKHEAARLEENLKSRSAAVSEOQOLEQKTLEVEKRSV- 1878
qq	2440
δ	9QCLYTSSAFPSGKPOPHSSV-VYSEAGKDKGPPPKSRYEEELRTRG 192
qq	2479 NKOQOMFNSFLGTMAFGKPIGNIAPDKAFEMYNRAAAMGFPKDFAKDNSCQLQQQQQQQQ 2538
οy	1924 KTTITAANFIDVIITRQIASDKDARERGSQSSDSSSSLSSHRYETPSDAIEV 1975
qq	2539 SPQVTTNKQQANQQTQQQPQQSQSQPHLTQLQTALSQNYQQQQQTQAQK 2590
οy	1976 ISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGPLHHYRPQQESPSPQQQLPPSSQ 2035
qq	
δλ	2036AEGMGOVPRT-HRLITIADHICQIITQDFARNQVSSQTPQQPPTSTFQN- 2083
qq	2634 STVAAAVSESSSNAMNLPSTAHQHHLSQTHHLAAYNKPTPPPPQTYSNP 2682
οy	2084SPSALVSTPVRTKTSNRYSPESQAQSVHHQRPGSRVSPEN 2123
qq	2683 IMQSMLGYAGNYFDKTMPPAAHMYSASSAASAYGNPAQQLPGNYVPGNN 2732
οy	2124 LVDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVHEKQDSLLLLSQRGAEPA 2176
qq	2733 NPAHQQQQQQQQQQQQQAPAVPPAEVKAPAKRGRKKKAATIAAEAAAAAKQQQQQ 2790
οy	2177 EQRNDARSPGSISYLPSFFTKLENTSPWVKSKKQE
đ	2791 QOQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ
δλ	2215 KLNSSGGGDSDMAAAQPGTEIFNLPAVITSGSVSSR-GHSFADPASNLGLEDIIRKAL 2271
QQ	2845 SMASAAAATNNQLQAHAQALQOGFQLYAGLKSGGVSSPVGSSAATPVNSGG 2895
Qy	2272 MGSFDDKVEDHGVVMSQPMGVVPGTANTSVVTSGETRREEGD 2313
qq	2896 -STINQTAADAAAISLKTSTGGMVPGSAFNFAPTPG-TLGLYGDQAAAASSYLDQFRDAP 2953
Qy	2314PSP-HSGGVCKPKLISKSNSRKSKSPIPGGGYLGTERPSSVSSVHSEGDY 2362
QQ	AHSGTAANPSGNAADKGQ
ΟY	2363 HRQTPGWAWEDRPSSTGSTQFPYNPLTWRMLSSTPPTFLACA 2404
qq	3005aaaayppadpnsqlyqqylrrddfhtrmifnqsllggpaaaaaagygqpppppsayq 3062
οy	2405 PSAVNQAAPHQONR 2418 : :

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1052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----LQQQQQQLRRRPSLLSEFHPGSDRPQERRTSYEPFHPGPSPVDHDSLESKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DAEADEGWAGAQMEVDYTEQLNFSDDDEQGSNSPKENNSE------DQGSKASEN 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 PRLEQVSDSHFQRVSAAVLPL---VHPLPEGLRASADAKKDPAF----GGKHEAPSSP-- 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              510 QEEKVEEKEEDKAEKTEKKEEE---KKDEEEKDEKEDSKENTKEKDKIDGTAEETEEREQ 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQPRPAVLSGYFKQFQKSLPPRFQRQGEQMKQQQWQQQQQGGVLPQTVPSQPSSSTV--- 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 YPPLHGPM----RFPP-SLSETNKGLRGRGPPPSWASEPERPSILSASELKELDKFDNL 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             602 AATEEPPPPLPPPPEPISTEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAKMVGTKSEAQ 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   413 LAQQHPPPDRQAVPGRPGPFPSKQQVAD------EDEIWKQRRRQQSEISAAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDTKVYHENIKTNQVMRKKLILFFKRRNHARKQREQKICQRYDQLMEAWEKKVDRIENNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRKAKESKTREYYEKQFPEIRKQREQQERFQRVGQRGAGLSATIARSEHEISEIIDGLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           450 DKFIQHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YPPNQGAFSTEQSRYPPHSVQYTFPNTRHQ---QEFAVPDYRSSHLEVSQASQL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISGQPCGDDQNASPSK----LSKEELIQSMDRVDREIAKVEQQILKLKKKQQQ----LEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAAKPPEPEKPVSPPPVEQKHRSIVQIIYDENRKK--AEEAHKIFEGLGPKVELPLYNQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           461 RARKRRE-----EEERR-----MEEORKAACAEKLKRLDEKLG----ILEKQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Length 2701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 514; Conservative 338; Mismatches 910; Indels
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Rhodes S., Huckle E.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
EMBL, AL096857, CAB51071.1; -.
Hypothetical protein.
SEQUENCE 2701 AA; 295828 MW; D2043FF9840ADECD CRC64,
                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 489.5; DB 4 Pred. No. 7.5e-18;
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1867 ALASTSAPTPAPAASSPAAPVITAPTIPASAPTASVPLAPASASAPAPAPTPVSAPNPAP
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                                                                                                                                                                                                     -----FDLNNYASVVIIDDHP------EVTVIEDPQ------SNLNDDGFTEV
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                                                                                                 ----INGSSAHHQEGVPNGTGQK-----NSKDSTGKKREDPKPGPKKPKEKVDALSQ-
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MICROTUBULE ASSOCIATED PROTEIN (MAP) (FRAGMENT).
Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1578 PPSKSGKRG------PFDDQPAGTIGVDL-
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117;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=SPRAGUE-DAWLEY, TISSUE=BRAIN;
MEDLINE=92347374; PubMed=1639092;
Rauner W., Kratz J., Staunton J., Feick P., Wiche G.;
Zauner W., Kratz J., Staunton T., Feick P., Wiche G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 LLSTTHPAN------KASLTLFCP------EEGDWKNSNLDRHNLQDFINIKLNSASIL 125
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| S59 NGQEVDIPISYLASVSSLIVWHPANPAEKIIRVLFPGNSTQYNILEGLEKLKHLDFLKQP 418
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4ammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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Matches 494; Conservative 360; Mismatches 946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257 LGPKVELPL--YNQPSDTKVYHENIKTNQVMR-----
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EEML, X60370, CAC16162.1; -.
NON TER
SEQUENCE 2364 AA, 259022 MW,
                                    NCBI_TaxID=10116
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RSLMSSPEDLTKDFEELKAEEIDVAKDIKPQLELIEDEEKLKETEPGEAYVIQKETEV	ETAPSTSPSLAVPSTKPAEDESVETQVNDSI	SKGSAESPDEGITTTEGEGECEQTPEELEPVEKQGVDDIEKFEDEGAGFEESSEAGDYEE	SAETAEQMDVDQQEHSAEEGSVCDPPPATKADSVDVEVRVPENHASKVEGDNTKERDL         : : :   :				VVDKAAEAGVTEDQYDFLGTPAKQPGVQSPSREPAS	IKAMHESALLEEQRQRQEQID		LPTTRPTRPPPPLIPSSRTTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQ ::		: :   : :     :::::   : : ::::   : EXSKPVVASFN-GLSDGSKTDATDGRDYNASASTISPPSSMEEDKFSKSALRDAY		RPEETDVKTGAELDIKOVSDERLSPAKSPSLSPSPPSPIEKTPLGERSVNFSLTPNEIKA	POTGIPTEALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIKN		AREGTRSPRTAHEISLKRSY-ESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDL :		::   :   :	TIKEMGKSIHEIP-RQDILTQESRKTPEVVOSTRPIIEGSI-SQGTPI		KFDNNSGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVRAGETVRSRH :			GSPMMNRTSDVTIPPNKSTNHERKSTLTPTQRESIPAKSPVPGVDPVVSHSPFDPHRGS	:  :		QSAMSIEFGQESPEHSLAMDFSRQSPDHPTVGAGMLHITENGPT		EVDYSPSDIQDSSLSHKIPPTEEPSYTQDNDLSELISVSQVEASPSTSSAH	TPPMDRITYIPGTQITFPPRPYNSASMSPGHPTHLAAAASAERERERERERERERERIAA 1731 
724	758	782	789	847	902	907	946	964	982	1024	1077	1011	1125	1125	1173	5811	1228	1287	1287	1343	1341	1389	1449	1450	1495	1501	1555	1538	1612	1582	1672 1633
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-----LTPRESSP-----TYSPGFSDSTSGAKESTAAYQ----TSSSPPIDAAA 1722
                                                                           1792 QLRIMPLPAGGPSISQGLPASRYNTAADALAALVDAAASAPQMD------V 1836
                                                                                                                                                        1837 SKTKES------KHEAA------RLEENLRSRSAAVSEOOOLEOKTLEVEK 1875
                                                                                                                                                                                 1772 ESTIESPDEEDYDYESHEKTIQAHDVGGYYYEKTERTIKSPCDSGYSYETIEKTTKTPED 1831
                                                                                                                                                                                                                                        1876 RSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDV 1935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2127 KSRGSRPGKSPERSHVS--SEPYEPISP-PQVPVVHEKQDSLLLLSQRGA----EPAEQR 2179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2180 NDARSPGSISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGGGDSDMAAAQPGTEIFNLP 2239
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                                                                                                                                                                                                                                                                                                                       1936 IITRQIASDKDARERGSQSSDSSSLSSHRYET-----PSDAIEVISPASSPAPPQE 1987
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Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta,

Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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MEDLINE-20157049; PubMed-10655223;

Rebay I., Chen F., Hsiao F., Kolodziej P.A., Kuang B.H., Laverty T., Suh C., Yoas M., Williams A., Rubin G.M.;

Suh C., Yoas M., Williams A., Rubin G.M.;

A Genetic Screen for Novel Components of the Ras/Mitogen-Activated Protein Kinase Signaling Pathway That Interact With the yan Gene of Drosophila Identifies split ends, a New RNA Recognition Motif-Containing Protein.";
                                                                                                                                                                                                                                                                                                                                                                                                   1988 KLQTYQ--PEVVKANQAENDPTRQYEGPLHHYRPQQESPS------PQ
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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SO	InterPro; IPR000504; SEQUENCE 5476 AA; 590531 MW; 93FAA8C7860770C2 CRC64;	qq	3358
č	2 08. Const 406. The C. Tonneth	Qy	854
žăń	Vuciy match Best Local Similarity 18:18; Pred. No. 3:46-17; Matches 551: Conservative 389: Mismatches 1057: Indels 1054: Gans 139:	qq	3400
ò	98 Basical Respective Control of the Control o	Qy	914
, a	SOPADITINGE PLADAGETREGISDEROKERHDRASTEREKTATE	qq	3445
2	TATEL TO A CONTROL OF THE PROPERTY OF THE PROP	Qy	974
<u> </u>	RETRABLEDE	qq	3500
3 8	131 UDI DEGLI INCOLLI ILGUNDI SELLINUNUNGONANTANDOSTAD. ISANGIFUM.	Qy	1033
<u> </u>	TELEFOLE - KASALAKAN - DEAFFOCKREAFSSTISGÜPCGDÜÜNASFSALISKELIÜSM 	qα	3542
3 8	GEKKNHREKRERRKENLKNM	QY	1082
5 5	2700 TEATVDNSDFT.NPTSRFR.SKFRRHIRKKKKKKMINCANTKTVNSGAHDSTGSTAD 2769	qq	3602
2	KDVGDDDVBORHDCTVOTTVDBNDKRABBAUKTBOT	Qy	1130
, a	TPTSAPSTAOTSKREDEMERIFFELISDEESOPPEARTHKUIIPSSVSTHCPIVSAAL	QQ	3652
2	DI VODGOTAR AND ENTRE THE THE TABLE	Qy	1181
, e		qq	3706
3 8	KAAANGA CATINOONIN DENIN TERMINA KEDANGA KARANGA CATIOONIN TERMINA TER	QY	1240
<u> </u>	3.13 QLAREANVORIENNYKARRANGSAIKEIIENQEFFEIKÄRKEQÜEKFÜKVÖÜKGAGLSAI 3/2 2872	qq	3766
2	TANASCHETCH TONNENDER TON	Qy	1300
, d	THE CELEBOLIST STATE OF THE CONTROL OF T	qa	3814
3 8	TODO PARAGRAPHIA PARAGRAPA TAREST POR CURPOSA TAREST PARAGRAPA TAREST PARAGRAPAN TAREST PARAGRAP PARAG	Qy	1352
ž	DAGE MATCHES ALLE RADE LEGIT AND CLICAS LEGIT STOCKED I I LEGIT MALVER LEGIT LEGIT MATCHES L	qq	3863
3 8	FUINT TOTENT TOTENT TOTENT TO THE TOTENT TOTENT TOTENT TO THE TOTENT TOT	Qy	1393
3 E	THE CONTROL OF THE CO	qa	3923
3 :	NIOS V DRI INGO VASEQUEQUASS DANANANAS BERNELLINGUANES LE V TACIO A BERNELID SA DATA NO CABRACA PARA IN TACIO A SERVICIA DE SERVICA DE SE	QY	1443
i d	300 NITOTABELEBREVALFRORNIANOGENANGKLIK***********************************	q	3980
3 2	THE STATE OF THE S	0y	1492
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3 8	PUMPUNKKET VEHED DAMAN TAKARES	δλ	1536
5 6	INCIDENTAL OF THE STANK OF THE	qq	4092
3 ;	1 Y 1050ALATI I F 105 I RARO Y SEAF CHUNS F 10ASAQUANNA EST I FOF DOMINIS DESAY	QY	1568
<u> </u>	OCT STREET TO STREET ST	QQ	4142
2	DIEASNEERNDEDSEVEAVKDSFDSFNATSBCNAF	QY	1615
3 6	DIEGOS DE CONTROLOS DE CONTROLO	QQ	4199
3 2	DAVELEDTTETADSTROBEL AV DELETET DY TREFDEERALMANALEIAGEFROID - EE	Qy	1662
5		q	4259

q	3300 PEMEPEREAEPD	EMEPEREAEPDPDPEAEIESEPVVEVLDPEELNKAVQSLKHEDMMDIKADTPQSERD 3357
Oy	795 -QMDVDQQEHSAEEGSVCDPPPAT	KADSVDVEVRVPENHAS
QQ	3358 LQIDTDTEENPDE-	
οy	854 EPRDEDLVVAQQIN	EPRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDVDGEPERQRMFPMDSKPSLLNPTGS 913
qq	3400 TPRETANIDIPNVESQ-	SQPKLSNESTPQPSVITKLPFLDTPKTV-PAG- 3444
Oy Op	914 ILVSSPLKPNPLDLPQLQH           : : 1   3445 -LPPSPVKIEPPTISKLQQ	ILVSSPLKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALL 973
Qy	974 EEQRQRQEQIDLEC	P- 103
qq	3500	
Qy	1033PPPL	PPPLIPSSKTTVASEKPSFIMG-GSISQGTPGTYLTSHNQASYTQETPKP 1081
qq	3542 QAIRTQSLIMQPPT	QAIRTQSLIMQPPTISIPEQTPHFAVPQMVLSPQSHHPQQPGTYMVGIRAPSPHSPLHSP 3601
Qy	1082 SVGSIS	VGSIS-LGLPRQQESAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHE 1129
qq	3602 GRGVAQSRLVGQLS	GRGVAQSRLVGQLSPVGRPWVSQPSPQQQVQQTQQQHALITSPQSSNISP 3651
δλ	1130 GVVRGTAGAIQEGSITRGTPTSKIS	ALP
QQ	3652 -LASPTIRVLS	SSSNSPITSKVNSYQPRNQQVPQQPSPKSVAEVQTTPQLMITPLQ 3705
δλ	1181 ALVKGSISRMPIED	ALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIK-NAREGTRSPRTAH 1239
Д	3706 КМТРІДУРННРТІІ	KMTPIQVPHHPTIISKVVTVQPQQATQSQVASSPPLGSLPPHKNVHLNAHQNQQQPQVIA 3765
οy	1240 EISLKRSYESVEGN	EISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIMQG 1299
QQ	3766 КМТАНОНООНМООЕМНООМІОРО	MHQQMIQRQQHMQQQQLHGQSQQITSAPQHQMHQ 3813
δλ	1300 TPRATTESFEDGLKYPKQ	YPKQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSI 1351
qa	3814 ОНОАОООООННИОО	ОНОАОООООННИООНГИОО ГНАООНРТОКОНОАООЕ ИООТО
δλ	1352 HEIPRODILTQE	SRKTPEVVQSTRPIIEGSISQGTPIKFDN 1392
qq	3863 НО ОООО ОПОВОДЕНТ	HOVOQONOAQQQHLSQQQHQSQQQLNQQHQAQQQQLQQTQKLQQMHGPQQQQXSPQGVGH 3922
δy	1393 NSGQSAIKHN	KHNVKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVKAGE 1442
qq	3923 LGGSTSIFASQQHN	LGGSTSIFASQQHNSQLPARGVPQQQHPQQLSHSSPCKPNTLVSVNQGVQPPAILTR 3979
Qy	1443 TVRSRHTSVVSSGP	TVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVS-YQNT 1491
g	3980 VGSHSQPNQQQQLP	VGSHSQPNQQQQLPHQQSSSGHPHQKQLSSPGANLPLQTPLNVIQNTPKIIVQQHIV 4036
0y	1492 -MSRGSPMMNRTSD	MSRGSPMMNRTSDVTIPPNKSTNHERKSTLTPTQRESIPAKSPV 1535
qq	4037 AQNQVPPPQTQGNAIHYPQNQG	IHYPQNQGKDSTPPGHVEPTPAMSAQKTSESVSVIRTPTPT 4091
οy	1536 PGVDPVVSHSPFDPHHRGSTAGEV	HHRGSTAGEVYWSHLPTQ 1567
đ	4092 TGL-AVIS	:    : ANTVGSLLTEENLIKISQPRQDELIEQDSKEVDSDYWSAKEVN 4141
Qy	1568 LDPAMPFHRALDPAAAAYLFQRQL-	HRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTIL 1614
QQ	4142 IDSVIKKLDTP	LASKDAKRAVEMQAIAPAPIPNPQPGNQSMAQETALPTTSMSVNNS 4198
Qγ	1615 NDYITSQQMQVNLR	NDYITSQQMQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPPT 1661
g	4199 NDHDTEDETETROL	NDHDTEDETETRQLPPAKPPIPTVGRPPGRGGSAKRGRQPRGAKKVGGFPLNSVTAAPPG 4258
Qy	1662 ILVPHPGGTST	FMDRIT 1679
qq	4259 VDSLVVQPGDNGVQ	VDSLVVQPGDNGVQTRLRKPVTAPVTRGRKGRPPRNLLLQQQQLQQQQLDIQRKGMEMVT 4318

01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

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       1680 YIPGTQITFPPRPYNSASMSPGHPTHLAAAASAERERERERERERERERIAA---ASSDL 1736
                                                                                                            4424 QQSEVISNTDPIGGDNSESCNTRKSRRLQEKEDRSTVDDIIEDVVRNTNTPTGTGPHLPK 4483
                                                                                                                                                                                            4540 VAASHLAPPEGAGVESHVPQLDAKEVEPVSVVTPISTPAPVSVAAPVTVPVPAMVPVKPT 4599
                                                                                                                                                                                                                                                                                                                    4718 QINTTLIPSGLPNPITALGKSVQLETSAAALL-----NKPVSVLVKGNA----SQVIQ 4766
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                                                                                                                                            4484 GAQTPPRRSGRNAQAKKTDAVQIINAVGRPR----RSKDRKTIGEQTANLIEEVTASNAT
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                                                Y--LRPGSEQPGRPGSHGYVRSPSPSVRTQE----TMLQQRPSV------FQGT
                                                                                                                               1808 GLPASRYNTAADALAALVDA----AASAPQMDVSKTKESK---HEAARLEENLRSRSAA
                                                                                                                                                                                                                                                        4658 VTGVITAGMPQGKEGNLPAATAAAPANSSNEDGQAAPPPQLQHQQQQQHPQQPPQQQANL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AS--AAQPQILHVVSSKASVVPQPQ-----QQQLPPTSSTGPHLQLAKP-----
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                                                                                                                                                                        1860 V------SEQQQLEQKTLE-------
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                                                                                      1779 NGTSVITPLDPTA-------
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5533 AA.

PRELIMINARY;

RESULT 10 Q9VPL2 ID Q9VPL2

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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Ra Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Ra Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.E., Gocyge R.A., Lewis S.E., Ilp P.W., Hoskins R.A., Galle R.E., Gocyge R.A., Lewis S.E., Ilp P.W., Hoskins R.A., Galle R.E., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Ra Brandon R.C., Rogars Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxerer E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Abbayani A. An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew M., Basu A., Barman B.P., Bandari D., Botchar D., Botchan M.R., Bouck J., Bayraktaroglu L., Beasley E.M., Ballew M., Basu D.A., Butler H., Cadieu E., Center A., Chandra I., Burkis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Burkis K., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doug L.E., Cownes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Andrews M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Podson K., Doug L.E., Gornell J.H., Gu Z., Guan P., Harris M., Andreil B.C., Goriell J.H., Gu Z., Guan P., Harris M., Harris M., Hastell B.E., Kodira C.D., Kraft C., Kravitz S., Liang Y., Lin X., Lasko P., Lei X., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Martei B., McIntosh T.C., McLeod M.P., Mirphy B., Murphy, L., Mursy D., Markell B.C., Staden-Kiamos I., Simpson M., Stupski M.P., Shith T., Rusher D.A., Nixon K., Nusskern D.R., Wang X., Mang Z.-Y., Nasarman D.A., Weinsenbach J., Shue B.C., Staden-Kiamos I., Simpson M., Stupski M.P., Shith T., Ryith Genome Sequence of Drosophila melanogaster.", The Genome Sequence of Drosophila melanogaster.", The Farbor. Tephonofal.
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                                        Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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Best Local Similarity 18.1%; Pred. No. 3.5e-17;
Matches 551; Conservative 389; Mismatches 1057;
                                                                                                                                                                                                                                                                                                         MEDLINE-20196006; PubMed-10731132;
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	LPA	TPTSAPSTAQTSKRGEDKMEFIFGIISDEESQFPEQAETNKDIIPSSVSTTGFIVSAAL	264 PLYNQPSDTKVYHENIKTNQVMRKKLILFFKRRNHARKQREQKICQRYD 3 	QLMEAWEKKVDRIENNPRRKAKESKTREYYEKQFPEIRKQREQOERFORVGQRGAGLSAT		IARSEHEISEIIDGLSEQENNEKQMRQLSVIPPMMFDAEQRRVKFINMNGLMEDPMKVYK	2950AQKSSKVETKVDDDNSVDMDEAGRALEAQLMSD 2	433 DRQFMNVWTDHEKEIFKDKFIQHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYKALVR 4	3 RNYGKRRGRNOOIARPSOEEKVEEKEEDKARFEKEEEKKDEEEKDEKEDSKENTKEKD		553 KIDGTAEETEEREQATPRGRKTANSQGRRKGRITR	:  :  :	SMINEAAAAAAAAATEEPPPPLPPPPEPISTEPVETSRWTE	3119 DDDALHTPKAKPTTPSSRGNDGLTPSREKPRLISPIPKTPTIANSSTLSTQSAETPVSSG 3	631 EEMEVAKKGLVEHGRNWAAIAKWVGTKSEAQCK	3179 TVISSSALATTPTSSTAAGVSAAPGLDNSPTSASAQCKKKESFIPGFDGQLDDRISESAV 3	-NFYFNYKRHNLDNLLQQHKQKTSRKPREERDVSQCESVASTVSAQEDE	3239 QSISAEFNSTSLLDNIADEPKIPVASPPRATKPLDKLEESKSRVTISQEETESAVSALLG 3	3DIEASNEEENDEDSEVEAVKPSEDSPENATSRGNTE	9 ESFGTSSTTDYSLDGMDEMSSVNELETPTLVIAEPDEEAALAAKAIETAGEPASILEE	749 PAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAE 7   1:1	795 -QMDVDQQEHSAEEGSVCDPPPATKADSVDVEVRVPENHASKVEGDNTKERDLDRASEKV 8	3415 LQIDTDTEENPDEADSSGPSLKIDETVQSSSSPEKSISNNSP 3	854 EPRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDVDGEPERQRMFPMDSKPSLLNPTGS 9	11:	ILVSSPLKPNPLDLPQLQHRAAVIPPWVSCTPCNIPIGTPVSGYALYQRHIKAMHESALL	-LPPSPVKIEPPTISKLQQPLVQPVQTVLPAPHSTGSGISANSVINLDLSNVISSC	974 EEGRQRQEQIDLECRSSTSPCGTSKSPNREWEVLQPAPHQLITNLPEGVRLPTTRPTRP- 1	DATE POWER THE CONTRACT OF THE CONTRACT THE CAST	1033PPFLLFSSKTTVASEKPSFIMG-GSISQGFFGTVITSHNQASYIQETPKP 1 ::
	6 Pp		Oy .		Dp 56		Dp 53	Oy 4	•		δλ	Dp 3(	ολ	Db 31	δλ	Db 31		32	•		Oy 7 Db 33	0y	Db 34	Qy	Db 34		Dp 35	6 4 G		Ā

Q	3599	QAIRTQSLIMQPP11S1PEQTPHFAVPQMVLSPQSHHPQQPGTYMVGIRAPSPHSPLHSP 3658
δ	1082	SVGSIS-LGLPRQOESAKSATLPYIKOEEFSPRSQNSQPEGLLVRAQHE 1129
qq	3659	GRGVAQSRLVGQLSPVGRPMVSQPSPQQQVQQTQQQHALITSPQSSNLSP 3708
Qγ	1130	GVVRGTAGAIQEGSITRGTPTSKISVESIPSLRG-SITQGTPALPQTGIPTE 1180
qq	3709	:     :     :     :     :       :         :         :           :   :         :   :         :   :         :   :         :   :         :   :         :   :         :   :       :   :       :   :     :   :     :   :     :   :   :     :   :   :   :   :   :     :
δy	1181	ALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIK-NAREGTRSPRTAH 1239
Q	3763	KMTPIQVPHHPTIISKVVTVQPQQATQSQVASSPPLGSLPPHKNVHLNAHQNQQQPQVIA 3822
Qy	1240	EISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIMQG 1299
g	3823	KWTAHQHQQHWQQFWHQQMIQRQQHWQQQQLHGQSQQITSAPQHQMHQ 3870
ΟŸ	1300	TPRATTESFEDGLKYPKQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSI 1351
qq	3871	ОНОАОООООННИООН ПИОО ГНАООНРТОКОНОАООО РИОСТО
0y	1352	HEIPRQDILTQESRKTPEVVQSTRPIIEGSISQGTPIKFDN 1392
QQ	3920	HQVQQQNQAQQQHLSQQQHQSQQQLNQQHQAQQQQLQQTQKLQQMHGPQQQQKSPQGVGH 3979
δy	1393	NSGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVKAGE 1442
qq	3980	LGGSTSIFASQQHNSQLPARGVPQQQHPQQLSHSSPCKPNTLVSVNQGVQPPAILTR 4036
οy	1443	TVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVS-YQNT 1491
qq	4037	VGSHSQPNQQQQLPHQQSSSGHPHQKQLSSPGANLPLQTPLNVIQNTPKIIVQQHIV 4093
Qy	1492	-MSRGSPMMNRTSDVIIPPNKSINHERKSTLIPTQRESIPAKS
qq	4094	AQNQVPPPQTQGNAIHYPQNQGKDSTPPGHVEPTPAMSAQKTSESVSVIRTPTPT 4148
οy	1536	PGVDPVVSHSPFDPHHRGSTAGEVYMSHLPTQ 1567
qq	4149	TGL-AVISANTVGSLLTEENLIKISQPKQDELIEQDSKEVDSDYWSAKEVN 4198
Οy	1568	LDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTIL 1614
qq	4199	IDSVIKKLDTPLASKDAKRAVEMQAIAPAPIPNPQPGNQSMAQETALPTTSMSVNNS 4255
Οý	1615	NDYITSQOMQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPPT 1661
QQ	4256	NDHDTEDETETRQLPPAKPPIPTVGRPPGRGGSAKRGRQPRGAKKVGGFPLNSVTAAPPG 4315
δy	1662	ILVPHPGGTSTMDRIT 1679
qq	4316	VDSLVVQPGDNGVQTRLRKPVTAPVTRGRKGRPPRNLLLQQQQLQQQQLDIQRKGMEMVT 4375
οy	1680	YIPGTQITEPPRPYNSASMSPGHPTHLAAAASAERERERERERERERIAAASSDL 1736
οp	4376	SATSSTPLPTPIPTSSVLTAAEKKARNQALTQAQEQNQVASQVGTGQDI 4424
δλ	1737	HGYVR
qq	4425	YEFHEDGGEEP-KPKTISSVAPSAEDQRPRLILTINKTQPSIKNISEMEQTIQQQQQ 4480
δλ	1779	NGTSVITPLDPTAQLRIMPLPAG-GPSISQ 1807
QQ	4481	QQSEVISNTDPIGGDNSESCNTRKSRRLQEKEDRSTVDDIIEDVVRNTNTPTGTGPHLPR 4540
δγ	1808	GLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAA 1859
QQ	4541	GAQTPPRRSGRNAQAKKTDAVQIINAVGRPRRSKDRKTIGEQTANLIEEVTASNAT 4596
δy	1860	VSEQQQLEQKTLE1872
qq	4597	VAASHLAPPEGAGVESHVPQLDAKEVEPVSVVTPISTPAPVSVAAPVTVPVPAMVPVKPT 4656

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                                                                                                                                                     1932 -FIDVIITRQIASDKDARERGSQSSDSSSSLSSHRYETPSDAIEVISPASSPAPPQEKLQ 1990
                                                                                                                                                                                           QINTTLIPSGLPNPITALGKSVQLETSAAALL-----NKPVSVLVKGNA----SQVIQ 4823
                                                                                                                                                                                                                                1991 TYQPEVVKANQAENDPTRQ----YEGP----LHH-----YRPQQ------ESPSPQQQ 2029
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Newberry E.P., Latifit T., Towler D.A.;
Newberry domain of MINT, a novel msx2 binding protein, recognizes iregulates the rat osteocalcin promoter.";
Biochemistry 38:10678-10690(1999).
Binchemistry 38:10578-10690(1999).
InterPro: IPR000504; -...
InterPro: IPR001993; -...
                        | | | : :|: || | 4 657 MPQHPKKKAIAAAEIESYQAI--NSSIPSGGLPMHQTAAPATQKITGGVADAVSKALVDP
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                                                                              -------PPPKSRYEEELRTRGKTTITAAN-
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
MSX2 INTERACTING NUCLEAR TARGET PROTEIN.
MUS MUSCULUS (MOUSE).
------VEKRSVQCLYTSSAFPSGKPQPHSSVVYS
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118;
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                                                                                                                                                                                                                                                                          -MOOKEKEK-----AAETKEPEPKA 1580
                                                                                                                                                                                                                                                                                                                                                                                                              1640 PVEQPRQSDVPPGEDSRDSQDSAALAPSAPQESAATDAVPCVNAEPLTPGTTVSQVESSV 1699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVAAKDR------KTNKSKRSKTSVQAAAASVVEKPVTR------KSERIDR 1799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKLKRSSSPRGEAQKLLELK------MEA--EKITRTASKSSGGDTEHPEPSLPLSRS 1849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --------AVVPP----TTPRRGR-----PP----KTRRRAEEDGEHERK- 1919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEEPAPEHGHKPAHQASE--TELAAAIGSIISDASGEPENFSAPPSVP----PGSQTHPR 2195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2057 AAASPQESESPQKGSGSSPQLANNPADPDREAEEESAS-----ASTAPPEGTQ 2104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKLILFFKRRNHARKQREQKICQRYDQLMEAWEKKVDRIENN-------PRRKA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQENNEKQMRQLSVIPPMMFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHEKEI 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----RPSQEEKVEEKEEDKAEKTEKKEEEK---KDEEEKDEKEDSKENTKEKDKIDG 556
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                                                                                                                                         Gaps
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                                                                                                                                                                         SGYPP-----NGGAFSTEQSRYPPHSVQYTFPNTRHQQEFAVPDYRSSHLEVSQASQ 55
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                                                                                                                                                                                                                                          56 LLQQQQQQLRRRPSLLSEFHPGSDRPQERRTSYEP-FHP-GPSPVDHDSLESKRPRLEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                -----EAAKPPEPEKPVSPP
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                                                                                                                                                                                                                                                                                                           114 VSDSHFQRVSAAVLPLVHPLPEGLRASADAKKDPAFGGKHEAPSSPISGQ------
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                                                                                                    3.8%; Score 484.5; DB 11; Length 3576; 19.9%; Pred. No. 2e-17;
                                                                                                                                         Indels
            Matches 492; Conservative 298; Mismatches 875;
Pfam; PF00076; rrm; 3.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1
                                                                                                                       Similarity
                   PROSITE;
SMART; SM
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ą	3067	:    :  	3079
λ	1784	AALVDAAASAPOMDVSKTKESK	1843
ą	3043		3066
۲	1724	RERERIAAASSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSV 1/	1783
q	3001	SQGEVRMSTPTLPSITYSIRPETLHSPRAPLQPQQIEARAPQ3	3042
λχ	1668	NSASMSPGHPTHLAAAASAEREREREREKE	1723
ď	2952	.	3000
λ	1608		1667
ą	2913	STPADRIIAHLATPKPDTHS29	2951
λ	1554	YPSQYQLYAME	1607
q	2873	LKIETKVLQPANLGPTLTPHHPPALPSKLPAEVNHVPSGP 2	2912
λ	1494	VDPVVSHSPFDPHHRG	1553
ą	2829	PYTQGGTVKVLTQGINTPPVLVHNQLVLTPSIVTTNKKLADPVT 20	2872
λ	1437	NTMS	1493
ą	2773		2828
λ	1379	EGSISQCTPIKFDNNSGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVERGKYE 1.	1436
- q	2721		2772
ά	1323	PPIRAFEGAITKGKPYDGITTIKEMGRSIHEIPRQDILTQESRKTPEV-VQSTRPII 1	1378
ž g	1266	SAPLEGLICRALPRGSPHSDLKERTVLSGSIMOGTPRATTESFEDGLKYFKQIKRES I:	1322
q	2608	LKGLVSTPAGPVNLLKGPVNVLTGPVNVLTTPVSATVGTVNAAPGPVTAACGVTATTG 2	2665
λ̈́ζ	1206	SKGHVIYEGKSCHILSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQCMSMRESPV I	1265
ą	2555		2607
ζ	1149	PTSKISVESIPSLRGSITQGTPALPQTGIPTEALVKGSISRMPIED-SSPEKGREEAA 1.	1205
q	2507	:	2554
λζ	1091	IKQEEFSPRSQNSQPEGLLVRAQHEGVVRGTAGALQEGSITRGT	1148
q	2453		2506
λ	1044	VASEKPSFIMGGSISOGTPGTVLTSHNOASYTOETPKPSVGSISLGL 1	1090
ą	2400		2452
ά	1002		1043
ą	2351		2399
à	944	2	1001
. a	2301	AEEATAATPEAPQEEKPSEKPSSPABCTFDPSKTPPAESLSQENSAAEK 2	2350
2	2248		2300
oy.	830	ENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCS 88	84
	830		84

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SEQUENCE FROM N.A.
Kuang B., Wu S., Shin Y.-A., Luo L., Kolodziej P.;
Kuang B., Wu S., Shin Y.-A., Luo L., Kolodziej P.;
Split ends encodes large nuclear proteins that regulate neuronal cell fate and axon extension in the Drosophila embryo.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR221715; AAF3461.1;
FlyBase; FBgn0016977; spen.
InterPro; IPR000504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1222 PAQQITHT-OFPVASSISLASRIKTSAQVPPEGEPLQSTQSAQPAPSTQATQPIPPAPPC 3280
1844 HEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEA 1903
                                                                       ---HPHVTAV---- 3113
                                                                                                                                              1904 GKDKGPPPKSRYEEELRTRGKTTITAANFIDVIITRQIASDKDARERGSQSSDSSSSLSS 1963
                                                                                                                                                                                                                                                                                                1964 HRYETPSDA-IEVISPASSPAPP---QEKLQTYQPEVVKANQAENDPTRQYEGPLHHYRP 2019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2073 POOPPTSTFQNSPSALVSTPVRTKTSNRYSPESQ-AQSVHHQRPG-----SRVSPENLV 2125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2170 ORGAEPAEORNDAR-SPGSISYLPSFFTKLENTSPMVKSKKOEIFRKLNSSGGGDSDMAA 2228
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
SPLIT ENDS LONG ISOFORM.
SPEN OR CG18497.
Drosophila melanogaster (Fruit fly).
Brosophila melanogaster (Fruit fly).
Brosophila metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Meeptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  2020 QQESPSPQQQLPPSSQAEGMGQVPRTHRLITLADHICQII-----TQDFARNQVSS-QT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 1085;
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                                                                                                                                                                                                                     3114 -----SEQPRATEGVVKVPPANKAPQQLVKEAVKTSDAK------
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                                                                   -----VQSEVLVMQSEYRLHPYTV---PRDVRIMV----
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                                                                                                                                                                                                                                                                                                                                                                   ---AVPAPAPVPVPVPTPAPPPHGEARILT------
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Š	1062 SVGSIS-LGLFKQGESAKSATLFYIKQEEFSFKSQNSQFEGLLVKAQHE 1129
QQ	3653 GRGVAQSRLVGQLSPVGRPMVSQPSPQQQVQQTQQQHALITSPQSSNISP 3702
Oy Dp	1130 GVVRGTAGAIQEGSITRGTPTSKISVESIPSLRG-SITQGTPALPQTGIPTE 1180 :
ογ	1181 ALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIK-NAREGTRSPRTAH 1239
đ	3757 KMTPIQVPHHPTIISKVVTVQPQQATQSQVASSPPLGSLPPHKNVHLNAHQNQQQPQVIA 3816
ço f	1240 EISLKRSYESVEGNIKQGMSMRESPVSAPLEGELICRALPRGSPHSDLKERTVLSGSIMQG 1299 3817 KWRADDAGDAGADAGADAGADAGADAGADAGADAGADAGADA
3 8	MATANAGAQUAQQEMAQQATQAQQHMQQQQQLHQQQQQIISAFQAQQQQIISAFQAQQAQ
B t	1300 TPRATTESFEDGLKYPROIRRESPPTRAFEGATTRCRPYDGITTIEMGRSI 1351 ::   ::   ::   ::   ::   ::   ::   ::
δ	1352 HEIPRODILTQESRKTPEVVQSTRPIIEGSISQGTPIKFDN 1392
qq	3914 HQVQQQNQAQQQHLSQQQHQSQQQLNQQHQAQQQQLQQLQQLQQKLQQMHGPQQQQKSPQGVGH 3973
ογ	1393 NSGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVKAGE 1442
qq	3974 LGGSTSIFASQOHNSQLPARGVPQQQHPQQLSHSSPCKPNTLVSVNQGVQPPAILTR 4030
δy	1443 TVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVS-YQNT 1491
qq	4031 VGSHSQPNQQQQLPHQQSSSGHPHQKQLSSPGANLPLQTPLNVIQNTPKIIVQQHIV 4087
QY	1492 -MSRGSPMMNRTSDVTIPPNKSTNHERKSTLTPTQRESIPAKS
qq	4088 AQNQVPPPQTQGNAIHYPQNQGKDSTPPGHVEPTPAMSAQKTSESVSVIRTPTPT 4142
δλ	1536 PGVDPVVSHSPFDPHHRGSTAGEVYMSHLPTQ 1567
QO.	4143 TGL-AVISANTVGSLLTEENLIKISQPKQDELIEQDSKEVDSDYWSAKEVN 4192
δy	1568 LDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTIL 1614
QQ	4193 IDSVIKKLDTPLASKDAKRAVEMQALAPAPIPNPQPGNQSMAQETALPTTSMSVNNS 4249
δy	1615 NDYITSQQMQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPPT 1661
qq	4250 NDHDTEDETETRQLPPAKPPIPTVGRPPGRGGSAKRGRQPRGAKKVGGFPLNSVTAAPPG 4309
δy	1662 ILVPHPGGTST
QQ	4310 VDSLVVQPGDNGVQTRLRKPVTAPVTRGRKGRPPRNLLLQQQQLQQQQLDIQRKGMEMVT 4369
ογ	1680 YIPGTQITFPPRPYNSASMSPGHPTHLAAAASAERERERERERERERIAAASSDL 1736
qq	4370SAISSTPLPTPIPISSVLTAAEKKARNQALTQAQEQNQVASQVGTGQDI 4418
δý	HGYVRSPSP
QΩ	4419 YEFHEDGGEEP-KPKTISSVAPSAEDQRPRLILTINKTQPSIKNISEMEQTIQQQQQ 4474
οy	1779 NGTSVITPLDPTA
qq	4475 QQSEVISNTDPIGGDNSESCNTRKSRRLQEKEDRSTVDDIIEDVVRNTNTPTGTGPHLPR 4534
Οy	1808 GLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAA 1859
q	4535 GAQTPPRRSGRNAQAKKIDAVQIINAVGRPRRSKDRKTIGEQTANLIEEVTASNAT 4590
ΟŊ	1860 VSEQQQLEQKTLE
q	4591 VAASHTADDRIGAGURSHUDOTIAK RURDVSUUTET STEDADVSUAADUTUDUDAMUDUKET 4650

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4870
                                                                                              1932 -FIDVIITRQIASDKDARERGSQSSDSSSSLSSHRYETPSDAIEVISPASSPAPPQEKLQ 1990
                                                                                                                                                                                                                              1991 TYQPEVVKANQAENDPTRQ----YEGP----LHH-----YRPQQ------ESPSPQQQ 2029
                                                                                                                                                                                                                                                                                                                                                                                                               --NYSYAP---TVLTPTLPAVQQQQQHLYKQNNQQKGAQIQMPPHGIIMPTHPGMLLQQ 5060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5202 MLYQHHLMRGGDYDDKMGSS------PPLELRRPGSGPPRTI-------AVPHS--- 5242
                                  4651 MPOHPKKKAIAAAEIESYQAI--NSSIPSGGLPMHQTAAPATQKITGGVADAVSKALVDP 4708
                                                                                                                                                                                                                                                                                                                                                                                     2076 -PPTSTFQNSPSALVSTPVRTKTSNRYSPESQAQSVHHQRPGSRVS-----PENLVDKSR 2129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2185 PGSISYLPSFFTKLENTSPMVKSKKQE-IFRKLNSSGGGDSDM-----AAAQPGTEI-F 2236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------PKLISKSNSRKSKS 2337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GWAWEDRPSSTGSTQFPYNPLTMRMLSSTPPTFPIACAPSAVNQAAPHQQNR 2418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                                                                                                                                                                        4769 QINTTLIPSGLPNPITALGKSVQLETSAAALL-----NKPVSVLVKGNA----SQVIQ
                                                                                                                                                                                                                                                                   4818 QQQPQIVA-----PAKQPIILQQNPLPTVLHHAQHTTVRPPQPLKAHVLNREKNIQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4964 AS--AAQPQILHVVSSKASVVPQPQ-----QQQLPPTSSTGPHLQLAKP-----
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                                                                                                                                                                                                                                                                                                           2030 LPPSSQAEGMGQVPRTHRLITLADHICQIITQDFARNQ-----VSSQTPQQ-----
                                                                                                                                                                                                                                                                                                                                               4871 LTPTKQAVAQ---PPQH-----APHSGHMLLTDTAGNQQLVQPQIIARHLQQQQHLQVNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2130 GSRPGKSPERSHVSSEPYEPISPPQVPVVHEKQDSLLLLSQRG-----AEPAEQRNDARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2237 NLPAVTISGSVSSRGHSFADPASNLGLEDIIRKALMGSFDDKVEDHGVVMSQPMGVVPGT
                                                                            ------PPPKSRYEEELRTRGKTTITAAN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2338 PIPGQGYLGTERPSSVSSVHSEGDY------HRQ----TP-----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5145 VLP-PGISGV--PPFDASLHDLGAYVSGRRTQSPPPAHQQASPITPNDSTYRGVTASRDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=BERKELEY;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
  --VEKRSVQCLYTSSAFPSGKPQPHSSVVYS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2297 ANTSVVTSGETRREEGDPSPHSGGVCK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5243 ------DSPQDRTAADS 5254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, SPEN PROTEIN.
                                                                            -----EAGKDKG-----
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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
R. Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazel R.G., Nelson C.R., Miklos G.L.G.,
Abril J.E., Agbayani A., An H.-J., Andrews-Ffankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Barnedale J., Bayraktaroglu L., Basaley E.M.,
Ballew R.M., Basu A., Barnedale J., Bayraktaroglu L., Basaley E.M.,
Ballew R.M., Basu A., Bannedale J., Bayraktaroglu L., Basaley E.M.,
Ballew R.M., Basu A., Bannedale J., Brokstein P., Brottier P.,
Bartis R.C., Busan D.A., Buller H., Caddeu E., Center A., Chandra I.,
R. Borkova D., Botchan M.R., Baller H., Caddeu E., Center A., Chandra I.,
R. Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
Borkova D., Botchan A., Bouck J., Brokstein P., Brottier P.,
R. Choff S., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dun P.,
Bodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dun P.,
R. Glodek A., Gorrell J.H., Gu Z., Gunn P., Harris M.,
R. Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
R. Harris N.L., Harvey D., Helman T.J., Wei M.-H., Ibegwam C.,
Allall M., Kalush F., Karpen G.H., Ke Z., Kennison J.A.,
R. Harris N.L., Marvey D., Helman T.J., Wei M.-H., Ibegwam C.,
R. Allall M., Kalush F., Karpen G.H., Ke Z., Kennison J.A.,
R. Marko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
R. Mattei B., McIntogh T.C., Morris J., Moshrefi A.,
Relson D.R., Nalten G.S., Pan S., Pollard J., Puri V., Reese M.G.,
R. Alber B.C., Siden-Kiamos I. Singbson M., Strong R., Shen H.,
Spire E., Spradling A.C., Staplecon M., Strong R., Shen H.,
R. Mang Z.-Y., Wassarman D.A., Reinstock G.M., Weissenbach J.,
R. Hilliams S.M., Wooden T., Worter J.C.;
R. Hilliams S.M., Wooden T., Worter J.C.;
R. Hilliams S.M., Wooden T., Wolley C., Scheeler F., Wang X.,
R. Hilliams S.M., Wooden T., Wolley C., Scheeler F., Wang X.,
R. Hilliams S.M., Wooden G. Drosophila Melanguser P., Shang C., Shang C.,
Scheeler S., Stand S., Shang S., Shang S., Shang S., Shang S., Shang 141; 2589 QSQPAPDLTIKQEH-PIAPAQEIKREQLSDEEQKFKSR-----HDSNSSIEERKLKTE 2640 2757 TEATVPNSPTTNDTSSEKLSKEERHRLKKSKKSKSMDNSCNTKIYNSSGAHPSTSPSLPA 2816 2817 TPTSAPSTAQTSKRGEDKMEFIFGIISDEEESQFPEQAETNKDIIPSSVSTTGPIVSAAL 2876 2877 QTYKQEPSTPNSKNEEAHIQLTVHEPEQQQQLERSRLSGGSSSSSHADRERH----- 2928 ----TSYEPFHPGP----SPVDHDSLESKRPRLEQVSDSHFQRVSAAVLPLV- 130 131 HPLPEGL---RASADAKK--DPAFGGKHEAPSSPISGQPCGDDQNASPSKLSKEELIQSM 185 --AAKPPEPE 220 313 OLMEAWEKKVDRIENNPRRKAKESKTREYYEKQFPEIRKQREQQERFQRVGQRGAGLSAT 372 36 QEFAVPD--YRSSHLEVSQASQLLQQQ---QQQQLRRRPSLLSEFHPGSDRPQERR---- 86 2641 REIKTELGDFYNSSEYTYTGKLKEYSPETRKKHKKSKRRLKSSSTAD---TSAAQTPLVM | : : | : | | | | :::|
TPLTPSIFDVHSSSECKTKFENFDDLKTECSSIPLE-ISAGERRKHKERKEKLRNM KPVSPPPV------GPKHRSIVQIIYDENRKKAEEAHKIFEGL------GPKVE--L 264 PLYNQPSDTK------VYHENIKTNQVMRKKLILFFKRRNHARKQREQKICQRYD Indels 1085; Length 5560; 599996 MW; 58F19621AF40D2A8 CRC64; Best Local Similarity 18.1%; Pred. No. 3./e-1/; Matches 556; Conservative 389; Mismatches 1050; 3.8%; Score 484.5; DB 5; ---DRVDREIAKVEQQILKLKKKQQQLEEE----Pred. No. 3.7e-Pfam; PF00076; rrm; 3. PR000504; 5560 AA; Similarity InterPro; SEQUENCE Query Match 221 87 186 ğ g 셤 q Q Qγ Qγ ŏ g δŻ g

2929	9KSOREÒONOI	2949
373	TARGEHET CETT DCT GEOFUND KOMBO! CVT DBMWD	
2950		2982
433	DRQFMNVWTDHEK	492
2983		3015
493	3 RNYGKRRGRNQOIARPSQEEKVEEKEEDKAEKTEKKEEEKKDEEEKDEKEDSKENTKEKD	552
3010		3064
3065	S NVASTSSAPPTP-GKLTVNVQAASKHADLQLDAKHISSPPVCKPSPSLFCLIGDD	387 3118
588		930
3119	9 DDDALHTPKAKPTTPSSRGNDGLTPSREKPRLISPIPKTPTIANSSTLSTQSAETPVSSG	3178
631		663
3179	9 TVISSSALATTPTSSTAAGVSAAPGLDNSPTSASAQCKKKESFIPGFDGQLDDRISESAV	3238
664	4 -NFYFNYKRRHNIDNILQQHKQKTSRKPREERDVSQCESVASTVSAQEDE	712
3239		3298
713	3DIBASNEEENPEDSEVEAVKPSEDSPENATSRGNTE	748
223		3356
3357	9 PAVELEPITETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAE    :	794 3414
795	-QMDVDQQEHSAEGGSVCDPPPATKADSVDVEVRVPENHASKVEGDNTKERDLDRASEKV	853 3456
854	EPRDEDLVVAQQINAQRPEPQS	913
3457		3501
914	4 ILVSSPLKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALL	973 3556
974	PRODUCTION TO THE PRODUCTION OF THE PRODUCT THAT DESIGN DEPENDENT	2001
3557		3598
1033	PPPLIPSSKTTVASEKPSFIMG-GSISQGTPGTYLTSHNQASYTQETPKP	1081
3599	QAIRTQSLIMQPPTISIPEQTPHFAVPQMVLSPQSHHPQQPGTYMVGIRAPSPLHSP	3658
1082	SVGSIS-LGLPRQQESAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHE	1129
3659	GRGVAQSRLVGQLSPVGRPMVSQPSPQQQVQQTQQQHALITSPQSSNISP	3708
1130	GVVRGTAGAIQEGSITRGTPTSKISVESIPSLRG-SITQGTPALPQTGIPTE	1180
3709	- LASPTTRVLSSSNSPTTSKVNSYQPRNQQVPQQPSPKSVAEVQTTPQLMITPLQ	3762
1181	ALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIK-NAREGTRSPRTAH	1239
3/03	AMTELUVEHHETLISKVYTVUPUUATUSUVASSEPLGSLEPHKNYHLNAHUNQUOPUVIA	3822
1240 3823	EISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIMQG ::: : :     :	1299 3870

1393 NSGOSAI----KHNVKSLITG-----PSKLSRGMPPLEIVPENIKVVERGKYEDVKAGE 1442 |: |:| TGL-AVIS------ANTVGSLLTEENLIKISQPKQDELIEQDSKEVDSDYWSAKEVN 4198 4316 VDSLVVQPGDNGVQTRLRKPVTAPVTRGRKGRPPRNLLLQQQQLQQQQLQQQQLDIQRKGMEMVT 4375 1680 YIPGTQITFPPRPYNSASMSPGHPTHLAAAASAERERERERERERERERIAA---ASSDL 1736 | | | | | | | | 4597 VAASHLAPPEGAGVESHVPQLDAKEVEPVSVVTPISTPAPVSVAAPVTVPVPAMVPVKPT 4656 3871 QHQAQQQQQHHNQQHLNQQLHAQQHPTQKQHQAQQQFNQQIQ------QHQSQQQ 3919 ---SRKTPEVVQSTRPILEGSISQGTPIKFDN 1392 4037 VGSHSQPNQQQQLPHQQSSSGHPHQKQLSSPGA---NLPLQTPLNVIQNTPKIIVQQHIV 4093 PGVDPVVSHSPFDPHHRGSTAGEV------YWSHLPTQ 1567 I--LVPHPG--GTST------MDRIT 1679 1737 Y--LRPGSEQPGRPGSHGYVRSPSPSVRTQE----TMLQQRPSV------FQGT 1778 4481 QOSEVISNTDPIGGDNSESCNTRKSRRLQEKEDRSTVDDIIEDVVRNTNTPTGTGPHLPK 4540 GLPASRYNTAADALAALVDA----AASAPQMDVSKTKESK---HEAARLEENLRSRSAA 1859 | | | | : :|-||| 4657 MPQHPKKKAIAAAEIESYQAI--NSSIPSGGLPMHQTAAPATQKITGGVADAVSKALVDP 4714 4775 QINTTLIPSGLPNPITALGKSVQLETSAAALL-----NKPVSVLVKGNA----SQVIQ 4823 1991 TYOPEVVKANQAENDPTRO----YEGP----LHH-----YRPQQ------ESPSPQQQ 2029 ----IKRESPPIRAFEGAITKGKPYDGITTIKEMGRSI 1351 1443 TVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVS-YQNT----- 1491 LDPAMPFHRALDPAAAAYLFQRQL-----SPTPGYPSQYQLYAMENTRQTI--L 1614 NDYITSQQMQVNLRPDVARGLSPREQPLGLPYPATRG-------IIDLTNMPPT 1661 -------QLRIMPLPAG-GPSISQ 1807 4715 VTGVITAGMPQGKEGNLPAATAAAPANSSNEDGQAAPPPQLQHQQQQQHPQQPPQQANL 4774 -FIDVIITRQIASDKDARERGSQSSDSSSLSSHRYETPSDAIEVISPASSPAPPQEKLQ 1990 -MSRGSPMMNRTSDVTIPPNKSTNHERKSTLTPTQRESIPAKS--------PV 1860 V-----SEQQQLEQKTLE---------VEKRSVQCLYTSSAFPSGKPQPHSSVVYS-NGTSVITPLDPTA------1300 TPRATTESFEDGLKYPKQ-HEIPRODILTQE----3920 1536 4149 1568 4199 1615 4256 1662 4425 1779 1808 1902 1352 1492 1873 g δ qq δ Q ò В g S q g Qy ρp qq g δλ Q δy qq δ oy Dp οy οy οy ò 셤 ò 셤 ŏ g οy q δ

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3015 2698 TPLTPSIFDVHSSSECKTKFDNFDDLKTECSSIPLE-ISAGERRKHKERKEKKREKLRNM 2756 2817 TPTSAPSTAOTSKRGEDKMEFIFGIISDEEESOFPEQAETNKDIIPSSVSTTGPIVSAAL 2876 3065 NVASTSS----APPTP-GKLTVNVQAASKHADLQLDAKHISSPPVCKPSPSLPCLIGDD 3118 DDDALHTPKAKPTTPSSRGNDGLTPSREKPRLISPIPKTPTIANSSTLSTQSAETPVSSG 3178 : : | : | 3238 2641 REIKTELGDFYNSSEYTYTGKLKEYSPETRKKHKKSKRRLKSSTAD---TSAAQTPLVM 2697 P--EMEPEREAEPDPDPEAEIESEPVVEVLDPEELNKAVQSLKHEDMMDIKADTPQSERD 3414 264 PLYNQPSDTK------VYHENIKTNQVMRKKLILFFKRRNHARKQREQKICQRYD 312 HPLPEGL---RASADAKK--DPAFGGKHEAPSSPISGQPCGDDQNASPSKLSKEELIQSM 185 313 QLMEAWEKKVDRIENNPRRKAKESKTREYYEKQFPEIRKQREQQERFQRVGQRGAGLSAT 372 373 IARSEHEISEIIDGLSEQENNEKQMRQLSVIPPMMFDAEQRRVKFINMNGLMEDPMKVYK 432 433 DRQFMNVWTDHEKEIFKDKFIQHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYKALVR 492 493 RNYGKRRGRNQQIARPSQEEKVEEKEEDKAEKTEKKEEEKKDEEEKDEKEDSKENTKEKD 552 914 ILVSSPLKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALL 973 ---TSYEPFHPGP----SPVDHDSLESKRPRLEQVSDSHFQRVSAAVLPLV-------DRVDREIAKVEQQILKLKKKQQQLEEE------AAKPPEPE KPVSPPPV------GKHRSIVQIIYDENRKKAEEAHKIFEGL------GPKVE--L ------SDNED-----SDNED----------SMTNEAAAAAAAAATEEPP--PPLPPPP-----EPISTEPVETSRWTE ------DIEASNEEE-----DEDSEVEAVKPSEDSPENATSRGNTE 3299 ESFGTSSTTDYSLDGMDEMSSVNELETPTLVIAEPDEEAALAAKAIETAGEPASIL--EE -QMDVDQQEHSAEEGSVCDPPPATKADSVDVEVRVPENHASKVEGDNTKERDLDRASEKV **EPRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDVDGEPERQRMFPMDSKPSLLNPTGS** 631 EEMEVAKKGLVEHGRNWAAIAKMVG-----TKSEAQCK-------3415 LQIDTDTEENPDE-----ADSSGPSLKIDET----VQSSSSPEKSISNNSP--PAVELEPITETAPSTSPSLAVPSTKPAE-----DESVETQVND---SISAETAE----NFYFNYKRRHNLDNLLQQHKQKTSRKPREERDVSQCESVAS--TVSAQEDE----------RREKREKKRRE-----KSQREQQNQI-----553 KIDGTAEETEEREQATPRGRKTANSQGRRKGRITR-----δy

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36 QEFAVPD--YRSSHLEVSQASQLLQQQ----QQQQLRRRPSLLSEFHPGSDRPQERR----

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3502 -LPPSPVKIEPPTISKLQQPLVQPVQTVLPAPHSTGSGISANSVINLDLSNVISSC 3556	974 EEQRQRQEQIDLECRSSTSPCGTSKSPNREWEVLQPAPHQLITNLPEGVRLPTRPTRP- 1032	3557SNTSAASATASASASISFGSPTASQNAMPQASTPKQGPITPQ 3598	PPPLIPSSKTTVASEKPSFIMG-GSISOGTPGTYLTSHNQASYTQETPKP	QALKTQSLIMQPPTISIPEQTPHFAVPQMVLSPQSHHPQQPGTYMVGIRAPSPHSPLHSP	1082 SVGSIS-LGLPRQQESAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHE 1129 1659 GRGVAQSRLVGQLSPVGRPMVSQPSPQQQVQQTQQOHALITSPQSSNISP 3708	1130 GVVRGTAGALQEGSITRGTPTSKISVESIPSLRG-SITGGTPALPQTGIPTE 1180	3709 -LASPITRVLSSSNSPITSKYNSYQPRNQQVPQQPSPKSVAEVQTTPQLMTIPLQ 3762	1181 ALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIK-NARECTRSPRTAH 1239 3763 KMTPIOVPHHPTIISKVVTVOPOOATOSOVASSPPIGSLPPHKNVHINAHONOOOPOVTA 3822	EISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIMQG	3823 КИТАНОНООНМООРМНООМІОРО	TPRATTESFEDGLKYPKQIKRESPPIRAFEGAITKGKPYDGITIKEMGRSI	3871 QHQAQQQQQHHNQQHLNQQLHAQQHPTQKQHQAQQQFNQQIQQHQSQQQ 3919	1352 HEIPRODILTQESRKTPEVVQSTRPIIEGSISQGTPIKFDN 1392   :: :  :   :   : :  : 320 HOVOOONDAOOOHISOOODIAOOHOAOOOTAKIOONHGPOOOOKSPACH 3979	**************************************	1339 INSQUALT RANKYSLITGE FEATURE FELT FERLY VERGATED VALUE 1442  3980 LGGSTSIFASQQHNSQLPARGVPQQQHPQQLSHSSPCKPNTLVSVNQCVQPPAILTR 4036	1443 TVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVS-YQNT 1491	4037 VGSHSQPNQQQQLPHQQSSSGHPHQKQLSSPGANLPLPTPLNVIQNTPKIIVQQHIV 4093	1492 -MSRGSPMANRTSDVTIPPNKSTNHERKSTLTPTQRESIPAKS	1536 PGVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQ 1567	:  :   :   :  ANTVGSLLTEENLIKISÕPKÕDELIEQDSKEVDSDYWSAKEVN 4198	1568 LDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTIL 1614	NDYITSQQMQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPPT 16		1662 ILVPHPGGTSTPP	4316 VDSLVVQPGDNGVQTRLRKPVTAPVTRGRKGRPPRNLLLQQQQLQQQLDIQRKGMEMVT 4375	1680 YIPGTQITFPPPRPXNSASMSPGHPTHLAAAASAERERERERERERERIAAASSDL 1736	4376SATSSTPLPTPIPTSSVLTAAEKKARNQALTQAQEQNQVASQVGTGQDI 4424	1737 YLRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGT 1778 	1779 NGTSVITPLDPTA
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4597 VAASHLAPPEGAGVESHVPQLDAKEVEPVSVVTPISTPAPVSVAAPVTVPVPAMVPVKPT 4656
                                                                                                                                                                               | | | | : :|||| | : 4057 MPQHPKKKAIAAAEIESYQAI--NSSIPSGGLPMHQTAAPATQKITGGVADAVSKALVDP 4714
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1808 GLPASRYNTAADALAALVDA----AASAPQMDVSKTKESK---HEAARLEENLRSRSAA 1859
                                                                                                                                                                                                                                                                                                                                                 4775 QINTTLIPSGLPNPITALGKSVQLETSAAALL-----NKPVSVLVKGNA----SQVIQ 4823
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
WUGSC:H_DJ0784G16.1 PROTEIN (FRAGMENT).
                                                                           1860 V------SEQQQLEQKTLE------
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MEDLINE=99063792; PubMed=9847074;
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                                                         Kraemer J., Wollam C., Wohldmann P., McGrane B.;
"The sequence of Homo sapiens PAC clone DJ0784G16.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases EMBL; AC004886; AAD21789.1; -. InterPro; IPR002965; -.
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            "Toward a complete human genome sequence."; Genome Res. 8:1097-1108(1998).
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Waterston R.H.;
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122;
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--PQVPVVHEKQDSLLLLSQRGAEPAEQRNDARSPGSISYLPSFFTKLENTSPMV 2205
                                                                                                                                                                                                         2641 TWARAKILQDIDREL-----DLVERESAKLRKKQAELDEEEKEIDAKLRYLEMGINRRK 2694
                                                                                                                                                                                                                                                   EGDPSPHSGGVCKPKLISKSNSRKSKSPIPG-----QGYLGTERPSSVSSVHSEGD 2361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GR---RGEGDAPFSEPGTTSTQRPSSPETATKQPSSPYEDKDKKEKSATRP--SPSPE 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 GLRASADAKKDPA-----FGGKHEAPSSPISGQPCGDDQNASPSK----LSKEEL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 IQSMDRVDREIAKVEQQILKLKKKQQQLEEEAAKPPEPEKPVSPPPVEQKHRSIVQIIYD 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PQSS---SSESSPPSPQPTKVSR-----HASSSPESPKPA---PAPGSHREISSSPTS 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENRK----KAEEAHKIFEGLGPKVELPLYNQPSDTKVYHENIKTNQVMRKKLILFFKRRN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 RHQQEFAVPDYRSSHLEVSQASQLLQQQQQQLR-----RRPSLLSEFHPGS 79
                                                                                                                      ------TSSGAOKKVKRTLPNPPPEEISTGTO----STFSTMGTVSRRRICRTN
                                                                                                                                                                  PASNLG-LEDIIRKALMGSFDDKVEDHGVVMSQPMGVVPG----TANTSVVTSGETRRE
                                                                                                                                                                                                                                                                                                                                    2362 YHRQTPGWAWEDRPSSTGSTQF------PYNPLTMRMLSSTPPTPIACAP
                                   2540 KVLHPDMAKVPPASPKTAKMMQRSMSDPKPLSPTADESSRAPFQYTEGYTTKGSQTM---
                                                                              KSKKQEIFRKLNSSGGGDSDMAAAQP-----GTEIFNLPAVTTSGSVSSRGHSFAD
                                                                                                                                                                                                                                                                                          -----LLKEREKRERAYLQGVAEDRDYMSDSEVSSTRPTRIESQHG---
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Catarrhini; Hominidae; Homo.
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Ohtaki S., Umeki K., Sawada Y.;
"Homo sapiens mRNA for RNA binding protein, complete cds.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB016092; BAA83718.1; -.
InterPro: IFR002965; -.
SEQUENCE 2752 AA; 299671 MW; 109C64F181097123 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 19.2%; Pred. No. 6e-17;
Matches 554; Conservative 316; Mismatches 1121; Indels
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                       2406 SAVNQAAPHQONRIWEREPAPLLSAQYET 2434
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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(TrEMBLrel. 13, I
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01-MAY-2000 (TrEMBLre
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RNA BINDING PROTEIN.
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090035
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ΟP	1481 DSSPEPKALPQTPRPRSRSPSSPELNNKCLTPQRERSGSESSVDQKTVARTPLG 1534
ογ	1132 VRGTAGAIQEGSI-TRGTPTSKISVESIPSLRGSITQGTPALPQTGIPTEALVKGSIS-R 1189
QQ	1535 QRSRSGSSQELDVKPSASPQERSESDSSPDSKAKTRTPLRQRSRSGSSPEVDSKSRLSPR 1594
Qy	1190 MPIEDSSPE-KGREEAASKGHVIYEGKSGHILSYDNIKNAREGTRSPRTAHE 1240
q	1595 RSRSGSSPEVKDKPRAAPRAQSGSDSSPEPKAPAPRALPR 1634
οy	1241 ISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIMQGT 1300
g	1635 RSRSGSSSKGRGPSPEGSSSTESSPEHPPKSRTARRGSRSSPEPKTKSRTPPRRRSSRSS 1694
ογ	1301 PITKGKPYDELKYPKQIKRESPPIRAFEGAITKGKPYDGI 1341
QQ	1695 PELTRKARLSRRSRSASSSPETRSRTPPR-HRRSPSVSSPEPAEKSRSSRRRRSASSPRT 1753
٥y	1342 TIIKEMGRSIHEIPRQDILTQESRKTPEVVQSTRPIIEGSISQGTPIKFDNNSGQSAIKH 1401
qa	1754 KTTSRRGRSPSPKPR-GLQRSRSRSRRRRTRTTRRDRSGSSQSTSRRRQRSRSRVTR 1812
δλ	Α
q	1813 RRRGGSGYHSRSPARQESSRTSSRRRRGRSRTPPTSRKRSRSRTSPAWKRSR 1865
Οÿ	1454SGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSPMNNRTSD 1504
අු	1866 SRASPATHRRSRSRTPLISRRRSRSRTSP-VSRRRSRSRTSVTRRRSRSRASPVSRRRSR 1924
Qy	VPGVDPVVSHS
QQ	1925 SRTPPVTRRRSRSRTPTTRRRSRSRTPPVTRRRSRSRTP 1963
ďδ	1560 YWSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILN 1615
qq	1964PVTRRSRSRTSPITRRRSRSRTSPVTRRSRSRTSPVTRRSRSRT 2010
Qy	1616 DYITSQQMQVNLRPDVARGLSPREQPLGLPYPAT-RGIIDLTN 1657
qq	2011 SPVTRRRSRSRIPPAIRRRSRSRIPLLPRKRSRSRSPLAIRRRSRSRTPRIARGKRSLTR 2070
δy	1658 MPPTILVPHPGGTS 1PPMDRITYIPGTQITFPPRPYNSASM 1698
qq	2071 SPPAIRRRSASGSSSDRSRSATPPATRNHSGSRTPPVALNSSRMSCFSRPSMSPTP 2126
ΟŊ	1699SPGHPTHLAAAASAERERERERERERERERERERERERERERERERE
qq	2127 LDRCRSPGMLEPLGSSRTPMSVLQQAGGSMMDGPGPRIPDHQRTSVPENHAQSRIALALT 2186
Qy	RPG
q	2187 AISLGTARPPPSMSAGLAARMSQVPAPV-PLMSLR 2221
δy	1795 IMPLPAGGPSISQGLPASRYNTAADALAALVDAAASAPQMDVS-KTKESKHEAARLEENL 1853
qa	2222 TAPAANLASRIPAASAAAMNLASARTPAIPTAVNLADSRTPAAAAAMNL 2270
Qy	1854 RSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKS 1913
q	2271 ASPRTAVAPSAVNLADPRTPTAPAVNLAGARTPAALAALSLIGSGT-PPTAA 2321
Qy	1914 RYEEELRTRGKTTITAANFIDVIITRQIASDKDARERGSQSSDSSSSLS 1962
qq	2322 NYPSSSRTPQAPASANLVGPRSAHATAPVNIAGSRTAAALAPASLTSARMAPALSGANLT 2381
Qy	1963 SHRYETPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGP 2013
qa	2382 SPRVPLSAYERVSGRISPPLLDRARSRIPPSAPSQSRMISERAPSPSSRMGQAP 2435
Qy	2014 LHHYRPQQESPSPQQQLP-PSSQAEGMGQVPRTHRLITLADHICQ 2057

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                                                                                                                                                                                                                                                                                                                                             2277
  SQSLLPPAQDQPRSPVPSAFSDQSRCLIAQTTPVAGSQSLSSGAVATT--TSSAGDH--- 2490
                                                                                                                                                                                          ----RKPI----D 2683
                                                                                                                                                                                                                                                                                                                                                                                                                                     2278 KVEDHGVVMSQPMGVVPGTANTSVVTSGETRREEGDPSPHSGGVCKPKLISKSNSRKSKS 2337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLRDSRSLSYSPV-----SSSSERGSR- 2720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----SPRPMRHRSSRS 2751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Structural analysis of Arabidopsis thaliana chromosome 5. II. Sequence features of the regions of 1,044,062 bp covered by thirteen physically assigned Pl clones."; DNA Res. 4:291-300(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                               2058 IITQDFARNQVSSQTP-----QQPPTSTFQNSPSALVS-TPVRTKTSNRYSPESQAQS
                                                                              2110 VHHQRPGSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEP-----ISPPQVP--VVHE
                                                                                                                                                                                                                                             2161 KQDSLLLLSQRGAEPAEQRNDARSPGSISYLPSFFTKLENTSPMYKSKKQEIFRKLNSSG
                                                                                                                                                                                                                                                                                                                                        2221 GGDSDMAAAQPGTEIFNLPAVTTS---GSVSSRGHSFADPASNLGLEDIIRKALMGSFDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2338 PIPGOGYLGTERPSSVSSVHSEGDYHRQIPGWAWEDRPSSTGSTQFPYNPLTMRMLSSTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2910 AA; 325351 MW; A847EC3FE1427DF7 CRC64;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; M
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MEDILDE-99439764; PubMed-10508862;
Wang X., Kibschull M., Laue M.M., Lichte B., Petrasch-Parwez
Kilimann M.W.;
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PROSITE; PS00499; C2_DOMAIN_2; 1.
SMART; SM00239; C2, 1.
SEQUENCE 4833 AA; 524996 WW; 7597642E508D8F35 CRC64;
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ЕМВС: X19186; САВ60732.1; -.
HSSP; P04410; 1A25.
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InterPro; IPR000008; -.
InterPro; IPR01178; -.
Pfam; PF00168; C2; 1.
Pfam; PF00595; PD2; 1.
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ογ	235	IVQIIYDE
g	1361	PSETRDISISEEEIKESQEKKVTSKKDSAQGFPSRKEHKENPELVDDLSPR 1411
οy	270	SDTKVYHENIKTNQVMRKKLILFFKRRNHARKQREQKICQRYDQLMEAWEKKVDRI 325
рр	1412	RASYDSVEDSSESENSPVARRKRRTSIGSSSSEEYKQEDSQGSGEDEDFIRKQII 1466
ŏ		ENNPRKAKESKTREYYEKOFPEIRKQREQOERFORVGQRGAGLSATIARS 376
g G	1467	EMSADEDASGSEDEEFIRSOLKEIGGVTESOKREETKGKGKSPAGKHRRLTRKSSTSFDD 1526
οy	377	EHEISEIIDGLSEQENNEKQMRQLSVIPPRMFDAEQRRVKFINMNGLME 425
a	1527	DAGRRHSWHDEDDETFDESPELKFRETKSQESEELVVAGGGGLRRFKTIELNSTVT 1582
οý	426 1	DPMKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNFGLIASYLERKSVPDCVLYY 478
QQ	1583	
ογ	479	ALVRRNYGKRRGRNQQIARPSQEEKVEE
qq	1641	SLDEDSDSSPSHKKGESKQQRKARHRSHGPLLPTIEDSSEBEELREBEBELLKEQEKQREL 1700
λά	536	EEKDEKEDSKENTKEKDKIDGTAEETEEREQATPRGRKTANSQGRRKGRITRSMTNEAAA 595
qq	1701	
δ	296	ASAAAAAATEEPPPPLPPPPEPISTEPVETSRWTEBEMEVAKKG- 639
q	1753 1	
οy	640	Transport of the state of the s
g	1813 (	 QKALKSAEEMYEENMHKPHKYKAFPAANERDEVFEKEPLYGGMLIEDYIYESLVEDTYNG 1872
δy	648 1	AAIAKMVGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRKPREERDVSQCESV- 702
q	1873	: : :   :   :
οχ	703	720
В	1930	PQEDIVSSSYIIPESHEIVDLGSMYTSTSEEKKLLDADAAYEELMKRQQMQVTDGSSLIQ 1989
δ	721	DSEVEAVKPSEDSPEN
qq	1990	: : : : :     ::     ::     ::     ::     ::     ::       ::     ::       ::       ::       ::         ::         ::
ολ	754	
q	2050 1	YVTDYTREIQEIIAHESLILTYSEPSESATSVPPSDTPSLTSSISSVCTTDSSSPVTTLD 2109
οy	787	SISAETAEQMDVDQQEHSAEE GSVCDPPP
g	2110	::
ογ	816	ADSVDVEVRVPENHASKVEGDNTKERDLDRASEKVEP 855
g	2170 1	
οy	856 1	RDEDLV VAQQINAQRPEPQSDNDSSATCSADEDVDGEPERQRWFPMDSKPSLLNPTG 912
g	2230	SEAELTKISLPETGLAPTPSSQTKEQPGSPHSVSGEISGQEKPTYRSPSG 2279
δ	913 8	SILVSS-PLKPNPLDLPQLQHRAAVIPPMVSCTPCNIP 949
g	2280	
οy	950	IGTPVSGYALYQRHIKAMHESALLEEQRQRQEQIDLECRSSTSPCGTSKSPNREW 1004
q	2340 F	KRKLAAAAPVAPTAIVTAHADAIPTVEATAARRSNGLPATKICAAAPPP 2388

Οy	1005 EV	HOLITNLPEGVRLPTTRPTRPPPLIPSSKTT	1059
QQ	2389	:     :     : :     : :     :     :     :       :	2437
δ, d	1060 GT	GTPGTYLTSHNQASYTQETPKPSVGSISLGLPRQQESAKSATLPYIKQEEFSPRSQN 	1116
ò	117	RGTAGAIOEGSITRGTPTSK - ISVESIPSI-RGSITC	1173
2 점		:	2530
δλ	1174 QT	GIPTEACIPTEA	1207
qq	2531 ST	: : :	2590
Qy	1208 GH	GHVIYEGKSGHILSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSA	1267
qq	2591	SVAPRSVSIPIPPEPLALDRHQYKENGKL	2619
Qy	1268 PL	PLEGLICRALPRGSPHSDLKERTV-LSGSIMQGTPRATTESFEDGLKYPKQIKRES	1322
q	2620 PL	SEVKVTEKCMD	2670
Qy	1323 PP	PPIRAFEGAITKGKPYDGITTIKEMGRSIHEIPRQDILLQESRKTPEVVQSTRPIIEGSI	1382
qq	2671 PS	INLESASSLGTPVTMDS-KTVAVVTCT	2699
οy	1383 SQ	SQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVKAGE	1442
qq	2700	DTTIYTTGTESQVGIEHAVTSPLQL	2724
Qγ	1443 TV	TVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRT	1502
qq	2725 -T	TSKHTELQYRKPSSQAFPMIRDEAPINLSLGPSTQAVTLAVT	2767
δλ	1503 SD	SDVIIPPNKSTNHERKSTLTPTQRESIPAKSPVPGVDPVVSHS 	1545
qq	2768 KP	KPVTVPPVGVTNGWTDSTISQGITDGEVVDLSTSKSHRTVVTMDESTSNVVTKIIEDEEK	2827
Qγ	1546 PF	WSHLPTQLD	1584
qq	2828 PVD	DLTAGRRAVCCDMVY	2872
Qy	1585 YL	RQTILNDY	1627
Q	2873 YO	YOYDRSGPYGYRGIGGMKPSMSDINLAEAGHFFYKSKNAFDYSGGTEAAVDLISG	2927
δλ	1628 RP	RPDVARGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRITYIPGTQIT	1687
qq	2928 RV	RVSTGEVMDYSSKTTG-PYPETRQVISGVGISTPQYSTARMT	2968
Qy	1688 FP	PRP-YNSASMSPGHPTHLAAAASAERERERERERERERERERERESSDLYLRPGSEQPG	1746
Q	2969 PP	PPPGPQYGVGSVPPPGPQYGVYSSVATPIPS	2998
δy	1747	GTSV	1787
QQ	2999 TF	AITTOPGSIFSTTVRDLSGIHTTDAITSLSALHQSQPMPRSYFITTGASETDISVTSI	3058
QY	1788 DP	DPTAQLRIMPLPAGGPSISQGLPASRXNTAADALAALVDAAASA	1831
QQ	3059 bI	DINASLQTITMETLPAETMDSVPTLTTASEVFSEVVGEESTLLIVPDEDKQQ	3110
Qy	1832 PQ	PQMDVSKTK	1840
qq	3111 00	OLDLERELLELEKIKQQRFAEELEWERQEIQRFREQEKIMVQKKLEELQSMKQHLLYQQ	3170
οy	1841 ES	ESKHEAARLEENLRSRSAAVSEQQQLEQKT-LEVEKRSVQCLYTSSAFPSGRPQPH	1895
QQ	3171 EE	EEERQAQFMMRQETLAQQQLQLEQIQQLQQQLHQQLEEQKLRQIYQYNYEPSGTASPQTT	3230
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3231 TEQAILEGQYVATEGSQFWATEDATTTASTVVAIEI------PQSQGWYTVQSDGVTQY 3283
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EGDKTKPPSKVSSVAVQTVAEISVQTEPLGTI-RTPSIRARVDAKVEIIKHISAPEKTYK 3460
                                                                                                                                                                                                                                                                                                                                                                     2065 RNQVSSQTPQQPPTSTFQNSPSALVSTPVRTKTSNRYSPESQAQSVHHQR-----PG 2116
                                                                                                                                                                                                                                                                                                                                                                                                    3284 IAPPGILSTVSEIPLTDVVVKEEKQPKK--RSSGAKVRGQYDEMGESMADDPRNLKKIVD 3341
                                                                                                                                                                                                           2025 SPQQQLPPSS-----TQDFGMGQVPRTHRLITLADHICQII-----TQDFA 2064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRVSPENLVDKSRGSRPGKSPERSHVSSEPYE----PISP-----PQVPVVHEKQD 2163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3573 KMMQRSMSDPRPLSPTADESSRAPFQYSEGFTAKGSQTTSGTQKKVKRTL-----P 3623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSDMAAAQPGTEIFNLPAVTTSGSVSSRGHSFADPASNLG-LEDIIRKALMGSFDDKVED 2281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3720 AYLQGVAEDRDYMSDSEVSSTRPSRVESQHG-----IERPRTAPQTEFSQFI 3766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----PYNPLTMRMLSSTPPTPIACAPSAVNQAAPHQQNRIWEREPAPLLSAQ 2431
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MEDLINE-99439764; PubMed-10508862;
WRDLINE-99439764; PubMed-10508862;
WRDLINE-99439764; PubMed-10508862;
WRDLINE 99439764; PubMed-10508862;
Kilimann M.W.; Laue M.M., Lichte B., Petrasch-Parwez E.,
Kilimann M.W.; Solk putative scaffolding protein of presynaptic active
zones, shares homology regions with rim and bassoon and binds
profilin.",
J. Cell Biol. 147:151-162(1999).
EMBL: Y19185; CAB60731.1;
FNBL: Y19185; P04410; 1A25.
                                                                        -----TITAANFIDVIITRQIASDKDARERGSQSSDSSSSLSSHRYETPSDAIEVIS
                                                                                                                                                                       1978 PASSPAPPQEKLQTY-----QPEVVKANQAENDPTRQYEGPLHHYRPQQ-----ESP
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Q9QYX7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 RRPSLLSEFHPGS-----DRPQERRISYEPFHPGPSPVDHDSLESKRPRLEQVSDSHF 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      426 DPMKVYKDRQFMNVWTDHEKEIFKDKFIQHPK-----NFGLIASYLERKSVPDCVLYY 478
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                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 1029; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                479 YLTKKNE---NYKALVRRNYGKRRGRNQQIARPSQEEKVEEKEEDKAEKTEKKEEEKKDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEKDEKEDSKENTKEKDKIDGTAEETEEREQATPRGRKTANSQGRRKGRITRSMTNEAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 326 ENNPRRKAKESKTREYYEKQFPEIRKQREQQERFQR--VGQRGAGLSATIARS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----EHEISEIIDGLSE---QENNEKQMRQLSVIPPMMFDAEQRRVKFINMNGLME
                                                                                                                                                                                                                                                                                                                                                                  Length 5038;
                                                                                                                                                                                                                                                                                 577A7B2530F54C5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                  DB 11;
                                                                                                                                                                                                                                                                                                                                                               Query Match 3.7%; Score 467.5; DB 11; Best Local Similarity 18.3%; Pred. No. 2.7e-16; Matches 562; Conservative 393; Mismatches 1079;
                                                                                                                                                              Prodom; PD000535; -; 1.
PROSITE; PS00499; C2_DOMAIN_1; UNKNOWN_1
PROSITE; PS50004; C2_DOMAIN_2; 2.
                                                                                                                                                                                                                                                                                 547541 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 PPHSVQYTFPNTRHQQEFAVP----
                         InterPro; IPR000008; -. InterPro; IPR001427; -. InterPro; IPR001478; -.
MGD; MGI:1349390; Acz.
                                                                                                          Pfam; PF00168; C2; 2. Pfam; PF00595; PDZ; 1
                                                                                                                                                                                                                                                 SMART; SM00239; C2; 1
SEQUENCE 5038 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235
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703	-	y 754	787 SISAETAEQMDVDQOEHSAEEGSVCDPPP	::         : :	y 816ATKADSVDVEVRYPENHASKVEGDNTKERDLDRASEKVEP 855   1	Y 856 RDEDLVVAQQINAQRPEPQSDNDSSATCSADEDVDGEPERQRMFPMDSKPSLLNPTG 912 :	913 SILVSS-PLKPNPLDL	950IGTPVSGYALYQRHIKAMHESALLEEORQRQEQIDLECRSSTSPCGTSKSPNREW	1005 EVLOPAPHQLITNLPEGVRLPTTRPTRPPPLIPSSKTTVASERPSFIMGGSISQ	D Z389VPFKPSSIPTGLVFTHRPEASKPPIAFKPAVPEIPVTTGKTTDTCPKPT 2437 y 1060 GTPGTXLTSHNQASYTQETPKPSVGSISLGLPRQOESAKSATLPYIKQEEFSPRSON 1116		y 1117 SQPEGLLVRAQHEGVVRGTAGAIQEGSITRGTPTSK-ISVESIPSLRGSITQGTPALP 1173	Y 1174 QTGIPTEA	y 1208 GHVIYEGKSGHILSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSA 1267             1514     1616   2591SVAPRSVSIPIPPEPLALDRHOYKENGKL	1268 PLEGLICRALPRGSPHSDLKERTV-LSGSIMQGTPRATTESFEDGLKYPKQIKRES	1323 PPIRAFEGAITKGKPYDGITTIKEMGRSIHEIPRQDILLTQESRKTPEVVQSTRPIIEGSI		y 1383 SQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVKAGE 1442 	1443 TVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRT	2725 -TTSKHTELQYRKPSSQAFPMIRD	y 1503 SDVTIPPNKSTWHERKSTLTPTQRESIPAKSPVPGVDBVVSHS 1545   155   1545   1555   15	y 1546 PFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAA 1584
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  3819
                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophillade; Drosophila.
3767 PPQTQTEAQLVPPTSPYTQYQXSS-PALPTQ-APTPYTQOSHFQOQTLYHQOVSP----
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                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                               2897 AA
                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBgn0026577; BEST:LD14959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       319165 MW;
                                                                                                                                                                                                                                                                                             01-MAY'2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2001 (TrEMBLrel. 16,
CG8677 PROTEIN.
BEST:LD14959 OR CG8677.
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                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00628; PHD; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                  2432 YET 2434
                                                                                                     3820 YOT 3822
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SEQUENCE
                                                                                                                                                                                                                                                                      Q9VID9;
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09VID9
AC 09VID9
AC 09VID9
DT 01-MAX
CC EUKATY
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Score 465.5; DB 5; Length 2897; Pred. No. 1.6e-16;

3.7%;

Query Match Best Local Similarity

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97;
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                                                                                                                            1005 SEEETIPRKRINSETLVP-----AIPASNVLCQPDERHRKRRSS------EDANE 1048
                                                                                                                                                                                                                                               1049 AFSKESSPIEVPPSAVSEKLKRNNEQDIQEEVED-----PLAMSVKDSLRSAKD 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | : :| ||: | : :| ||: | | 10.48 TMKQELKKKKKA-EKEADPTVLEPSGEESEASEASEAEEARNKKKKKCPGKDGWSSDSEE 1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1307 QPESEEBEBEPPHYETDPGSPLFRSDHEFSP------ESELEDESQVVPM---KR 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1192 PKVGRGRGPRKK----REVDITNIIETNDSETPVROSRRIAQOKIKEEAERRKOEEVALR 1247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1877 SGKQPR-----SQPLKPT-------ASSTLTGKGKG---KGKAKKKQVS 1911
                                                                                                                                                                                                  84 ERRTSYEPFHPGPSPVDHDSLESKRPRL-EQVSDSHFQRVSAAVLPLVHPLPEGLRASAD 142
                                                                                                                                                                                                                                                                                                                                  143 AKKDPAFGGKHEAPSSPISGQPCGDDQNASPSKLSKEELIQSMDRVDREI-AKVEQQILK 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        412 QRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNFGLIASYLERKSV 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309 ---QRYDQLMEAWEKKVDRIENNPRRKAKESKTREYYE-----KQFP-----EIRK 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               906 SLLNPTGSILVSSPLKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTPVSGYALYQRHIK 965
767; Gaps
                                                              24 SVQYTFPNTRHQQEFAVPDYRSSHLEVSQASQLLQQQQQQQLRRRPSLLSEFHPGSDRPQ 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 LKKKQQQLEEEAAKPPEPEKPVSPPVEQKHRSIVQIIYDENRKKAEE------A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HKIFEGLGPKVELPLYNQPSDTKVYHENIKTNQVMRKKLILFFKRRNHARKQREQKIC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       352 QREQQERFQRVGQRGAGLSATIARSEHEISEIIDGLSEQENNEKQMRQLSVIPPMMFDAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1353 ARTVRKENADDLEEE-----WILLCOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1391 PICNKGYHCSCLSPVLFYIPEGDWHCPPCQQEQLIAALERQLEQYDTLVAQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        503 QQIARPSQEEKV--EEKEEDKAEKTEKKEEEKKDEEEKDEKEDSKENTKEKDKIDGTAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     561 TEER-----EQATPRGRKTANSQGRRKGRITRSMTNEAAAAAAAAAATEEPPPPLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1494 VKRRRGDGRINRRAAKRG--TRRRRGNESDSSHRKSLGSGSRSGSDSSSDNSTSFSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         658 SEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRKPREERDVSQCESVASTVSAQEDE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTETAPSTSPSLAVPSTKPAEDESVETQVNDS-ISAETAEQMDVDQQEHSAEEGSVCDPP
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   Indels
Mismatches 901;
Conservative 302;
Matches 445;
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ò	996	AMHESALLEEQRQRQEQIDLECRSSTSPCGTSKSPNREWEVLO 1008	
q	1912	:     :       :  :     :  :  :  :  :  :	
δ	1009	PAPHQLITNLPEGVRLPTTRPTRPPPLIPSSKTTVASEKPSFIMGGSISQGTPGTYLTS	
9 2	1069	KRMLAEKNAEGAKIAATPRLTPLKSGVTASEKRTPG 2005 HNOASYTOFTDKPSVGSTSLERDOOFSAKSAPLDVIKORFFSDBSONGODESLIVDBOU 1198	
; 음	2006		
οy	1129	EGVVRGTAGAIQEGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGIPTEALVKGSIS 1188	
Q	2035		
Qγ	1189		
q	2069	RNVEEEEQFSAEVAARELPGAEE	
δ	1249	SVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIMQGTPRATTESF 1308	
g	2092	TELLATION OF THE CONTROL OF THE	
δ	1309	EDGLKYPKQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHEIPRODILTQES 1364	
Q <sub>O</sub>	2119	TSGLQEPHRKRLPWPTMHPPLLRHQFPISAGPSHSPASLV2158	
δγ	1365		
g	2159	PPHAAQGMHPMLQRHLSQTVPPPQAMHLLQNALSAPLGQP 2198	
ΟÝ	1425	ENI	
qq	2199	:	
δ	1484		
q	2243		
οy	1544		
QQ	2299	QPLFKPHEDAAPSAPASQASVITRMPSLLPPAHGRNHGPPSGLYPSSAD 2347	
ογ	1603	LYAMENTRQTILNDYITSQQMQVNLRPDVARGLSPREQPLGLPYPATR 1650	
g	2348	LARFYGQVANQQPIPAVPGSRSPSSTSGPPRHLLRPQMPPGLPPPHASLRPTYGPPPLR 2407	
δ	1651	GIIDLINMPPTILVPHPGGTSTPPMDRITYIPGTQITFPPRPYNSASMSP- 1700	
Q	2408	GSGPPTSTFTTNSRPAYLHGAEHHGGPSGPPMGGV-FSSGPPPARHATPHLNPY 2462	
ολ	1701	GHPTHLAAAASAERERERERERERERIAAASSDLYLRPGSEQPGRPGS 1750	
qq	2463	RAPPIYGNPNYSPRLGGAPGTGSMRPGAVDYVAGPRGYSP 2502	
δý	1751	HGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMPLPAGGP 1803	
g	2503	YGYYPPPPPLSTPSAHAATSSVIVSAPHILIPINHSVPTLTHGKTPPQQTP 2553	
ογ	1804	SISQGLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAVSEQ 1863	
QQ	2554	TOSSGPPPAAAPPPTITSETSSHKPPLASVITSKKLTTLEA 2594	
ç q	1864 2595	QQLEQKTLEVEKRSYQCLYTSSAFPSGKPQPHSSVVYSBAGKDKGPPPKSRYEBELRTRG 1923 ::::::::::::::::::::::::::::::::::::	
à	1924		
g P	2635	2635 PSSATGTAVV	

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RNBLITAXNID=1217;
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RAMAMER M.D. Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
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RAMAME M.D., Celniker S.E., Hill R.A., Evans C.A., Gocayne J.D.,
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Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeliffer B.D.,
RAMADI J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
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RAMEN M. Cawley S., Dahlke C., Davenport L.B., Davies P.,
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                                               2084
1984 P---PQEKLQTYQPEVVKANQAENDPTRQYEGPLHHYRPQQESPSPQQQLPPSSQAEGMG 2040
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Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Bukaryota; Neotera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
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CG3996 PROTEIN.
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2877 PAQISPPERVADKLE 2891
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693 ERDVSQCESVASTVSAQE : ::   ::   :: 1320 TKPATKSQSTSAEVKTQR	726 SEVEAVKPSEDSPENATS   :::    :   1380 KEGDSQQPEESQHKGKNQ	784 VNDSISAETAEQMDVD	1420 MSSKNOFSETVDEALERI	818 KADSVDVEVRVP         :    1480 KHVDVAIEAHIPSPPPPF	851 EKVEPRDEDLVVAQQINA		905 PSLLNP				995 GISKSPNK-EWEVLQPAE 	1021 GVRLPTTRP-TR	1738 GESKPTTEDLTRLEQLE	1061 TPGTYLTSHNQASYTQET		111/ SQFEGLLVKAQHEGV : :  :  :   1851 AVTDEKSVQDQNVVDKK	1160SLRGSITOGTPALPOT		1216 SGHILSYDNIKNAREGTF	1963TETQKSKE	1276 ALPRGSPHSDLKERTVL- :     :  :			1385 GTPIKFDNNSGOSAIKHN		1442 ETVRSRHTSVVSSGPSVI		1497 PMMNRTSDVTIPPNKSTN : ::  ::  ::  :2220	HR
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A Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; The genome sequence of Drosophila melanogaster.";		k Incerpro; IPROJIOUS; R Pfam; PF00566; TBC; 1. R PROSITE; PSO0037; MXB_1; UNKNOWN_1.		<pre>7%; Score 463.5; DB 5; Length 3111; 1%; Pred. No. 2.3e-16;</pre>	Matches 516; Conservative 401; Mismatches 1076; Indels 857; Gaps 113;	28 TFPNTRHQQEFAVPDYRSSHLEVSQASQLLQQQQQQLRRRPSLLSEFHPGSDRPQER		621 GTGGGGSSTDTSLCDDDPRXTERSPKQKAKLARKLKEQKQLAGSRETSLERQRPKSWA	128 PLVHPLPEGLRASADAI	:	173PSKLSKEELIOSMDRVDREIAKVEQQILKLKKKQQQLEEEAAKPPEPEREV	727	24 SFFFEDAR STATES STAT	260KVELPLYNQPSDTKVYHENIKTNQVMRKKLILFFKRNHARKQREQK		307ICORYDOLMEAWEKKVDRIENNPRRKAKESKTREYYEKQFPEIRKQREQOERF	o 911 TRSSTIEIEERYQALERRISQDQPSGDRQAKYIPSTAALEERFNTLEKQLSAEKQR 966	7 360 QRVGQRGA 389 7 160 QRVGQRGA 389 8 17 18 18 18 18 18 18 18 18 18 18 18 18 18	390 QENNEKQMRQLSVIPPMM	::   : :   : : :   :  : :     :  :     :	427PMKVYKDRQFMNVWTDHE	0 1087 NALERKMSVQKSSPSKNKKEPPDBE	482 KKNENYKALVRRNYGKRRGRNQOIARPSQEEKVEEKEEDKAEKTEEKKEEEKKDE 535	111/ NEFEEFEESERAN-ERISCROIFTARRUSCHARSEINENUSFIRMUSFIRMUSFIRMUSFIRMUSFIRMUSFIRMUSFIRMUSFIRMUSFIRMUSFIRMUSFIRM 536 EEKDEKEDSKENTKEKDKIDGTAEEFEEREOATPRORKTA		576	: :         : : :    :   :  :   :  :   :  :	635 VAKKGLVEHGRNWAAIAKMVGTKSEAQCKNFYFNYKRR	1285 PRKSPPSTEELEKRFNALEKQMSTTNLBTTKEPDO 1319
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qq	1320	TKPATKSQSTSAEVKTQKSMKSFDDKIKEVNVAIEKEQSRVEVEVNAEKKRKNVEEAPKN 1379
Qy	72	AVKPSEDSPENATSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQ 783
ΩD	1380	KEGDSQQPEESQHKGKNQRRASEPPSTEDLEKRYETLKRR 1419
ΟŊ	784	NDSISAETAEQMDVDQQEHSAEEGSVCDPPPA
යි	1420	14
Qy	818	50
<b>Q</b>	1480	
Qy	851	VAQQINAQRPEPQSDNDSSATCSADEDVDGEPERQRMFPMDSK 904
qq	1540	7
Qy	905	PSLLNPCLOHRA 934
qq	1593	ADLENRLQFLERQLYKKFYKQRCASDSEVASRVKLPPEDQPSTSRQARKQEAEGQLEQRV 1652
Øλ	935	AVIPPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEQRQRQEQIDLECRSSTSPC 994
QQ	1653	LALEKQLS ENSLKLLEAMRERHRSAD 1678
Qy	995	GTSKSPNR-EWEVLQPAPHQLITNLPE 1020
ΩD	1679	-DSGSPRRLSTETIDATGKELVRYTQNIGELEEVDAHKPINISINIKMMVNKDSESKQPK 1737
ΟŊ	1021	PSS
q	1738	GESKPTTEDLIRRLEQLEQQLLEERAKNGSIPPENEVLEEKPEKLEEKDSCKK 1790
Ογ	1061	TPGTYLTSHNQASYTQETPKPSVGSISLGLPRQQESAKSATLPYIKQEEFSPRSQN 1116
a	1791	QEKNCHNQHVKGDEVEKTEIPADRKIEPASAKEIKTLENVEKAQIRAKVVDTEKSVKDQN 1850
οy	1117	SQPEGILVRAQHEGV VRGTAGAIQEGSITRGTPTSKISVESIP 1159
Q	1851	AVTDEKSVQDQNVVVDKKADRKILDKKDKSPAAGKSEDTRQTSGKKEKSEDIKQASEAPK 1910
Οy	1160	SLRGSITQGTPALPQTGIPTEALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGK 1215
අ	1911	AGASKETSTRGKPSETKLEKPTIKESVLKETFPKKENLESEKPKSKENEATK 1962
Qy	1216	SGHILSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICR 1275
qq	1963	TETQKSKETPTVAVSPKESKVSSKQMTEKKETIKDSSKELPEKMVIN 2010
Qy	1276	ALPRGSPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYPKQIKRESPPIRAF 1328
g	2011	STDVGPMDPNGKTVVLLMDNEHRASKVRRLTRANTEELEDLFQALEKQLNDRNLVKSE 2068
Qy	1329	BGAITKGKPYDGITTIKEMGRSIHBIPRQDILTQESRKTPEVVQSTRPIEGSISQ 1384
q	2069	DGRLIRVDPKPSAEQV-EQTQAISDLTKEIEDFTSAKPEBENPKEAAKEDKPEPE 2122
Qy	1385	GTPIKFDNNSGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVKAG 1441
đ	2123	-EPEDFDWGPNTVKHHLKRKTVYLPSTKELESRFRSLERQIKLLEDVEKIDVE 2174
ΟŊ	1442	ETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRIPVSYQNTMSRGS 1496
q	2175	QRINEIERKIKLQYSLSHEKDLNKYLELCEGKGLDDDEPVPVETP 2219
οy	1497	PMMNRTSDVTIPPNKSTNHERKSTLTPTQRESIPAKSPVPGVDPVVSHSPFDPH 1550
<b>Q</b> O	2220	TKEAEITTARDRSRSPGRKALATKSPYTSPSRKATIKTPHTSPTRKPIIK-SPYTSP 2275
Qy	1551	HRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMEN 1608

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-----PR-PYNSA 1696
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----TSTTSAVSTSSLTH 3061
2372 DADAIPTIGELEHRIRVLDEKLKSPAKTRSKSRSRSPTIEDIKRQKMRDEKKPRTPVHNL
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                                                                                                    1609 TRQTILNDYITSQQMQVNLRP-DVARGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHP
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 16, Last annotation update)
MULTIDOMAIN PRESYNAPTIC CYTOMATRIX PROTEIN PICCOLO.
Rattus norvegicus (Rat).
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          2276 SRKS-AKSPYTS--PSR-----NR-
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   Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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                                                                                                                                         MEDLINE-20170257; PubMed-10707984;
Fenster S.D., Chung W.J., Zhai R., Cases-Langhoff C., Voss B.,
Fenster S.D., Kaempf U., Kindler S., Gundelfinger E.D., Garner C.C.
"Piccolo, a Presynaptic Zinc Finger Protein Structurally Related t.
Bassoon.";
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llarity 18.2%; Pred. No. 5.2e-16;
Conservative 398; Mismatches 1066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002965; -.
Pram, PR00168; C2; 1.
PRINTS, PR001217; PRICHEXTENSN.
PROSITE; PS00499; C2_DOMAIN_1; UN
PROSITE; PS50004; C2_DOMAIN_2; 1.
SMART; SM00239; C2; 1.
Matrix protein.
SEQUENCE 4880 AA; 530148 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.7%;
Similarity 18.2%;
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InterPro; IPR000008; -.
InterPro; IPR001478; -.
                                                                                                                                                                                                                                                               Bassoon.";
Neuron 25:203-214(2000)
Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                   SEQUENCE FROM N.A.
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Matches 569;
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182	1 9 1	IN 674 SQ 1938	7S 707			807 3178			918 vF 2339	:A 958		S 107				:- 1271 iD 2670	tA 1327	
	EPVETSRWTEEEMEVAKG		LDNLLQQHKQKTSRKPREERDVSQCESVARJVS 	ENPEDSEVEAVKP: :::	TSEEKKLLDADSAYEELMRRQQVQVTDGSSPVQTTIGDDMAESTLDFDRVQDASLTSSIL SEDSPENATSRGNTE-PAVEL	SGRALIDISSATUSIPUNITUORSABELEDIYUNITRELUULIAHESLILIYSEESEE PTTETAPSTSPSLAVP-STKPAEDESVETQNNDSISAETAEQMDVDQQEHSAEE	-GSVCD	VRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQI :::	PMDSKPSLLNPTGSILVSS    :   :  :  : EKPTYRLPSGSLPVSTHPSKSRPF		LYORHIKAMHESALLEEOROROEGIDLECRSSTSPCGTSKSPNREWEVLQPAPHQLITNL 	-PEGVRLPTTRPTRPPPPLIPSSKTTVASEKPSFIMGGSISQGTPGTYLTSHNOAS    ::	EFSPRSQNSQPE	-GLLVRAQHEGVVRGTAGAIQEGSITRGTPTSK-ISVESIPSLRGSITQGTPALPQTGIP 	-LVKGSISR-MPIEDSSPEKGREBAASKGHVIX                   QTVPTSLTQFLPAEASKPEVSAVSSAVP	EGKSGHILSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPLEG- 	-LICRALPRGSPHSDLKERTV-LSGSIMQGTPRATTESFEDGLKYPKQIKRESPPIRA 	FEGALTKGKPYDGITTIKEMGRSIHEIPRQDILITQESRKTPEVVQSTRPIIEGSISQGTP
: 	ЭКРИК	KNFYF!   : - NGFM(	HEIVDI	NPEDS!	RVQDAS	SHSAEI SHSAEI	PPATKA   :	AOAPS	LVSS   :  VSTHE	IGJ : KLAVAZ	COPAPE : 1   /PPKPS	PGTYL7	SOPE      SSPRYS	GTPAI	REEAAS 1 I AVSSAV	RESPVS	QIKRE	TIEGE
-   -	reemm	SEAQCI     DEEQ-	IIPESI	⊠   	TLDFD	OVDQQ!	SVGTKI	PEPGL	PTGS11  :  : PSGSL1	NIP      YPKKK	REWEV	LSOGI	PRSQNS       PHSNKS	RGSIT(	SPEKGI  -  (PEVS)	GMSMI	GLKYPF	OSTRE
::	SAEEM	MVGTK: ::  : LL-TR	VSSSY		DMAES'	TAEOMI TAEOMI TEPAI	PSWE	TKISL	PSLLN   : PTYRL	SCTPCI	SKSPNI	IMGGS	QEEFSI    LSI	SIPSE]	PIEDS:	EGNIK(   : NGKL-:	SSFEDG	CTPEV
MERT.H.	OKALK	AAIAKU : SVDGS:	POEDI		TTIGD	SISAE	FSGMA	RDEDL : :  SEAEL	PMDSKI	IPPMV: :   LPPAT:	SPCGT	EKPSF:	LPYIK(    SP	- ISVE:  - -  LVSLE	ISR-MI	SYESVI	PRATTI	LTQESRKT
 	AKKG-  :  QKEGV	HGRNW.   DTYNG	-HKQKTSRKPREERDVSQCESV      : : :     DPMQKISDLQKEFYELESLHSVVPOE		SSPVQ	SGRALIDISSATUSIPUNTITURSABELEDIYUNITRELUULIAHESLILTY. PTTETAPSTSPSLAVP-STKPAEDESVETQNNDSISAETAEQMDVDQQEHSAEE-	RIVES	HASKVEGDNTKERDLDRASEKVEPRDEDL 	NAQRPEPQSDNDSSATCSADEDVDGEPERQRMFPMDSKPSLLNPTGSILVSS- 	-PLKPNPLDLPQLQHRAAVIPPMVSCTPCNIP- 	DLECRSSTSPCGTSKSPN :	TTVAS:   : IPVTT	TTQETPKPSVGSISLGLPRQQE-SAKSATLPYIKQEEFSPRSQNSQPE- 	-GLLVRAQHEGVVRGTAGAIQEGSITRGTPTSK-ISVESIPSL 	TEASPEKGREBASK : : SASQPTLYTSGALGTFSVTPAVTASLFQTVPTSLTQFLPAEASKPEVSAVSSAVP	KNAREGTRSPRTAHEISLKRSYESVEGNI 	-LICRALPRGSPHSDLKERTV-LSGSIMQGTPRATTESF :	RQDIL.
  -  -  -	-TEEEMEVAKKG     :   :   :   PTDEQSVMQKEG	LVE      ESLVE	RDVSQ :: YELES		DVTDG	DESVE	RTNED	LDRAS       LDAYK	DVDGEPERQRMF    :   -VSGKISGQ	OLOHR	OIDLE	IPSSK : : VPQ	QQE-SI : : SADYN	SITRG'       SWPLG	ASLFQ	RTAHE	-LSGS	THEIP
EDAGE	WTE	EDYIY	KPREE : <del> </del> LOKEF		RRQQV VEL  ::	VALTO TKPAE : SVCTT	IMPES	TKERD	ADEDV	PLDLP               	ESALLEEQRQRQEQI ::  TWVEAAARRS	PPPPL     -PKPA	LGLPR       LNLVT	AIQEG   AQAIT	TPAVT	GTRSP   SVSIP	- ERTV  : :	EMGRS
- TGP.TN	-PVETSRW-	GGMLI	OKTSR 	NEE -	YEELM TE-PA	AVP-S	ISVSLDRTI	VEGDN 1- ETGDG	SATCSA	PLKPN     PPPPP	LLEEQ: ::  MVEAA	TRPTR	VGSIS  :: TSTMSI	RGTAG	STESV	KNARE   SVAPR	SDLK-	ITTIK
	VYKLP	KEPLY	HK	-DIEASNEE-	TSEEKKLLDADSAYEELMRRQQ SEDSPENATSRGNTE-PAVEL-	TSPSL :	EDISV	-HASK     IKGKK	SDNDS	SAQPP	MHESA: : LTI	PEGVRLPTTRPTR    ::   VFTHRPEAIKPPIA	S' : TGLSL'	HEGVV)   EPGTP'	 TSGAL	SYDNI	RGSPH:	KPYDG
:   ERPKTPP-	IEVQK		LDNLLQQ   :  KVRLQEQIY	AQEDE   ::	EKKLL SPENA	ETAPS	-GSVCD	VRVPEN	NAQRPEPQSD     1 KEQHVSPHS-	SSLDIS	LYQRHIKAME: :  :  : IVTTHVDAL-	PEG    	YTQETPKPS-        : -TDTCPKPTG	LVRAQI : ITLPSI		SGHIL	CRALP	AITKG!
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q	5 G	Q Pp	S G	δλ	a & 1	3 6 8	O.Y O.	Oy Dp	Oy Dp	Oy Dp	Oy Db	O O O	O O	Q P	Oy Ob	Oy Dp	à é	λ̈́o

Q C	2/22 LSAA	AASSLGTPDTT Z/48
Οy	1388 IKI	SLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVKAGET
Д	2749' IY	
οy	1448 HTS	TSAR
qq	2775 HTI	HTELPYRKPSSQAFPTIRDEAPINLSLGPSAQAVTLAVTKPVTV 2818
Oy	ω	SPFDPH 155 
qq	819	WTDSTLSQGVADGEVVDLSTSKSHRTVVTMDESTSNVVTKIIEDDEKPVD 287
ΟŸ	HR	SHLPTQLDPAMPFHRALDPAAAAYLFQR
q	2877	-LTAGRRAVCCDMVYTLPFGRSCTAQQPATTLPEDRFGYRDDHYQYDR 2923
δλ	1590 OLS	QLSPIPGYPSQYQLYAMENTRQTILNDYITSQQMQVNLRPD 1630
q	2924	SGPYGYRGIGGMKPSMSDINLPEAGHFFYKSKNAFDYSGGIGAAVDLISGRVS 2976
ζŏ	1631 VA	VARGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRITYIPGTQITFPP 1690
QQ	2977 TGI	TGEVMDYSSKTTG-PYPETRQVISGVGISTPQYSTARLTPPP 3017
δλ	1691 RP	YNSASMSPGHPTHLAAAASAEREREREREKERERERIA. 
Ωp	3018 GPC	κς.
ογ	1747	-RPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPT 1790
QQ	3048 IT	IFSTTVRDLSG
Οy	1791 AQI	AQLRIMPLPAGGPSISQGLPASRYNTAADALAALVDAAASAPQM 1834
qq	3108 ASI	
δλ	1835 DVS	DVSKTKESK 1843
q	3160 DL	DLERELLELEKIKQQRFABELEWERQEIQRFREQEKIMVQKKLEELQSMKQHLLYQQEEE 3219
Qy	1844 HE	HEAARLEENLKSRSAAVSEQQQLEQKT-LEVEKRSVQCLYTSSAFPSGKPQPHS 1896
Q	3220 RQ	AQFWMRQETLAQQQLQLEQIQQLQQQLHQQLEEQKLRQIYQYNYDPSGTSSPQTTTEQ 3279
Qy	1897 SV	SVVYSEAGKDKGPPTI 1927
Q	3280 AII	AILEGQYAATEGSQFWATEDATTTASTVVAIEIPQSQGWYTVQSDGVTQYIAPPGILSTV 3339
δy	1928 TA	TAANFIDVIITRQ1959
qq	3340 SE	SEIPLTDVVVKEEKQPKKRSSGAKVRGQYDEMGESVADDPRNLKKIVDSGVQTDDBETAD 3399
οy	1960 -SI	-SLSSHRYETPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQYE 2011
QQ	3400 RS	YASRRRRTKKSVDTSVQTDDEDQDEWDMPSRSRRKARTGKYGDSTAEGDKTK 3453
δy	2012 GPI	GPLHHYRPQOESPSPQQQLPPSSQAEGMGQVPRTHRLITLADHICQIITQDFAR 2065
qq	3454 -PL	LSKVSSVAVQTVARISVQTEPVGTI-RTPSIRARVDAKVEIIKHISAPEKTYKG 3507
Qy	2066 NQ	NQVSSQTPQQPPTSTFQNSPSALVSTPVRTKTSNRYSPESQAQSVHHQRPGS 2117
qq	3508 GSI	GSLGCQTETDSDTQSPPYLGATSPPKDKKRPTPLEIGYSSSHLRADPTVQLAPSP 3562
Qy	2118 RVS	RVSPENLVDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVHEKQDS 2164
qq	3563 PKS	PKSPKVLYSPISPLSPGNALEPAFVPYEKPLPDDISPQKVLHPDMAKVPPASPKTAK 3619
QY	2165 LLI	LLLLSQRGAEPAEQRNDARSPGSISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGGGDS 2224
q	3620 MMC	MMQRSMSDPKPLSPTADESSRAPFQYSEGFTTKGSQTMTASGTQKKVKRTLPNPPPEE 3677

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1297 SSSQQPKSPQGLSDTGYSSDGISGS-LGEIPSLIPSDEKDLLKGLKKDSFSQESSPSSPS 1355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0T-2001 (TrEMBLrel. 16, Last annotation update)
MULTIDOMAIN PRESYNAPTIC CYTOMATRIX PROTEIN PICCOLO.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 QQEFAVPDYRSSHLEVSQASQLLQQ--QQQQQLRRRPSLLSEFHPGSDR-----PQERR 86
                                                                                                                                                                                                                                                                                                               ------PYNPLTMRMLSSTPPTPIACAPSAVNQAAPHQQNRIWEREPAPLLSAQYE
                                                                 ----VSTGTQ----STYSTMGTASRRMCRTNTMARAKILQDIDREL-----DLVERES
                                                                                                                2284 VVMSQPMGVVPG----TANTSVVTSGETRREEGDPSPHSGGVCKPKLISKSNSRKSKSP
                                                                                                                                                             3724 AKLRKKQAELDEEEKEIDAKLRYLEMGINRRKEA-------LLKEREKRERAY
                                                                                                                                                                                                                                                            LOGVAEDRDYMSDSEVSSTRPSRVESQHG------VERPRTAPQTEFSQFIPP
                                                                                                                                                                                                             IPG-----QGYLGTERPSSVSSVHSEGDYHRQTPGWAWEDRPSSTGSTQF-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 5085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF227534; AAF63196.1; -
InterPro; IPR001408; -
InterPro; IPR001478; -
InterPro; IPR001478; -
Pfam; PF00168; C2, 2, 2
PRINTS; PR001217; PRICHEXTENSN.
PROSITE; PS00499; C2_DOMAIN_1; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5085 AA.
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Matrix protein.
SEQUENCE 5085 AA; 5
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1882 NERDEVFEKEPLYGGMLIEDYIYESLVEDTYNGSVDGSLL-TRQEEQ--NGFWQQRGREQ 1938
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                             SGVGESQKREEAKG-KGKGVAGKHRRLTRKSSTSFDDDAGRRHSWHDEDDETFDESPELK 1591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERPKTPP----SNLSPIEDASPTEEL-RQAAEMEELHRSSCSEYSPSIESDPEGFEISP 1821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1999 TSEEKKLLDADSAYEELMRRQOVQVTDGSSPVQTTIGDDWAESTLDFDRVQDASLTSSIL 2058
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                                                                                                                       NRKKAEE------AHKIFEGLGPKVELP-LYNQPSDTKVYHENIKTNQVMRKKLILFF 293
                                                                                                                                                                                                                                                                                                                                                                       350 RKQREQQERFQRVGQRGAGLSATIARSEHEISEIIDGLSEQEN--NEKQMRQLSVIPPMM 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F-----DAEQ-----RRVKFINMNGLMEDPMKVYKDRQFMNVWTDHEKEIFKDKF 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          453 IQHPK-----NFGLIASYLERKSVPDCVLYYYLTKKNE---NYKALVRRNYGKRRGRN 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EREQATPRGRKTANSQGRRKGRITRSMTNEAAAASAAAAATEEPPPPLPPPPE--PIST 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---LVEHGRNWAAIAKMVGTKSEAQCKNFYFNYKRHN 674
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EIAKVEQQILKLKKKQQQ--LEEEAAKPPEPEKPVSP--PPVEQKHRSIVQ----IIYDE 242
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                                                                                                                                                                                                                                               KRR----NHARKQREQKICQRYDQLMEAWEKKVDRIENNPRRKAKESKTREYYEKQFPEI
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qq	:  : ::   : Db 2400 IVTTHVDALTMVEAAARRSNGLPATKMCAIAPPP	:   :      :      :      :	
oy Ob	QY 1019PEGVRLPTTRPTRPPPLIPSSKTTVASEKPSFIMGGSISQGTPGTYLTSHNQAS	PSFIMGGSISQGTPGTYLTSHNQAS 1073	
O.y D.b	1074 YTQETPKPSVGSISLGLPRQQE-SAKSATLPYIKQ	(IKQEEFSPRSONSQPE 1120 	
oy D	OY 1121 -GLLVRAQHEGVVRCTAGAIQEGSITRGTPTSK-ISVESIPSLRGSITQGTPALPQTGIP	VVESIPSLRGSITQGTPALPQTGIP 1178  : ::  :	
8 8	1179		
og og	: : 2582 SASQPTLYTSGALGTFSVTPAVTASL		
Qy Db	OY 1213 EGKSGHILSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPLEG 	SSVEGNIKQGMSMRESPVSAPLEG- 1271   :       KRNGKIPIJGD 2670	
οy	1272	DGLKYPKQIKRESPPIRA	
a	2671	FTANEVYRRQISAVQPSIIN 2721	
oy B	1328 FEGAITKGKPYDGITTIKEMGRSIHEIPRQ   :     2722 LSAASSLGTP	DILTQESRKTPEVVQSTRPIIEGSISQGTP 1387 :  :            VIMDS-KTVAVVTCTDTT 2748	
δy	1388	PENIKVVERGKYEDVKAGETVRSR 1447	
q	2749 IYTTGTESQVGIEHAVTS	t: 1774	
\$ 6	1448 HISVVSSGPSVLRSTLHEAPKAQLSPGIYDDTS	ARRTPVSYQNTMSRGSPMMNRTSDVTI 1507	
3 8	1508 PPNKSTNHERKSTLTPTORESIPAKS	SECTION TO SECTION 155	
d d	2819 PPVGVTNGWIDSTLSQGVADGE	1	
δý	1551 н	ALDPAAAAYLFQR 1589	<u> </u>
Q	2877LTAGRRAVCCDMVY	TLPFGRSCTAQQPATTLPEDRFGYRDDHYQYDR 2923	
Oy Op	1590 QLSPTPGYPSQ           2924SGPYGYRGIGGMKPSMSDTNLPE	YQLYAMENTRQTILNDYITSQQMQVNLRPD 1630	
Qy	OY 1631 VARGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRITYIPGTQITPPP : :           : :         :         :	IPGGTSTPPMDRITYIPGTQITFPP 1690	
QQ	2977 TGEVMDYSSKTTG-PYPETRQVISGV	GISTPQYSTARLTPPP 3017	
δλ	QY 1691 RP-YNSASMSPGHPTHLAAAASAERERERERERERERERERIAAASDLYLRPGSEQPG	ERERIAAASSDLYLRPGSEQPG 1746	
Dp	3018 GPQYGVGSV	LRSSNGVVYSSVATPIPSTFA 3047	
දු පු	QY 1747RPGSHGYVRSPSPSVRTQETMLQQRPSVEQGTNGTSVITPLDPT :	RPSVFQGTNGTSVITPLDPT 1790	
δ	1791		
qq	3108	: :  FFSEVVGEESTLLIVPDEDKQQQQL 3159	
δχ	Qy 1835 DVSK	TKESK 1843	
qq	3160	KIMVQKKLEELQSMKQHLLYQQEEE 3219	
δý	OY 1844 HEAARLEENLRSRSAAVSEQQQLEQKT-LEVEKRSVQCLYTSSAFPSGKPQPHS	SSVQCLYTSSAFPSGKPQPHS 1896	

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: | | | : | | : | SEIPLIDVVVKEEKQPKKRSSGAKVRGQYDEMGESVADDPRNLKKIVDSGVQTDDEETAD 3399
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3220 RQAQFMMRQETLAQQQLQLEQIQQLQQQLHQQLEEQKLRQIYQYNYDPSGTSSPQTTTEQ 3279
                              SVVYSEAGKDKGPP-----TI 1927
                                                                                              TAANFIDVIITRQ------1959
                                                                                                                                                                                                                            2012 GPLHHYRPQQESPSPQQQLPPSSQAEGMGQVPRTHRLITLADHICQII-----TQDFAR 2065
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                                                                                                                                                                                                                                                                                                                                                                                                                        LLLLSQRGAEPAEQRNDARSPGSISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGGDS 2224
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
02013648.
Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Pteryotta: Metazoa: Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryotta: Metazoa: Arthropoda; Tracheata; Brachycera; Muscomorpha;
Ephydroidea: Drosophilidae; Drosophila.
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MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Annanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
                                                                                                                                                                                                                                                                                                                                                                           -SLSSHRYETPSDAIEVISPASS-----PAPPQEKLQTYQPEVVKANQAENDPTRQYE
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RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., And K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews Pfannoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Erotter P., Charler P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Dorlor A., Gorgeli J.H., Gu Z., Gelbart W.M., Glasser K., Glock A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harvey D., Helman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.H., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalali M., Kallush F., Karpen G.H., Ke Z., Kennison J.A., Mattis B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Liu X., Mattel B., Morthcos H.C., McLood M.P., McDherson D., Merkulov G., Milshian N.V., Mobarry C., Morris J., Moshrefi A., Mony M., Murphy B., Murphy L., Muzny D.M., Nelson D., Reinert K., Saunders R., Dollard J., Puri V., Resse M.G., Sher B.C., Spier K., Stone B.C., Stuppson M., Strong R., Sun R., San R., Shen H., Shillang S., Pan S., Pollard J., Puri V., Santh T., Shir R., Wang X., Wang Z.Y., Wangsarman D.A., Welson K., Welson K., Welson K., Stupski M.P., Santh T., Sauth H.O., Shir R., Wang X., Wang X.H., Rohn G., Zhan M., Zhang G., Zhao Q., Zheng L., The Genome Sequence of Drosonhila melanomaster."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEAAKPPEPEKPVSPPVEQKHRSIVQIIYDENRKKAEEAHKIFEGLGPKVELPLYNQPS 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FKRRNHARKQREQKICQRYDQLMEAWEKKVDRIENN-----PRRKAK-----E 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 CCPVRYSCDHENELDFMDQSTTTTTTTTTTTGFILASTMTPPTTTDCIHDGEIFADGAS 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               511
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llarity 19.5%; Pred. No. 2.9e-16;
Conservative 319; Mismatches 1010; Indels
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Science 287:2185-2195(2000).
EMBL; AE003750; AAF56376.1; -
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3E 2768 AA;
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Best Local Similarity
Matches 552; Conserva
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SEQUENCE
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1008 SVYLPPVSQEVPSSTAKVDNRNDFETE------KPT-LPPSGEDQSSEPLP--AMDL 1055 1022 VRLPT------TRPTRPPPPLIPSSKTTVASEKPSFIMGGSISQGTP-GTY 1065 ---KQEEF 1110 EEDSKPIDESEEDKKPVEESAEDKKPVEDSEEKEKPLPTVIPASEIEKESKPEDEKKTEA 1280 SPRSQNSQPEGLLVRAQHEGVVRGTA-GAIQEGSITRGTPTSKISVESIPSLRGSITQGT 1169 ||| | : | : | |: | : | |: EVPE--AEPADKDHKDEEDVQTATDL--PIKSDIGPPVVDTEATTGQPETSDETATDKPP 1007 P----AGIPGEGDCLVEGKTYANNTIVPATAPCDVSCKCISSLVACQQMECKLPEN-- 1107 LLEEQRQRQEQID----LECRSSTSPC----GTSKSPNREWEVLQPAPHQLITNLPEG 1021 -LEKCTVAADLLDGCCPTYICDESTESAEKDEESTAKPDNKIDEDVSEISTE---EIPKD 1163 DFAAPTEQPE----ATTPAQIADTAEKEVDDKLATTSAPVSG-EDELKPADEKKRTE-T 1333 PALPQTGIPTEALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIKNAR 1229 EGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPLEGLI-----CRALPRGSPH 1283 ------EVPTSASTENEIEESDKFTTVAPPKISA 1408 SDLKERTVLSGSIMQGTPRATTESFEDGLKYPKQIKRESPPIRAFEGAITKGKPYDGITT 1343 SDETEPTA-EEDLVPATFEPIESEFEVSTKKPAV---QGPPLPTLAPAQPEKKPVDAETS 1464 -----TPCNIPIGTPVSGYALYQRHIKAMHESA 971 EK-----VEEKEEDKAEKT-----EKKEEEKKDEEEKDEKEDSKENTKEKDKIDGTA 558 EESEEQDEGKSTEAPTSVDDIEPAKPTESSEEASGEG-----EDVAKETTPAGEASIA 608 GEEEIVKGTTPAGEPSSEGDEEIVKGTTPAEESSSESEDELTKVTTPAGEPSVAGEEEIA 668 -----KGLVEHGRNWAA----IAKMVGTKSEAQCKNFYFNYKRRHNL 675 ---SQCESV----ASTV 706 -----EENPEDSEVEAV 731 KP-SEDSPENATSRGNTEPAVE----LEPTTETAPSTS----PSLAVPSTKPAEDESV 780 EQDATDLPVEDVVQSTTAKTTTTEQPK---EESS-----TEAEDAEIEVTTSSPADKQ 951 -VSTSAPAKASPEEEVVTATTSAPTEEDVKPTTAGTISE----EEEEGKPTPAEEGSGEE 495 IKVTTPAGESSSEGDEEIVKESTPAGEPISEGEEDVIKATTSAPKSDIEGVKEPETATEV 781 EKDVKVTAAPEETEDEAKPTSAPVASDEKEQEPKPSEGSGDEELDLKPTTAPTAGATSAS 1164 VIMPTGITEQPLSHVKPDEEIQPVTSVPAQFDESTTAKVDKKP---IDESAEDKKPIGES EETEER-------EQATP-RGRKTANSQGRRKGRITRSMTNEAAAASAAAA RVPENHASKVEGDNTKERDLDRASEKVEPRDEDL---VVAQQINAQRPE----------PQSDNDSSATCSADEDVDGEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDL KETTPAGEPSIAGEEEIVKVTTPAGESSIAGEEEIVKVTTPAGESSSEG---ETQ-----VNDSISAETAEQMDVDQQEHSAEGSVCDPPPATKADSVDVEV-LTSHNQASYTQETPKPSVGSISLGLPRQQESAKSATLPYI-----:| || ::|| AQIPDAEIPASTDEPESSTELPTVDL--DKKPEEDSTKG-------ERDV----DNLLQQHKQKTSRKPRE-----SAOEDEDI ------EASNE---POLOHRAAVIPPMVSC----ESDKVP----556 949 1056 972 1066 1281 1170 1334 1230 1284 1409 441 496 603 609 637 699 707 732 902 952 873 928 1221 1111 1375 559 781 827 ă g g δ 셤 g ŏ ŏ g δ g q g g g οχ δŏ g ò g ŏ ò ò δ 8 δ δ g Ω g à g ò g à 셤

g ç	QY 1344 IKEMGRSIHEIPRQDILTQESRKTPEVVQSTRPIIEGSISQGTPIKFDNNSG DD 1465 II	GGSISQGTPIKFDNNSG  :     :   :  AGASCHDVDVGADEDKHDSH	1395	
ò	1396 QSAIKHNVKSLI	EDVKAGETVRSRHTSVVSSG	1455	
· අ	1514	: : : : : : : : : : : : : : : : : : :	1558	
δý	1456		1492	
a	1559 PSKDDGEQKPVEVEEKPIEDGQKPIE	SIEPESDRATTIAPSKEEPS	1615	
O.y Db	1493SRGSPMMNRTSDVIIPPNKSTNHERKSTLIPTQR 	ESIPAKSPVPGVDPV           :  TVAPAGEKIPTSSITPDEEPT	1541 1671	
٥y	1542	PAAAAYLFQRQLSPTPGYP	1598	
qq	1672	-PASSEEDENSSTDOIP	1712	
οy	1599 SOYQLYAMENTROTILNDYITSQQM  :	ARGLSPREQPLGLPYPATR	1650	
a	1713 SEVPEKKPETPAQTPEEGDIVGATAAPTTSDEV	PPVQRLPEEVLAEIPQPSTE	1765	
8 8	1651 GIIDLINMPPTILVPHPGGTSTPPMDRITYIPGTQITFPP	FPPRPYNSASMSP	1700	
2	QQ/T	VAPISEKDEKPTEEEKPVE	1815	
ζ Q Q	QY 1701 GHPTHLAAAASAERERERERERE-RIAAASSDLYLRPGSEQPGRPGSHGYV D		1754	
Qγ	1755 -RSPSPSVRT	-QETMLQORPSVF-QGTNG	1780	
qq	DD 1873 DKQPSSTAQAPVETIPEISTELPAQDGDKPTSEAPVDSDEDTSAPSDEKIPSVSGEEVEG	::     :   TSAPSDEKIPSVSGEEVEG	1932	
δ	Qy 1781 TSVITPLDPTAQLRIMPLPA-GGPSISQGLPASRYNTAAD	-ALAALVDAA	1828	
QQ	Db 1933 PEVTTASPQAAEEDELKTPAESEPSSTDKVPETEYQKPEDETKADETPESVTQVSDVATS	: :       TKADETPESVTQVSDVATS	1992	
οy	1829	QKTLEVEKRSVQCLY	1882	
QQ	Db 1993 TSAPVAGGDIEKDEQATTASPEEEEEIKPTIAPAAEIPQPSEKEPVDEQEVESGTKATPA	EKEPVDEQEVESGTKATPA	2052	
ογ	1883 TSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSF	NFID	1934	
Ор	2053 ESDGQPIDEIAPATSGPIDEASTAAPTKEE	-STTVASAASPAVHDDEIKD	2101	
ογ	1935		1970	
qq	Db 2102 VTTTQPVADEKEVAAPQDETKTSIDVSTDSPTAQDDEKQDKTEAPVAPTTVSSPTADSAA		2161	
δλ	1971		2022	
셤	Db 2162 DSSTPTVEVPSPVEIDTKPMDDIMSQTIAPHTADGAASTSTEDEDQAPVTVSPQDAEK		2219	
ΟŊ	Qy 2023SPSPQQQLPPSSQAEGMGQVPRT		2047	
qq	2220 TPVSP		2279	
οy	Qy 2048 LITLADHICQIITQDFARNQVSSQTP	dd00	2077	
ор	Db 2280 IQTTAAPLDEEKIPSTAAPLDDEKIPAPVSPVVFDVEPSSEKPAVSEYDGEESTEPPVHD		2339	
οy	2078		2135	
a a	2340 VETSTDEPTSDAKLKPPTSAPATPSESPATEAEIV	PETAAPELEKEVPEK	2389	
δŏ.	2136 SPERSHVSSE-PYEPISPPQVPVVHEKQDSLLLLSQRGAEPAEQRN		2194	
අ	2390 ATEQPELEKETPEKATEQPELEKE	TPEKATEQP	2422	

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Gaps 114;
                          2314
                                                                                                          2504
                                                                                                                                        2315 SPHSGGVCKPKLISKSNSRKSKSPIPGQGY-----LGTERPSSVSSVHSEGDYHRQTP 2367
                                                                                                                                                                                                                                      2549 ----EDEENTTVK------LSSSTTTSTTESPVTSAPSTTTVASQQQQ----PITPPPY 2593
2195 FTKLENTSPMVKSKKQEIFRKLNSSGGDSDMAAAQPGTEIFNLPAVTTSGSVSSRGHSF 2254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 RSSHLEVSQASQLLQQ-QQQQQLRRRPSLLSEFHPGSDRPQERRTSYEPFHPGPSPVDHD 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 REMRLSVNQVLPSTQRASSPETATKQPS----SPYEDKDKDKKEK-SATRPSPSP--- 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 SLESKRPRLEQVSDSHFQRVSAAVLPLVHPLPEGLRASADAKKDPAFGGKHEAPSSPISG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 QPCGDDQNASPSK----LSKEELIQSMDRVDREIAKVEQQILKLKKKQQQLEEEAAKPP 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPEKPVSPPPVEQKHRSIVQIIYDENRK----KAEEAHKIFEGLGPKVELPLYNQPSDTK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           274 VYHENIKTNQVMRKKLILFFKRRNHARKQREQKICQRYDQLMEAWEKKVDRIENNPRRKA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        492 RGRSRSRTP-----TKRGHSRSRSPQ---WRRSRSAQRWGR----SRSPQRRG 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 KESKTREYTEKQFPEIRKQREQQERFQRVGQRGAGLSATIARSEHEISEIIDGLSEQENN 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          533 RSRS------PQRPGWSRSRNTQRRGRSSARRGRS-HSRSPATRGRSRSTP 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nickerson J.A.
                                                                                                                                                                  2505 E-----VPAVVSEI-PQPSEEAVPTTGHPLFPHLASSTTTPPAVDDRVGE------
                                                                                                                                                                                                               2368 GWAWEDRPSSTGSTQFPYNPLTMRMLSSTPPTPIACAPSAVNQAAPHOONRIWEREPAPL
                                                                       2255 ADPASNLGLEDIIRKALMGSFDDKVEDHGVVMSQPMGVVPGTANTSVVTSGETRREEGDP
                                                                                                        -----EPVVKPSL----DSTEEDEESVESEEESADKKDKNKE--TEEDTDKKHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Usukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
3.6%; Score 453; DB 4; Length 2296;
Best Local Similarity 19.6%; Pred. No. 5.7e-16;
Matches 504; Conservative 288; Mismatches 979; Indels 796;
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Interpro; IPR002965; -.
PRINTS; PR01217; PRICHEXTENSN.
SEQUENCE 2296 AA; 251962 MW; 17C0BD4EA10A9CF9 CRC64;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Blencowe B.J., Bauren G., Eldridge A.G., Issner R.,
Rosonina E., Sharp P.A.;
"The SRM160/300 splicing coactivator subunits.";
RNA 0:0-0(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
SPLICING COACTIVATOR SUBUNIT SRM300.
                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 2296 AA
                                                                                                                                                                                                                                                                                        2428 LSA-QYETLSDSDD 2440
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2594 GHAPEYEDEYDEEE 2607
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Mọn Sep 10 08:14:30 2001

1914 EKOMROLSVIPPMWEDAEORRYNETHWIGLMEDDRKVYRDROPHNWTDHEKEIFRUKETE  1819   1   1   1   1   1   1   1   1   1
579 454 554 594 514 631 631 633 701 693 701 693 701 693 701 101 1014 1019 1074 1071 1101 1101 1101 1101 1101 1101

οy	1393	NSGQSAIKHNVKSLIIGPSKLSRGMPPLEIVPENIKVVERGKYEDVKAGETVRSRHISVV 1452
qq	1344	NTGFSSEVKEDLNGPFLNQLETDPSLDMKEQSTRSSGHSSSE 1385
λο,	1453	HEAPKAQLSPGIYDDTSARRIP
Q	1386	LSPDAVEKAGMSSNQSISSPVLDAVPRTP-SRERSSSASSPEMKDGLPRTP 1435
Qy	1509	HHRGSTAG
QQ	1436	SRRSRGGSSPGLRDGSGTPSRHSLSGSSPGMKDIPRTP-SRGRSECDSSPEPK 1487
Oy	1567	QLDPAMPEHRALDPAAAAYLFQRQLSPTFGYPSQYQLYAMENTRQTILNDYITSQQMQVN 1626
QQ	1488	AL-PQTPRPRSRSPSSPE-LNNKCLTPQRERSGSESSVDQKTVARTPLGQRSRSGSSQ 1543
οy	1627	IIDLTNMPPT
q	1544	-ELDVKPSASPQERSESDSSPDSKAKTRTPLRQRSRSGSSPEVDSKS 1589
٥y	1687	MSPGHPTHLAAAASAERER
q	1590	RLSPRRSRSGS-SPEVKDKPRAAPR-AQSGSDSSPEPKAPAPR 1630
δŏ	1746	GRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMP 1797
qq	1631	ALPRRSRSGSSSKGRGPSPEGSSSTESSPEHPPKSRTARRGSRSSP-EPKTKSRTPPRRR 1689
οy	1798	AADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSR
qq	1690	SSRSSPELTRKARLSRRSRSASSSPETR-SRT-PPRHRRS 1727
οy	1858	AAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEE 1917
q	1728	PSVSSPBPAEKSRSSRRRRSASSPRTKTTSRRGRSPSPKPRGLQRS 1773
δŏ	1918	ELRTRCKTTTTAANFIDVIITRQIASDKDARERGSQSSDSSSSLSSHRYETPSDA 1972
qq	1774	RSRSRREKTRITRRRDRSGSSQSTSRRRQRSRSRSRVTRRRGGSGYHSRSPA 1826
φy	1973	LQTYQPEVVKANQAEND   :::
QC	1827	RQESSRISSRRRGRSRIPPISRKRSRSRISPAPWKRSRSRASPATHRRSR 1877
οy	2021	QESPSPQQQLPPSSQAEGMGQVPRTHRLITLADHICQIITQDFARNQVSSQTPQQ 2075
QQ	1878	SRTPLISRRRSRSRTSPVSRRRSRSRTSVTRRSRSRASPVSRRSRSRTPPV 1930
οy	2076	PPTSTFQNSPSALVSTPVRTKTSNRYSPESQAQSVHHQRPGSRVSPENLVDKSRGSRPGK 2135
qq	1931	TRRRSRSRTPTTRRRSRSRTPPVTRRRSRSRTPPVTRRRSRSRTSPITRRSRSRT 1986
Qy	2136	SEPYEPISPPQV
g	1987	SPVTRRRSRSRTSPVTRRSRSRTSPVTRRSRSRTPPAQDQ 2028
Qy	2188	-ISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGGGD 2223
Q	2029	AQT
οy	2224	SDWAAAQPGTEIFNLPAVITSGSVSRGHSFADPASNLGLED 2265
QQ	2083	VPHSDVGEPPASTGAQQPSALAALQPAKERRSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS
δλ	2266	IIRKALMGSFDDKVEDHGVVMSQPMGVVPGTANTSVVTSGETRREEGDPSPHSGG 2320
qq	2140	SSSSDSEGSSFLCNLSGTEEVPSPTPAPKEAVREGRPPEPTP 2181
ΟŊ	2321	YHRQTPGWAWEDRPSSTGS 238
q	2182	-AKRKRRSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS

QY 2381 TQFPYNPLTMRMLSSTPPTPIACAPSAVNQAAPHQQNRIWERE-PAP 2426

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RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
Braddon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Frannkoch C., Baldwin D.,
RA Beeson K.Y. Basu A., Baxendale J., Bayraktarolu L., Bassley E.M.,
RA Beeson K.Y. Bancs P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis R.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
RA Burtis N.L., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
RA Burtis R.J., Evangelista C.C., Ferraz C., Ferriara S., Pleischman W.,
RA Glodek A., Gong F. Gorrell J.H., Gul Z., Gubart W.M., Glasser K.,
RA Hostin D., Houston K.A., Helman T.J., Hernandez J.R., Harris M.,
Alani M., Kalush F., Karpen G.H., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Wei M.-H., Ibegwam C.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., Inda Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., Norberson D.,
RA Hostin D., Houston K.A., Nixon K., Nusskern D.R., Pacheler F., Shen H.,
Rhont S.M., Moy M., Wurphy B., Murphy L., Murny D.M., Nelson D.L.,
Rhount S.M., Moy M. R.A., Nixon K., Nusskern D.R., Pacheler F., Shen H.,
Spier E., Spradling A.C., Stapleton M., Stupek H. P., Shen H.,
Rhont S.M., Wodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Rhos R., Horston C., Turner R., Venter E., Wang A.H., Wang X.,
Wang S.Y., Wassarman D.A., Walniscock M., Walssenbach J.,
Rhos R., Horston E.W., Rubin G.M., Stupek H. P., Shirth H.O.,
Rhos R., Horston E.W., Rubin G.M., Wangsenbach J.,
Rhos R., Horston E., Zaverli J.S., Zhan M., Zhang G., Zhao Q., Zhen S., Zhan S., Scheeler F., Schen S., Scheeler F., Scheeler F., Schen S., S
                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Petrygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
    --PCKAWPSGLAQTCKPQEATPWRAEVPQP 2259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FBGn0029875; CG3950.
2951 AA; 332269 MW; 85CCC0ABBDAC8AEB CRC64;
                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                   PRT; 2951 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BERKELEY;
MEDLINE=20196006; Pubmed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 287:2185-2195(2000).
                                                                                                                                 PRELIMINARY;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      CG3950 PROTEIN.
: 11:
2227 SSFPF-
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                                                                                       RESULT 26
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PNQGAFSTEQSRYPPHSVQYTFPNTRHQQEFAVPDYRSSHLEVSQASQLLQQQQQQLRR 67

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Ouery Match
3.6%; Score 450.5; DB 5; Length 2951;
Best Local Similarity 18.9%; Pred. No. 1.1e-15;
Matches 512; Conservative 357; Mismatches 1013; Indels 827;

Š	B o	KPGLLSEFHPGSDRPQERRTGXEPFHPGPS	/6
qq	629	AGKPSQSRPSNTGGSTTT	688
οy	86	PVDHDSLESKRPRLEQVSDSHFQRVSAAVLPLVHPLPEGLRASADAKKDPAFG 1	150
qq	689	KTTTTSEPLTRROLOKEREVDAAHRAFAASLRSSSPADSTTSVG 7	732
δ λ	151	PISGQPCGDDQNASPSKLSKEELIQSMDRVDREIAKVBQQIIK  GDDQNASPSKLSKEELIQSMDRVDREIAKVBQQIIK	201
a	(33	TRHITGENVIONITA	r)
<u>ک</u> ک	202	LKKKQQQLEEEAAKPPEPEKPVSPPPVEQKHRSIVQIIYDENRKK-AEEAHKI	253
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à É	407 840	FECULARIAE :::	0 6 0 0
3 8	296	KKVDRIENNPRRK	, (
· 8	868		S
οy	333	AKESKUREYYEKQFPEIR	361
QQ	952	FPRARSPEKTPGWIQPQVSPRQSPEKQLPRAQS	1011
δ	362		405
Op	1012	PEKVPAVRQPSVSPRQSPEKQIPDPKTRDQGPGLPRISPRQSPEKQLPKDVPQKSRQSPE 1	1071
δy	406		459
QQ	1072	KDLTNOGRREBEIFRSTITTTGKRITNNLNEEFITNERDNOPISEKKPQIPANAEPNT 1	1131
ογ	460	GLIASYLERKSVPDCVLYYYLTKKNBNYRALVRRNYGKRGR	501
qq	1132	KPSETIESPDGGFPSKTTEVEAQPEVKESPTYRKKGLTRRETFEDRCRQILGM 1	1184
οy	503	63	550
QQ	1185	NEQEDVNVSHTIETIQVKIEDCPNDDEDDKPRRVTETYVVRTQP	1244
δλ	55		97
g	1245	KIKVEEELEVDVTEAEDVEILVNPSKKSPKEEDSPKYPKGPETPKSPRNDQRIPSIPKKG	1304
δŏ.	59	AAAAAATEEPPPPLPPPPEPISTEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAKMV	4
Q D		TPRYPQEQERYPKEP-ETSQYPKESPRNPKEDAETININEETTIVITKE	m
Οy	655		712
Dp	1363	KSPSPRWSPSPERRVPKSQQPPSPTASPSVSPVSGRKIPN	1404
δy	713	DIEASNEENPEDSEVEAVKPSEDSPENATSRCNTEPAVELEPTTETAPSTSP 7	765
В	1405	EVESNEVTEKIIDCRGKTVVEKISQRPRTPSPTTPKKNTKPSQKIPERVPETESEPEKDS 1	1464
δy	166	SLAVPSTKPAEDESVETQVNDSISAETAEQMDVDQQEHSAEEGSVCDPPPATKADSVD E	823
qq	1465	ESETKKTISVSVTKTETERRNSRITKTKOPLPLKEPOSKVPAGKSPRKDSLIGRKRDSLV 1	1524
δλ	824	ASEKVEPRDEDLVVAQQINAQRPEP	873
Dp	1525	EETRITTTTTTRQGRKPSDINGSPSIKDRLRSSPRKQKISPQQTRTPTPAQTRNPED 1	1582
δÿ	87		21
g	1583	DVDGDSSSPDASPTRVGNERRRSSNISVHTEIIIDHMAPKSPKTERRSQGGTGNVPSPIR 1	1642
ĉ	922	DND: DIDOLOHDAAVIDDMVSCHPCNIPIGHDVSCYALYORHIKAMHESALLEEORORO-	980

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1698	1018 1758	1059	1103	1150	1921 1202 1980	1245	1283 2086	1333 2143	1382 2191	1419 2248	1434	1481 2368	1541 2408	1601 2451	1660	1716 2508	1775 2565	1834
:     :     :	981EQIDL-ECRSSTSPCGTSKSPNREWEVLQPAPHQLITNL 1	1019 PEGVRLPTTRPTRPPPLIPSSKTTVASEKPSFIMGGSISQ	1060GTPGTYLTSHNQAS-YTQETPKPSVGSISLGLPRQQESAKSATLP 1		SKISVESIPSLEGSITQGTPALPQTGIPTEALVKGSISRMPIEDSSPEKGRE	1203EAASKGHVIYEGKSGHILSYDNIKNAREGTRSPRTAHEISLKR 1:	1246 SYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPH 1	1284 SDLKERTVLSGSIMQGTPRATTESFEDGLK-YPKQIKRESPPIRAFEGAIT 1	1334 KGKPYDGITTIKEMGRSIHEIPRQDILTQESRKTPEVVQSTRPIIEGSI 1 :	1383 SQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSRGMPP 1 :     :     :     :       :	1420	1435YEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSA 1 	1482 RRTPVSYQNTMSRGSPMMNRTSDVTIPPNKSTNHERKSTLTPTQRESIPAKSPVFGVDPV 1 :	1542 VSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQY 1 :	1602 QLYA-MENTRQTILNDYITSQOMQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPP 1::	1661 TILVPHPGGTSTPPMDRITYIPGTQITFPPRPYNSASMSPGHPTHLAAAASAERER 1	1717 EREREKERERERIAAASSDLYLRPGSEQP-GRPGSHGYVRSPSPSVRTGETMLQQRPSVF 1   : ::::	1776 QGTNGTSVITPLDPTAQLRIMP-LPAGGPSISQGLPASRYNTAADALAALVDAAASAPQM 1
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RND [1]

RD SEQUENCE FROM N.A.

RX Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RADILINE-20196006; PubMed=10731132;

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RA Admantides P.G., Scherer S.E., Li P.W., Hooskins R.A., Galle R.F.,

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RA Besson K.Y. Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Gawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Goder C., Gabrielian A.E., Garrell J.H., Gu Z., Gunn P., Harris N.L.,

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RA Hostin D., Houston K.A., Howland T.J., Well M.-H., Ibegwam C.,

RA Hostin D., Houston K.A., Howland T.J., Well M.-H., Ibegwam C.,

RA Hostin D., Houston K.A., Howland T.J., Well M.-H., Ibegwam C.,
                                                                                                                                                                                                                                          2613 NGSTPRKGSTSSTTSSSGKITRIMISSSSTTTSSSSTTNTRNKQREEDSI-----TSSYGV 2667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2566 PGDRSTTTTTKVTTTSTTRGAPSKPAQGP----IWADR-----SKVLKGHATVPQT 2612
                                                                                                                                           1835 DVS-----KTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPS 1889
                                                                                                                                                                                                                                                                                                                                                                                                                          1890 GKPQPHSSVVYS-EAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVIITRQIASDKDAR 1948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2790 RKESSSST-----HSTHSSIAQSLVRHEDETEDDSESNDVCSVIEAPQMRQNQSHT 2840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2185 PGSISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGGGDSDMAAAQPGTEIFNLPAVTTS 2244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2007 TRQYEGPLHHYRPQQE--SPSPQQQLPPSSQAEGMGQVPRTHRLITLADHICQIITQDFA 2064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2065 RNQVSSQTPQQPPTSTFQNSPSALVSTPVRTKTSNRYSPESQAQSVHHQRPGSRVSPENL 2124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2125 VDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVHEKQDSLLLLSQRGAEPAEQRNDARS 2184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2885 -----MLPPTATG 2917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last an
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Q917U4;
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Gaps 104;
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., She B.C., Siden-Kiamoo I., Simpson M., Stupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wallams S. M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao G., Zhao X., Zhao X., Zhao X., Zhao S.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:: :| | | :: | :| | :: | 3098 QKKDKKSRSTKVPNEETPVQEQYAKV----NVVEEEA--PEQPEIPVQILEVKPVEVDVK 3151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :: | | | | : : | | | 3047 DDIHDYIQKLIELETPRTE-LEKYEKIEFEPIV------DVEDESPKEV 3097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----VDEEPEIASP-QSIEEHPEQSKEKLAPKPKTVRKVKKDDLSDYVKKLIEEEIPK 3251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.6%; Score 450.5; DB 5; Length 6815; Best Local Similarity 17.7%; Pred. No. 3.4e-15; Matches 430; Conservative 376; Mismatches 906; Indels 713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A4E244001A4EBA01 CRC64;
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                                                                    LSPGIYDDTSARRIPVSYQNTMSRGSPMMNRTS-DVTIPPNKST-----NHERKSTLTPT 1524
                                                                                                                                                                 QRESIPAKSPVPGVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAA 1584
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                    ------PIEEA-----
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4584 --TITEEIPTE--PEVQEIIEEIEEEEKPAEYVIEVKESQPEA----------
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STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
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                                                                                                                                                                                                             EPEK-PAEAIVEEEEPVVTE---
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298541
10 0208541
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DT 01-0CT
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DF X2C2A.
GN X2C2A.
GN Caenor
CC Eukary
CC Rhaddi
OX NCBLLI
RN [1]
RN SEQUEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297 FEQASTIPDRPPLPARLPTVDEPIVISEQHEEDRSSATSGADYERSFDQEVTYERSSPLL 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPARLPTVDEP--IVISEQHEEDRSSATSGAD------YERSFDQDVTYE--K
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                                                                                                                                                                                                                                                                                                                                                          Query Match 3.6%; Score 449.5; DB 5; Length 4900; Best Local Similarity 19.6%; Pred. No. 2.5e-15; Matches 584; Conservative 388; Mismatches 1098; Indels 917;
"Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                               SERAIN-BRISTOL N2;
STRAIN-BRISTOL N2;
Waterston R.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006731; AAF60483.1; -.
SEQUENCE 4900 AA; 551244 MW; D837F46317C902D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                          Query Match
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	696 937 747 997 800 1045 849 1104 872 1104 1124 958 1277 1081 1189 1183 1189 1189 1189 1189 1189 11	VSOCESVASTVSAQEDEDIE-ASNEEBRPEDSEVEAVKPSEDSFERATERGO  SEIDHIAMIQSIAEQSSPEGASTVPDRPPLPVRLPTVDEPIVSEGUEDDRSSATSGAD  TERAVELEPTTETAPSTSPIANPSTRPAEDESVETQWNDSISAETAEQUEOPEIDHIAMIOSIA  QCHERAREOSVODPPP ATKADSTVDVBPPLPVRLPTVDEPIVSEGUEDDRSSATSGAD  ### ASRKVEPRDEDLY	
g &	1811	APKA	
P C	1866	AFARQUESFGILD LISARRIFYSIQNIMSROS FMMMKISDYIIFFUNSINAE   :	
Qγ	1517	-RKSTLTPVPGVD-PVV 1542	

:|: || :| | :| | 1926 GDRSSATPGADYERSYDQDVTYERSSPLLEPKQSSFEQASTIPDRPPLPVRLPTVDEPIV 1985 1543 SHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRA---LDPAAAAYLFQRQLSPTPGYPS 1599 1600 QYQLYAMENTRQTILNDYITSQQMQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMP 1659 2069 VRLPTVDEPIVSSEQHEEDRSKQSSFEQASTIPDR----PPLPVRLPTVDEPIVSSEQHE 2124 TQETM-----LQQRPSVFQGTNGTSVITPLDPTAQLRIMPLPAGGPSISQGLPASRY 1814 2217 HEDDRSSATSGTDYERSFDQDVTYERSSPLLEPCEDPVMESKEP--ELTQEEIDHIAWIQ 2274 SIARQSSFEQ-----PIVSSEQHED 2313 LRTRGKTTITAANFIDVIITRQIASDKDAR-ERGSQSSDSSSS--LSSHRYETPSDAIEV 1975 ISPASSPA-----RQYEGPLH 2015 ODFTYBRSSPLLEPCEEPVMESKKPELTQEE------IDHIAWIQSIAEQSS 2469 ---SFDDKVEDHGVVMSQPMGVVPGTANTSVVTSGETRREEGDPSPHSGGVCKPKLISKS 2330 2673 YERSFD---QDVTYERSSFL-LEPCEEPVMESKEPELTQEEIDHIAWIQSIAEQSSFEQA 2728 ---PILLVP------HPGGTSTPPMDRITYIPGTQITFPPRPYNSASM-----SPGHP 1703 1704 THLAAAAS-AERERERERERERERIAAASSDLYLRPGSEQPGRPGSHGYVRSPSPSVR 1762 NTAADALAAL------VDAAASAPQMD----VSKTKESKHEAARLEENLRSRSA 1858 AVSEQUQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEE 1918 2364 IARIQSLAEQSSFEQASTVPDRPPLPVRLPTVDEPIVSSEQHEDDRSSATSGADYERPFD 2423 H---YRPQQ-----ESPSPQQQLPPSSQAEGMGQVPRTHRLITLADHIC--QIITQDFA 2064 2065 RNQVSSQTPQQPPTSTFQNSPSALVSTPVRTKTSNRYSPESQAQSVHHQRPGSRVSPENL 2124 2125 VDKSRGSRPGKSPERSHVSSEPY-EPISPPQVP-VVHEKQDSLLLLSQRGAEPAEQRNDA 2182 RSPGSISYLPSFFTKLENT-SPMVKSKKQEIFRKLNSSGGGDSDMAAAQPGTEIFNLPAV 2241 2624 IPTPSSSFEQASTVPDRPPLPVRLPTVDEPIVSSEQH------EDDRSSATSGAD 2672 STVPDRPPLPVR--LPTVDEPIVSSEQHEDDRSSATSGADYERSFDQDVTYERSSPLLEP 2786 NSRKSKSPIPGQGYLGTERPSSVSSVHSEGDYHRQTPGWAWE---DRPSSTGSTQFPYNP 2387 1986 SSEQHEDDRSSATSGADY----ERSIDQEVTYERSSPLLEPCEEPVMESKK-----2033 1660 1763 2169 1815 2275 1919 1976 2016 2424 2183 2566 2242 2274 2331 2729 1859 g δy 셤 οy Dp δ g δλ qq δ g δŽ Ω g g g δy οy g δy Dp δλ g В ŏ g οy δy οχ δ 음 ŏ

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                                                                                                                                                                                                                                                                                                               Science 270:293-296(1995).
-!- FUNCTION: THIS GIANT MUSCLE PROTEIN MAY BE INVOLVED IN MUSCLE ASSEMBLY AND IN MAINTAINING THE STRUCTURAL INTEGRITY OF SARCOMERES. MAY HAVE PROTEIN KINASE ACTIVITY.
-!- ALTERNATIVE PRODUCTS: A NUMBER OF FORMS OF THIS PROTEIN ARE PRODUCED BY ALTERNATIVE SPLICING WHICH DIFFER IN TISSUE DISTRIBUTION. DIFFERENT SIZE TRANSCRIPTS MAY ALSO EXIST WITHIN ANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6122 VSKKTVV----EEKRFVAEE--KLSFAVPORVEVTRHEVSAEEEWSYSEEEEGVSISVYR 6175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5901 HTKKMVISEEKMFFASHTEEEVSVTVPEVQKEIVTEEKIHVAVSKRVEPPPKVPELPEKP 5960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                || | ::: :: | : || || || 6064 VPEIPK--KKVPEERKPPPRKEEVPPPRKVPALPKKPVPEEKVAVPVPVAKKAPPPRAE 6121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 AFGGK-HEAPSSPISGQ----PCGDDQNASPSKLSK-----EELIQSMDRVDR---- 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYEPFHPGPSPVDHDSLESKRPRLEQVSDSHFQRVSAAVLPLVHPLPEGLRASADAKKDP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENIKTNQ------VMRKKLILFFKRRNHARKQREQKICQRYDQLMEAWE 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 HQQEFAVPD---YRSSHL--EVSQASQLLQQQQQQLRRRPSLLSEFHPGSDRPQ-ERRT 87
                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last annotation update)
TITIN, SKELETAL MUSCLE ISOFORM (EC 2.7.1.-) (CONNECTIN) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SIMILARITY: BELONGS TO IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 90 IMMUNOGLOBULIN C2-LIKE DOMAINS.
EMBL, X90569; CA6A6189.1; -.
HSSP: P56276; 1TLK.
InterPro; IPR003006; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; 1g; 59.
SMART; SW00408; IGc2; 1.
Muscle protein: Cytoskeleton; Structural protein; Phosphorylation;
Serinc-threonine-protein kinase; Alternative splicing; Repeat;
Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                               ONE TISSUE.
TISSUE SPECIFICITY: MUSCLE-SPECIFIC.
SIMILARITY: TO THE CATALYTIC DOMAINS OF OTHER SERINE/THREONINE
                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-SKELETAL MUSCLE;
MEDLINE-96026330; PubMed=7569978;
Labeit S., Kolmer B.;
"Titins: giant proteins in charge of muscle ultrastructure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.5%; Score 444; DB 4; Length 7962; Best Local Similarity 18.3%; Pred. No. 9.5e-15; Matches 463; Conservative 332; Mismatches 934; Indels 804;
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                    PRELIMINARY;
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                                                                                                                                                                             NCBI_TaxID=9606;
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Q10465;
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ATIARSEHE 379   : :   APVPKKEKV 6268	) RQFMNV 439 :   : FEKHMQI 6308	NENYKAL 490 	SEKKDEE 536	-REEEYEEYE 6414	TTNEAAA 595    ERYE 6445	AIAKMVG 655	-KVPVPIPKKL- 6497	DEDEDIE 715      : REKEQV- 6528	STSP 765	:  PRKEVAP 6557	ADSVDV- 824	ITEEEVVPVI 6611	EPOSDND 878	[ 914	PEVPKK 6731	KAMHESAL 972       -VDEFEVI 6785	_		: K 684	K 684	K 684 S 108 E 687	684 108 687 114	684 108 687 114 114	E 687 T 114 P 693 E 119	K 684 S 108 E 687 T 114 P 693: E 119:	K 684 S 108 E 687 T 114 E 119 E 125:	684 108 114 114 693 693 115 125 125	684 108 1108 114 119 693 125 125 131
ທີ່	EQENNEKOMRQLSVI PPMMFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNV ::	KDKFIQHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYKAL   : :	EDKAEKTEKKEEEKKDE	YTLEEEAVSVQ-REI	-DSKENTKEKDKIDGTAEETEEREQATPRGRKTANSQGRRKGRITRSMTNEAAA :      -   - FEEYEPTEEYDQYEEYEEREY	ASAAAAATEEPPPPLPPPEPISTEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAKWG  :	KAPPAKVLKKAVPEE-KVPVI	TKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRKPREERQVSQCESVASTVSAQEDEDIE	LEPTTETAP-	::      : EPAAKVPMKPKRVVAEEKVPVPRKEVA	AEQMDVDQQEHSAEEGSVCDPPPATKAD	IHEEEEFITE	EVRVPENHASKVEGDNTKERDLDRAS-EKVEPRDEDLVVAQQINAQRPEPQSDND  :	DVDGEPERQRMFPMDSKPSLLNPTGSI	:  :  : :   : :   :   :   :   :   :   :		VLFE		REEF	EEEF	REEF	DASY.	BEEF QASY VVRG EEPP	EEEF QASY VVRG EEPP GSIS	EEEF OASY VVRG EEPP GSIS APPA	TESTYPEEEEFVPEE  (LTSHNQASYTOETI  (LTSHNQASYTOETI  )  RAQHEGVVRGTAGA.  SEEIPEEPPSIEE  SALVK-GSISRMP-  PYQKKEAPPAKVPEI  TI    PYQKKEAPPAKVPEI  STRSPRTAHEISLKI  LEVVEAEVEEIPEEPEII  LEVVEAEVEEIPEE	PEEEEVLPEEEEVLPEEEETPPEEEETPPEEEEV-PPEEEVPEEEEVLPEUT	CERETY PPEEEEYVPEEEEFVPEEEVLPEV   CSISQGTPGTYLTSHNQASYTOETPKPSVG   CSISQGTPGTYLTSHNQASYTOETPKPSVG   CONTRACT   CONTR
EKOFPEIRKOREQOERFORVGORGAGI   :   EKKVPE	IPPMMFDAEQRRVKFII :   : VPPKVIK	KNFGLIASYLERK:   :  KR	VEEKE	-TEFRKRVVKEEKVSIEAPKREPOPIKEVTIMEEKERAYTLEEEAVSVO	AEETEEREQATPRGRKT/ 	PVETSRWTEEEMEN	1	HKOKISRKPREERI   :     : -KPPPPKVPEEPKI	TSRGNTEPAVELEP	TEPAAKVPA	TAEQMDVDQQEHS!		KERDLDRAS-EKVEPRDI  :::	-DVDGEPERQRMFI	:   :   :   PEVPKKPI	1 2	LEFOROROGO I DLECRSSTSPCGTSKSPNREWEVI OPAPHOLITA			Ţ.	; <b>5</b> ;	The problem of the property of the property of the problem of the	TAPPEEEEVPPEE TMGGSISQGTPGT) TMGGSISQGTPGT) PRSONSQPEGILLVF :   :   :   :   :   :   :     :     :					
SAIREII : : APKKIVP	NEKOMROLSVIPP   : :   PEKKVPP	KDKFIQHP   : :   KEAPPKARVPEEP	DIARPSQEEK-	KVSIEAPKREPQP	KEKDKIDGTAEET :   :    EEYDQYEEY	PPLPPPPEPISTE	PVKPVPEEPVPTK	KRRHNLDNLLQQ	EVEAVKPSEDSPENAT		AEDESVETQVNDSISAET	PEEVAFEEEVVTHVEEYLVEEEEEY	SDNTKERD		PVPKKVEAPPAKV	PQLQHRAAVIPPM : :    vpkkvrapppk	CRSSTSPCGTSK		: PEEEVLPEEE	: CPEEEVLPEEEE CTVASEKPSF	: LPEEEVLPEEEE TTVASEKPSF'   :     KKVTEKKVVIPK-	LPEEEVLPEEEE  TTVASEKPSF  I	CTVASEKPSF  TTVASEKPSF  (KVTEKKVVIPK-SATLPYIRGEFSI	: CTVASEKPSF  (TVASEKPSF              CKVTEKKVVIPK- SATLPYIKQEEFSI RILLPKEEEVLI RILLPKEEEVLI PSLKGSITGGTAFPAI PTPVKKVEAPPAI	LPEEEEVLPEEEIIPPEE TTVASEKPSFIMGGS K	TPEEEEVLPEEEE  TTVASEKPSF	TPEEEEVLPEEEE  TTVASEKPSF  (KUTEKVVIPK- SATLDF1KQEEES  AILLP-KEEEVL SERGSITGGTPA SELRGSITGGTPA STROWYYEGKSGH:	TTVASEKPSF  (KVTEKKVVIPK- SATLPYINGEES SATLPYINGEES SATLPKEEEVL SILLDKEEEVL SILLDKEEEVL STROPPRINGES SKGHVIYEGKSGH SKGHVIYEGKSGH SKGRTVLEEKVSV
KKVDRIENNPRRKAKESKTR   :        ::: KIPAKIEEPPPAKVPEAPKK	ISEIIDGLSEQENNEKQ : : :   : PPPKVPEEPKKPVPEKK	WTDHEKEIFKDKFIQHPK       : :     -TQEEKVLVAVTKKEAPPKARVPEEPK	VRRNYGKRRGRNQQIA	V-TEFRKRVVKEE	EKDEKE-DSKENTKEKDKI        :    :   : EYDYKEFEEYEPTEEYDQY	ASAAAAATEEPPI  :	<b>ЕНЕЕҮІТЕРЕКРІРУКРУРЕЕРУРТКР</b>	TKSEAQCKNFYFN	ASNEEENPEDSEVI		KPAEDE	PVRVPEV-PKELEI	EVRVPENHASKVEGDN  :    PVKVPEVPRKPVPEEK	SSATCSADE	: I VPKKPVPEEKVPVI	LVSSPLKPNPLDLPQLQHRAAVIPPMV  -  - 	LEEOROROEOIDLE		PEEEEVLPEEEEVLPEEEESTPPEEEEV	PEEEVLPEEEVLPEEEV PTRPPPPLIPSSKTTVASEK	PEEEEVLPEEEVLPEEEVLPEEE PTRPPPLIPSSKTTVASEKPS	PEEEVLPEEEEV PTRPPPLIPSSKI       :   PKVPYPAPVPEIKI ISLGLPRQOESAKG	PEEEEVLPEEEEVLPEEE PTRPPPLPSKTTVAS PKVPVPAPVPEIKKKVTE ISLGLPROGESAKSATLP I	PEEEEVLPEEEEVLPEEEE PTRPPPLIDSKTTVASEKPSF                 PKVPVPAPVPEIKKKVTEKKVVIPK- ISLGLPROGESAKSATLPYIKGEEFS                           	PEEEVLPEEEV PTRPPPLIPSSKY PKVPVPAPVPEIKI ISLGLPRQQESAKK :	PEEEVLPEEEEV PTRPPPPLIFIE PKVPVPAPVPEIKE ISLGLPRQGESAKE ISLGLPRQGESAKE ISTGLPRQESAKE VPKKVEE-KE RGTPTSKISVESIE H           RVPEVIKKAVPEA KGREEAAS	PEEEVLPEEEV PTRPPPPLISE PKVPVPAPVPIKE ISLGLPRQGESAKE ISLGLPRQGESAKE ISTGLPRYEE-KE VPKKVEE-KE KGTPTSKISVESIE H	PEEEEVLPEEEE PTRPPPLIPSSKTTVASE
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                                                                                                                                                                                                                                                                                                                                                                                                 1610 RQTILNDYITSQQMQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGG 1669
                                                                                                                                                                                                                                                                                                                                                                                                                                    1670 TSTPPMDRITYIPGTQI-----TFPPRPYNSASMSPGHPTHLAAAASAEREREREREK 1722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7317 PEVPP-TKVPEVPKVAVPEKKVPEAIPPKPESPPPEVFEEPEEVAL-----EEPPA 7366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | | | | : | : | : | 3367 EVVEEPEPAAPPQVTVPPKRAPAVVAKKPELPPVKVPEVPKEVVPE----KKV 7421
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                            ERERERIAAASSDLYLRPGSEQPGRPGSHGYVRSPS-PSVRTQETMLQQRPSVFQGTNGT 1781
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LKYPKQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHEIPRQDILTQESRKTPEVV 1371
                                                                                                                                                                                                                                       1492 MSRGSPMMNRTSDVTIPPNKSTNHERKSTLTPTQRESIPAK--SPVPGVDPVVSHSPFDP
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                                                                             QSTRPIIEGSISQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVE
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                                                                                                                                                                                                7179 PAK-----EVVPEKKVPV-----
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---RAESPPPEV-YEE------
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                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Bukaryota: Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pteryota: Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidea; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003598; --
Pfam; PF00018; SH3; 1.
Pfam; PF00011; fn3; 5.
Pfam; PF00041; fn3; 5.
PROSITE; PS00179; AA_TRNA_LIGASE_II_1; UNKNOWN_1.
SMART; SM00408; IGC2; 1.
SEQUENCE 16215 AA; 1841509 MW; 242C8765E00F7603 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.5%; Score 442; DB 5; Length 162
Best Local Similarity 18.9%; Pred. No. 3.2e-14;
Matches 482; Conservative 363; Mismatches 906; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 QGAFSTEQSRYPPHSVQYTFPNTRHQQEFAVPDYRSSHLEVSQASQLLQQQ-
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Zhang Y.Q., Broadle K.S.;
Zhang Y.Q., Broadle K.S.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, A371740; CAB93524.1; -.
Flybase; FBQM0010396; sls.
InterPro; IPR001452; -.
                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                      PRT; 16215 AA
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SLS OR KET OR D-TITIN OR CG1915.
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                                                                                                                01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                      PRELIMINARY,
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7850 -KHRFIADGKDRK 7861
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NCBI_TaxID=7227;
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Q9NFS3
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g	5628 GKKKIPKS	GKKKIPKSEPTEEVHPDEVDAQIETVVKEDEMIVEEKRRIKKTKRPKSTKEVTEELFEEQ	5687	
δy	346	LSE	389	
g	5688 PEEEISPE	PEERISPEEEVPQKEVIEEIEEIVEEKRRIKKTKKPKLTQQVTEEETPHEEII	5740	
6 6	390 QENNEKQM : :   5741 KESEEVVQ	IFK   IPT	449 5781	
ογ	450 DKFIQHPK	LERKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGRNQQI	505	
g	: :: 5782 EETVE	EEETAEDQQLVVEESKKVKKPTGTVEKTDVEELPGEEV	5827	
9 9	506 ARPSQEEK   :  5828PVEEVP	ARPSQEEKVEEKEEDRAEKTEKKEEEKKDEEKDEKENDKEKDKIDGTAEETE	562 5884	
οy	563		599	
g	5885 EEDQPEEE	EEDQPEEEVLQEEIIGEQEEITERQRKVKSIKKPKKVVTEKTVDQTEQPEKPEESQAEEV	5944	
6 G	600 AAAATEEPI           5945 KETVTEEPI	AAAATEEPPPPLPPPPEPISTEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAK	652 6004	
γ			709	
e G	6005 AEQPETPE	AEQPETPETEFEVKEFAITTTEDILDVTKKRVKKKKPVTKVAAE	6048	
oy B	710 EDEDIEAS   :   6049 ESTEEPAE	EDEDIEASNBEENPED-SEVEAVKDSEDSPENATSRGNTEPAV-ELEPTTETAPSTSPSL	767 6093	
ð á	768 AVPSTKPAI	AVPSTKPAEDESVETQVNDSISAETAEQMDVDQQEHSAEEGSVCDPPPATKADSVDVEVR	827	
3 3	;		/*10	
<u>6</u> 6	828 VPENH :   6148 LEEVDLQH	VPENHASKVEGDNTKERDLDRASEKV-EPRDEDLVVAQQINAQRPEPQSDNDSSATC:	883 6193	
ò t			928	
9 8			6243	
<u>8</u>	929 QLQHRAAVIPPMVSCT :   :   :   :   :   6244 EQQPEEVQLKPIPS	PCNIPIGTPVSGYALYQRHIKAMHESALLEEQRQROEQIDLECR 	988 6 <b>2</b> 89	
Š d	989 SSTSPCGT	SSTSPCGTSKSPNREWEVLQPAPHQLITNLPEGVRLPTTRPTRPPPPLIPSSKTTVASEK ::   : :   : : : : : : : : : : : : : :	1048	
2		GOOGG 1DISISSANGAGAGAGAAAAAAAAAAAAAAAAAAAAAAAAAA	1005	
; a	_ 4	EEDEVEEMPVDDVKVVAVSEDVLP-EEE	6366	
ογ	SAKSA :	PTSKISV :	1155	
g	6367 VVPTEETPI	LKEASVEGOPQLLEAAIAEIKEASVEGOPQLLEAAIAE	6407	
δ'n :		ESIPSLRGSITQGTPALPQTGIPTEALVKGSIS	1188	
8			6466	
දු පු	1189 -RMPIEDS:  :::     6467 RRVVLDDS(	-RMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIKNAREGTRSPRTAHEIS :  : ::	1242 6524	
ρλ			1300	
අ	6525 LVKKKKE	LVKKKKKEIKPPRITEKLRPROCVPEEPTVLECKVEGVPFPEIK	6568	

PRT; 5170 AA.

PRELIMINARY;

RESULT 31 Q17490 ID Q17490

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Gaps 126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1105 EHFEEQETGKSSPAPSSHVES-ERQVLESPVASDPRH-VMETTTTTTVTRQFHDDESERS 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1163 DSPNRDVV--EAQSIHSSNIESHQQFSEKDDDSQRGPSPVKSEDEPVKHESYKFETSTTE 1220
                                                                                                                                                                                                                                              MEDLINE-94150718; Pubmed-7906398; Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Jones M., Rershaw J., Kirsten J., Mortimore B., O'Callaghan M., Parsons J., Percy C., McMurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R., Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thiery-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watenstock L., Wilkinson-Sproat J., Wohldman P.; R.2. Mb of contiguous nucleotide sequence from chromosome III of C. elegans ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---YDENRKKAEEAHKIFEGLGPKVELPLYNQPSDTKVYHENIKTNQVMRKKLILFFKRR 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 QQQ--QLRRRPSLLSEFH-----PGSDRP----QERRTSYEPFHP-GPSPVDHDSLES 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 KRPRLEQVSDSHFQRVSAAVLPLVHPLPEGLRASADA-KKDPAFGGKHEAPSSPI----S 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            895 KVLGFAKKAGMVAGGVVAAPVALA---AVGAKAAYDAFEKDDEDDETSHSPESPVPEYQS 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQPCGDDQNAS-----PSKLSKEELIQSMDRVDREIAKVEQQILKLKKKQQQLEEE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NHARKQREQKICQRYDQLMEAWEKKV--DRIENNPRRKAKESKTREYYEKQFPEIRKQRE 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        355 QQERFQRVGQRGAGLSATIARSEHEISEIIDG-----LSEQE--NNEKQMRQLSVIP 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSEQQSEEPHIVKETTTTTTTTTTTELYDEPEKGNVTFSPAPSSHAESERQVPESPVVSHQE 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----AVPDYRSSHLEVSQASQLLQQQ 60
                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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575856 MW; 27C2DFBF4AE03A7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gattung S.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 AA-----KPPEPEK----PVSPPP---VEQKHRSIVQII----
                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
CODED FOR BY C. ELEGANS CDNA YK11B8.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 STEQSRYPPHSVQYTFPNTRHQQEF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 368:32-38(1994)
                                                                                                                         Caenorhabditis elegans
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EMBL; U50071; AAA93447
SEQUENCE 5170 AA; 5
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                          NCBI_TaxID=6239;
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ολ	405 PMMF	DAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHEKEIFKDKFIQHPK	459
qq	1221 TREF	: :     :     :     :     :     :     : :   : :     : :   :   : :     : : :   : : :   : : :   :	1261
δλ	460	GLIASYLERKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEK	513
qq	1262 SEYGSE	GHYPSVIETKTTTYTREFYDDDQDE	1313
ογ	514 VEEK 	EEDKAEKTEKKEEEKKDEEEKDEKEDSKEN :  :  :  :	568
qq	1314 HEGSI	HLFKETTTTTTTTTTTAREFYDEPENVEELQDPQFSPAPSSHVESGIHASESPVAQQQEI	1373
ΟŊ	569 PRGR	PRGRKTANSOGRRKGRITRSMINEAAAASAAAAAATEEPPPPLPPPPEPISTEP 	622
qq	1374 PQ	TREFHEDSPAAQYFHEEEYESHVLTEQAPLLTEQQHQPESGDE	1418
Qγ	623 VETS	VETSRWTEEEMEVAKK-GLVEHGRNWAAIA~KWVGTKSEAQCKNFYFNYKRRHNLDNLLQ	089
qq	1419 SDGE	GGLGSKVLGFAKKAGMVAGGVVAAPVALAAVGAKAAYDALKKDDDEEDQEERESLLR	1478
δλ	681 QHKQ	)DIEA	716
Q	1479 QERS	QERSIDSPHASEQSQIEEEHERFEESPVPSEKHHVTETTTTTTTTTTFDEHEPLVSQEI	1538
δλ	717 SNEE	SNEEENPEDSEVEAVKPSEDSPENAT-SRGNTEPAVE	752
QC	1539 EGEK	EGEKGSPADSEKSLPHVVETTTTTTTTTTTTTSEDKNDSESPVPSEKEQEPTTVSREVYETAEG	1598
QY	753 LEPT	TETAPSTEDESVE	781
qq	1599 DEPE	TKEVIDDSQEMGDDDEPKQESPQVVET	1658
Οy	782 TQVNDSI	QVNDSISAETAEQMDVATKADSVDV	824
qq	1659 SEAG	:	1718
δŏ	825 EVRV	EVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCS	884
qq	1719 EVRP	AAPISFS	1771
δλ	· 885 ADED	IdNd	932
qq	1772	HDQHDRESPVESEKSVKHTTETTTTTTTTTVTRQLYDDEASEIRGESPVATEEHEH	1824
Qy	933 RAAV	IPPMVSCTPCNIPIGTPVSG	982
qq	1825	VSSTKSDDESEQHVPSVIETTTTTTTTVTREFYDDQDELQRE	1866
Qy	983 IDLE	IDLECRSSTSPCGTSKSPNREWEVLQPAPHQLITNLPEGVRLPTTRPTRPPPPLIPS	1039
q	1867 TQSE	SERRSSIPTEETEHEDSHLIKETTTTTTTTTTFFYDEPENVEK	1911
ογ	1040 SKTT	VASEKPSFIMGGSISQGTPGTYLISHNQAS-YTQETPKPSVGSISLGLPRQQESAK	1098
qq	1912 LQDS	LODSQFSLSPSVAKQQEIPQ	1944
οy	1099	SATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVRGTAGAIQEGSITRGTPTS	1151
qq	1945 TREF	TREFHEDSPAAQYFHEDEYEHQVPTEQAP-LLTEQQHQPESGEESDGEGFG	1994
Qy	1152 KISV	KISVESIPSLRGSITQGTPALPQTGIPTEAL-VKGSISRMPIEDSSPEKGREEAASKGHV	1210
qq	1995 S-KV	KVLGFAKKAGWVAGGVVAAPVALAAVGAKAAYDALKKEDDEEDQEERESL	2045
δλ	1211 IYEG	YEGKSGHILSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPLE	1270
qa	2046 IREE	RSFDESPVPSEKH	2080
δλ	1271 GLIC	GLICRALPRGSPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYPKQIKRESPPIRAF	1328
Ę	2041 1000		2129

us-09-522-753-11.rspt

6 B 6	1329   BCAITKGKPYDGITTIKEMGRSIHEIPRODILIQESRKTPEVVQSTRPIIE	g & £	3031 SGSPVPSEKSVERVIEJ 2235 IFNLPAVTTSGSVSSRGHSFAL 3086 VHGOTOMMUMUMTSHEHVUD	ERVIE GHSFA I
8 8 8	2184 RQGSYSSGYSPKSPGGSITGLDEEKALSGVQEPEDRPENFAESHEKTE 2231 1428KVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTS 1480	k da		TRREEGDPSI
ç a	NTMSRGSPMANRTSDVTIPPNKSTNHERKSTLTPT-QRESIPAKSPVPGVD	δδ GD	2343GYLGTERPSSVSSV 13188 TTVTREHFDTEEDYIPSESRTE	SSVSSV   : SESRTS
oy do	PHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTEGYPS	Qy	IVESHEYKSES	PSSTGSTQF          SIPSEQDSTH-
oy B	1600 QYQLYAMENTROTILNDYITSQQMQVNLRPDVARGLSPREQPLGLPYPATRGII 1653 ::	Qy QD	2420WEREPAPLLSP :   :   : 3302 STAQYYKSESPVQTEKSLLLAR	-WEREPAPLLSP :   :   ! PVQTEKSLLLAR
\$ g	1654 DLTNMPPTILVPHPGGTSTPPMDRITYIPGTQITFPPRPYNSASMSPGHPTHLAAA 1709 	SU 73	LT 32 43 Q17343 PRELIMINARY	.RY;
o d	1710 ASAER		Q17343; 01-NOV-1996 (TrEMBLrel. 01-JAN-1998 (TrEMBLrel. 01-MAR-2001 (TrEMBLrel.	11. 01, 11. 05, 11. 16,
QY Dp	1746GETMLQQRPSVFQTN 1779 1746	OC C C C C C C C C C C C C C C C C C C		ıs. Tematod
Oy Dp	1780 GTSVITPLDPTAQLRIMPLPAG-GPSISQ	OC NR RP RP	Rhabditidae; Peloderinae; NCBI_TaxID=6239; [1] SEQUENCE FROM N.A.	nae; C
Oy Dp	1808GLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAVSEQQ 1864 	RX RA X	STRAIN=N2; MEDLINE=95263663; Pubmed=77 Otsuka A.J., Franco R., Yan Boontrakulpoontawee P., Jey	Med=77 , Yan , Jey
oy Ob	1865 QLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELR 1920 	RA RT RL	Sobery A.; "An ankyrin-related gene (uguidance in Caenorhabditis J. Cell Biol. 129:1081-1092	ene (u ditis 11-1092
oy Ob	1921 TRGKTTITAANFIDVIITRQIASDKDARERGSOSSDSSSLSSHRYETPSDAIEVISPAS 1980 1921 TRGKTTITAANFIDVIITRQIASDKDARERGSOSSDSSSLSSHRYETPSDAIEVISPAS 1980 2700 TETVRTTTVTREYLDDPOSVTRSRSPSEHDISEQYAPES 2738		[2] REVISIONS, AND SEQUENCE OF STRAIN=N2; Otsuka A.J.;	CE OF
ç q	1981	RL DR DR	Submitted (DEC-1996) to the EMBL; U39847; AAB41827.1; -EMBL; U21733; AAB38384.1; -HSSP; P42773; IIHB.	to the 7.1; -
oy Og	2018 2025       : 2797 KTTTTIKEVHVPVEEDVQISPVHSETSVSEKOLPADEQLDEPVTESTTATVTRERYEE 2856		InterPro; IPR000488; InterPro; IPR000906; InterPro; IPR001360; InterPro; IPR002110;	
oy Oy	2026 PQQQLPPS-SQAEGMGQVPRTHRLITLADHICQI-ITQDFARNQVSSQTPQQPPTSTFON 2083  :           :     :   :   :   :   :		InterPro; IPR002383; Pfam; PF00023; ank; 24. Pfam; PF00531; death; 1. Pfam; PF00791; ZU5; 1.	. <del></del> .
Qy Db	2084 SPSALVSTPVRTKTSNRYSPESQAQSV		PRINTS; PRO0001; GLABLOOD. PROSITE; PS50088; ANK_REPERPROSITE; PS50297; ANK_REP_REPROSITE; PS50017; DEATH_DOM	LOOD. REPEA REPEA
Oy	2123 NLVDKSRGSRPGKSPERSHVSSEPYEPISPROVPVVH-EKQDSLLLLSGRGAEPAEGRND 2181 1::	DR SO SO	PROSITE; PS00572; GLY SMART; SM00005; DEATH SEQUENCE 6994 AA;	COSYL_ 1, 1. 775364
0y	2182 ARSPGSISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGGGDSDMAAQPGTE 2234	eno	Query Match	3.5%;

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SPHSGGVCKPKLISKSNSRKSKSPIPGQ----- 2342
                                                                                                                               | : : | | | EDDHSHVVESQEYSASG----SPVPSEKSVERVIETTTT 3187
                                                                                                                                                                                                                                      DEPYNPLIMEMLSSIPPIPIACAPSAVNQAAPHQONRI-- 2419
                                              ADPASNLGLEDIIRKALMGSFDDKVEDHGVVMSQPMGVVP 2294
                                                                                                                                                                                                                                                            oda; Chromadorea; Rhabditida; Rhabditoidea; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7744957;
ang B., Shim K., Tang L.Z., Zhang Y.,
eyaprakash A., Hedgecock E., Wheaton V.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (unc-44) is necessary for proper axonal s elegans.";
92(1995).
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    Created)
    Last sequence update)
    Last annotation update)

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_REGION; 1.
OMAIN; 1.
L_HYDROL_F1_1; UNKNOWN_2.
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                                                                                                                                                                                                                                                                                                     SAQYETLSDSDD 2440
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AKQQQESGDESD 3333
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Best Local Similarity 18.7%; Pred. No. 1.7e-14; Matches 556; Conservative 356; Mismatches 1102; Indels 958; Gaps 126;	14 STEQSRYPPHSVQYTFPNTRHQQEFAVPDYRSSHLEVSQASQLLQQQ 60	61 QQQQLRRRPSLLSEFHPGSDRPQERRTSYEPFHP-GPSPVDHDSLES 106 : :   :	107 KRPRLEQVSDSHFQRVSAAVLPLVHPLPEGLRASADA-KKDPAFGGKHEAPSSPIS 161	162 GQPCGDDQNASPSKLSKEELIQSMDRVDREIAKVEQQILKLKKKQQQLEEE 212 	213 AA	240YDENRKKAEEAHKIFEGLGPKVELPLYNQPSDTKVYHENIKTNQVMRKKLILFFKRR 296 ::  :  :  :	297 NHARKQREQKICQRYDQLMEAWEKKVDRIENNPRRAKESKTREYYEKQFPEIRKQRE 354 	355 QQERFQRVGQRGAGLSATIARSEHEISEIIDGLSEQENNEKQMRQLSVIP 404  1 :	405 PAMFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNF 459	460GLIASYLERKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEK 513	514 VEEKEEDKAEKTEKKEEEKKDEEEKDEKEDSKENTKEKDKIDGTAEETEEREQAT 568  13138 HEGSHLFKETTTTTVTREFYDEPENVEELQDPQFSPAPSSHVESGIHASESPVAQQQEI 3197	569 PRGRKTANSQGRRKGRITRSMTNEAAAASAAAAATEEPPPPLPPPPEPISTEP 622	623 VETSRWTEEEMEVAKK-GLVEHGRNWAAIA-KMVGTKSEAQCKNFYFNYKRRHNLDNLLQ 680 : :	681 QHKQDIEA 716	717 SNEEENPEDSEVEAVKPSEDSPENAT-SRGNTEPAVE 752	753 LEPTTETAPST	782 TQVNDSISAETAEQMDVDQQEHSAEEGSVCDPPPATKADSVDV 824 1	825 EVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCS 884
Best Match						~		~					m				E	

q	3543	EVRPDEPHIIETTTTTTTTTTTTTTT37873595
οy	885	ADEDVDGEPERQRMFPMDSKPSLLINPTGSILVSSPLKPNPLDLPQLQH 932
qq	3596	HDQHDRESPVESEKSVKHTTETTTTTVTRQLYDDEASEIRGESPVATEEHEH 3648
δý	933	RAAVIPPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEQRQRQEQ 982
Оþ	3649	SSTKSDDESEQHVPSVIETTTTTTTTTTTTTTTTTT 3690
δ	98	CGTSKSPNREWEVLQPAPHQLITNLPEGVRLPTTRPTRPPPPLIPS 103
op ,	3691	RSSIPTEETEHEDSHLIKETTTTTTVTREFYDEPENVEK 373
ογ	4	FIMGGSISQGTPGTYLTSHNQAS-YTQETPKPSVGSISLGLPRQQESAK 109:    ::
qq	3736	LQDSQFSLSPSVAKQQEIPQ 3768
Qy	1099	SATLPYIKQEEFSPRSQNSQPEGLLVRAQHECVVRGTAGAIQEGSITRGTPTS 1151
qq	3769	TREFHEDSPAAQYFHEDEXEHQVPTEQAP-LLTEQQHQPESGEESDGEGFG 3818
å,	1152	KISVESIPSLRGSITQGTPALPQTGIPTEAL-VKGSISRMPIEDSSPEKGREEAASKGHV 1210
qq	3819	S-KVLGFAKKAGMVAGGVVAAPVALAAVGAKAAYDALKKEDDEEDQEERESL 3869
Qy	1211	IYEGKSGHILSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPLE 1270
QQ	3870	IREERSFDSPHASEQSQIEKEHKRFEESPVPSEKH 3904
δy	1271	GLICRALPRGSPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYPKQIKRESPPIRAF 1328
q	3905	HDQSSALPQESVSQPIEKESRTFNDESEFGVKSDHYTEDDQESLKSPKE 3953
δλ	1329	EGALTKGKPYDGITTIKEMGRSIHEIPRQDILTQESRKTPEVVQSTRPIE 1379
οp	3954	SGEAFSQFTSEKEQDRSDSPIHS-QKEDISQFQNESSPEDVKSEQPHDEEKPDLE 4007
δy	1380	GSISOGTPIKFDNNSGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENI 1427
QQ	4008	RQGSYSSGYSPKSPGGSITGLDEERALSGVQEPEDRPENFAESHEKTE 4055
Oy	1428	KVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTS 1480
QQ	4056	ATSDENLFESDKYAPASPVPSEDSSNRVIETTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
οy	1481	MNRTSDVT
qq	4105	YVVESQEYSSGSPVPSEKSVDRVIETTTTTVTREHFEAEDEIPTI- 4151
Qy	1540	PVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPS 1599
QO	4152	YESSHDDQAASPVPSEED 4169
Qy	1600	QYQLYAMENTRQTILNDYITSQQMQVNLRPDVARGLSPREQPLGLPYPATRGII 1653
q	4170	VHEQIQITITITITYKEHFVPDDEIDSEHMNESDKYASGSPVPSEEDSS 4218
Qy	1654	DLINMPPIILVPHPGGTSTPPMDRITYIPGTQITFPPRPYNSASMSPGHPTHLAAA 1709
qq	4219	RVTETTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
Οy	1710	ASAER
qq	4260	KSVERVIETTITITITITITITITITITITITITITITITITITI
δy	1746	GETMLQQRPSVFQGTN 1779
qq	4317	SNRDEEFVLPAIAPYKQPTEYGRVDSHDAPASPAPSAESPIQAYKQEESQEAHSLEGFQQ 4376
οy	1780	GTSVITPLDPTAQLRIMPLPAG-GPSISQ
qq	4377	RSSVSHEDSPAAQYFHDNESDHDSPVPSDRAPLLTEQQHQPESGEESDGEGFGSKVLGFA 4436

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SEQUENCE FROM N.A.
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                                                      QL----EQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELR 1920
                                                                                                                                                                    PVEQDPYVVEKTTTVIRQYHDEPPQEIEEQTIPEEVTVLREVYESP---EGDEPEQHYIET 4620
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          ---GLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAVSEQQ 1864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterrygota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                               4524 TETVRITI------VIREYLDD------PQSVIRSRSPSEH-----DISEQYAPES
                                                                                                                                                                                                                                                    -----PSPTEKSESQCY
                                                                                                 1921 TRGKTTITTAANFIDVIITRQIASDKDARERGSQSSDSSSSLSSHRYETPSDAIEVISPAS
                                                                                                                                               ----SPAPPQE-KLQTYQPEVVKANQAENDPTRQYEGPLHHY---
                                                                                                                                                                                                               KTTTTITKEVHVPVEEDVQISPVHSETSVSEKQLPADEQLDEPVTESTTTATVTRERYEE
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Last annotation update)
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                                                                          4490 VLVNPVEPSDSEISE--IELEYTS-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SISAETAEQMDVD----SUCDPPPATK 818
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                                                          development in
                                                                                                                                                                                                                                                                                                                                    Indels 709;
     ľ.,
                                                                                                                                                                                                                                                                             Length 1966;
  Roure A., Core N., Angelats C., Vola C., Fasano
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                                                                                                     Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AF217844; AAF34752.1; -. FlyBase; FBGn0020427; Gug. SEQUENCE 1966 AA; 208033 MW; 96AF90E2082E770C CRC64;
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                                                                                                                                                                                                                                                                          Query Match 3.4%; Score 433.5; DB 5; Best Local Similarity 19.6%; Pred. No. 5.3e-15; Matches 421; Conservative 243; Mismatches 770;
                                                       for proximal and ventral leg
Erkner A., Roure A.,
Kerridge S.;
"Grunge is required f
Drosophila.";
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ор	877	PLGRPFEPTGLMLKYGDPLAAKCGPPQDLKYPMPPVSQAGPADVKPYGGENLIKSSP 933		
οy	1056	SISQGTPGTYLTSHNQASYTQETPKPSVGSISLGLPRQQESAKSATLPYI 1105	δy	1959
q	934	YGPPPESPIDASARSTPGDOSQGSNSNSQP-PSPHP	QΩ	1808
ó	1106	KOEEFSPRSONSOPECLLVPAOHEGVVRGTAGAIOEGSITRGTPTSKISVESIP	Οy	1999
, d	626	SPHMPSP-AGGGLPPGMHPONI.THGPPPGAAGGSGPOPPPPTSLHOPTPTSAGPP	qa	1868
3 3	, ,	CONTROL OF THE PROPERTY OF THE	Qy	2044
<u>8</u>	1034	SLAKUSTUQUTPALPUTGIPTEALVKGSISKMPIEDSSPEKGREEAASKGH 1209    :	qa	1923
Qy	1210	VIYEGKSCHILSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVS 1266	RESULT	ILT 3
QQ	1076		0917 1D	703 Q917
Οy	1267	APLEGLICRALPRGSPHSDLKERTVLSGSIMQGT	AC DT	0917 01-M
QQ	1123	QQQQQQQQQQQP-GGPAGTVRTSSPAQQPPRSMHDPQSSREPPTSQ 1167	556	01-M
λo	1324	PIRAFEGAITKCKPYDGITTIKEMGRSIHEIPRQDILTQESRKTPEVVOSTRPIIEGSIS	GN OS	CG18 Dros
g ,	8011	PSTIMAGSSGFGGFPPPQSFHAHKISFLFGLAGSGFF-PFGLI	88	Euka
δ á	1384	OGTPIKFDSLITGPSLITGP	88	Ephy
2	1210		RN RP	$\frac{1}{8}$
ζς G	1411	SKLSRGMPPLEIVPENIKVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPK 1468  AII	R K C	STRA
3 8	1469	ACT COCTATION CADDIDAC COMMINDICATION TO DAIL CONTROL OF COMMINDICATION CONTROL CONTROL OF COMMINDICATION CONTROL COMMINDICATION CONTROL CONTROL COMMINDICATION CONTROL CONTRO	RA E	Aman
· 유	1316	ACLUS COLLUDOL CONTRACT V SU UN UN CONTRACTOR DE LA LITTE IN CONTRACTOR DE L'ACTUAL DE L'A	8 8 8	Sutt Bran
δ	1529	IPAKSPVPGVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPA 1581	RA RA	Wan
. q	1356		RA RA	Ball Bees
δy	1582	AAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITSQQMQVNLRP 1629	RA RA	Bork
Dp	1395	 AAAVAER	R R	Cher de P
<b>^</b>	1630	DVARGLSPREOPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTP 1673	RA RA	Dods
연	1449	HERPGASPPVIRHPOMPLPLALIAPGGGIPQIGV-HPGQSPYPHDLHPSVFYS	RA RA	Fosl
δ	1674	PMDRITYIPGTQITFPPRPYNSASMSPGHPTHLA 1707	<b>&amp;</b> &	Harr
qq	1502	:   :          PHHHPENSPYGYAPYGPEPAYMAAHHAGLQGPPPQQMRQDEQNA 1561	RA RA	Jala Kimm
ζý	1708	AAASAERERERERERERERI	RA RA	Lask Liu
ор	1562	:  :  :::   :::    :	ra Ra	Merk
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Ωp	1646	HGSPFAPQDGQPHGLKPTSHMDALRAHAHSANSAGMGGGHHPTEPLPIDIE 1696	8 8 8	Wang Will
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<u>8</u> 8		đ	152
à	-AAVLPLVHPL-PEGLRASADAKKDPAFGGKHEAPSSPISGOPCGDDONA	δò	104
g	:       PLRSTRPVPQPVEAEQKA	QQ	154
ò	SPSKLSKEELIOSMDRVDREIAKVEOOILKLKKKOOOLEEEAAKPPREP	οy	105
. a	YEEATDELTEEPIPQPQPVMWERGKKKPQKPQEEVTEIPKTLEIAVDTLEEEVRKPTEPQ	đ	16(
ò	221KPVSPPPVEOKHRSIVOIIYD	ΟŊ	115
ස	POPVLWARGOKRPOKPDEOKOELPKSLEIAVDTIEEDLIKPVOPEPOPVLWERKKKPOP	QQ	164
		QY	118
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ò	ROK TCORYDOL MEAWEKKUD	Oy	124
유	GKKKIPKSEPTEEVHPDAAOIETUVKEDEMIVEEKRRIKKTKRPKSTKEVTETIERET	qq	176
8		δy	13(
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g q	EBDOPEEEVLOEETIGEOEETTERORKYKSIKKPKKVYTEKTVOOTBOPEKPEESQAEEV	QO	198
ô	AAAATEEPPPPLPPPEPISTEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAK	Qy	159
. q		ΩD	203
2	MVGTKSFAOCKNEYFNYKRBHNI.DNI.J.OOHKOKTSBKBBFFRDVSDCFSVASTVSBO	Øλ	163
음	AEOPETPETEFEVEFAITTTEDILDVTKKVKKKKKKKKKKTK	QQ	206
ò	PTTETAPSTEPSI.	Οy	167
8	ESTEEPAEFEEFEEFATOPEEVOPVEEIPEEPOVKEVADERKTA	QQ	214
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QV Db	768	AVPSTKPAEDESVETQVNDSISAETAEQMDVDQQEHSAEEGSVCDPPPATKADSVDVEVR 827
ογ	828	NAQRPEPQSDNDSSATC
qq	1383	
Qγ	884	SADEDVDGEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLP 928
qq	1429	EEAEHIELEKOPKPEEDOPOVPWKRGEKKOPVEEVLEEKKWPSGKRRPLP 1478
δλ	929	QLQHRAAVIPPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEQRQRQEQIDLECR 988
qq	1479	EQQPEEVQLKPIPSKPIEEQKPEKAIPGPQLVPEEKPESEEELE 1524
δλ	989	SSTSPCGTSKSPNREWEVLQPAPHQLITNLPEGVRLPTTRPTRPPPPLIPSSKTTVASEK 1048
đ	1525	LKLPEDKKPKEPKAKKEKK
δý	1049	PSFIMGGSISQGTPGTYLLSHNQASYTQETPKPSVGSISLGLP
qq	1549	PKLKKAIPSVDEVSEEVAEPFDEPIAEEDEVEEMPVDDVKVVAVSEDVLP-EEE 1601
ΟŊ	1096	SAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVRGTAGAIQEGSITRGTPTSKISV 1155
q	1602	VVPTEETPEAKQKAHKKRTKRLKEASVEGQPQLLEAAIAEI 1642
δy	1156	ESIPSLRGSITQGTPAL1188
Dp	1643	EKVDEISQEISQKTITLLKKTEDTRPQF-ITTEQLIELDVEDVRRDLEMKVTSNIIKKEK 1701
οy	1189	-RMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIKNAREGTRSPRTAHEIS 1242
q	1702	REVYLDDSQPLPELELITQKR1QEGIDKVADEELIEDQQLIQNQQETTTSEVIGQERK 1759
ΟŻ	1243	LKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIMQGT 1300
qq	1760	LVKKKKKEIKPPRITEKLRPRQCVPEEPTVLECKVEGVPFPE
δy	1301	AFEGAITKGKPYD-G
q	1804	WYFNDILLFASEKYEITVMEQVAKLKIAKVTPSDVGVYTCEAKNEAGVAT 1853
δy	1355	PRQDILTQESRKTPEVVQSTRPILEGSISQGTPIKFDNNSGQSAIKHNVKSLITG-PS 1411
qq	1854	SRINIILEKEQGVPPQFTKPLKIEFIEEKQPERLKVTVTCQVTGKPNPE 1902
Qγ	1412	-KLSRGMPPLEIVP-ENIKVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKA 1469
qq	1903	VKWYRGIE-,-EVIPSETVQMFYDEKTGDVALEVINPTPNEAV 1942
Qy	1470	QLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTSDVTIPPNKSTNHERKSTLTPTQRESI 1529
q	1943	VQAQNQFGRAIGNANILSRVDEVPREILKAPTVTPLSAVVV 1986
ογ	1530	PAKSPVPGVDPVVSHS
qq	1987	PTGGTLFFEAKYDGLPRPEVKWMRNGREIIENEETIIETTETTTIK 2033
δy	1590	
qq	2034	VVNMTRKRTGKYEVWAKNKVGEAKSSGSVVVSDQKPDEQIKPPRFIQPLEPKYFGEH 2090
δy	1639	EQPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRI 1678
QQ	2091	EVAIIEAIVESEPLSSFQWFVHNEPIKSSNEVRIVSQAN-KSTLLIENFQSKFVGP 2145
Oy	1679	TYIPGTQITFPPRPYNSASMSPGHPTHLAAAASAERERERERERERERERIAAASSDLYL 1738
qq	2146	FTCRAENVGGSVTSTATVNLIPQEEAEFFESPRFVEELV 2184
VO.	• 1739	RPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPL 1787

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Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., II P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewiss S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
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Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Harris N.L., Harvey D., Helman T.J., Wei M.-H., Ibegwam C.,
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster (Fruit fly).
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Kimmel B.E., Kodiza C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Limmel B.E., Kodiza C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Lei Y., Lei Y., Lei Y., Lei Y., Lin X., A Lasko P., Lei Y., Lei Y., Lei Y., Lin X., A Liu X., Martel B.E., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mornt S.M., Moy M., Murphy B., Murskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Kemington K., Sauders R.D.C., Scheeler F., Shen H., Reinert K., Kemington K., Stungson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Sylvakas K., Tector C., Turner R., Wohler E., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Zhong K.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O., Chore, 287, 2185, 2195, 2000.
                    Ketchum K.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.4%; Score 432; DB 5; Length 1963; Best Local Similarity 19.0%; Pred. No. 6.4e-15; Matches 437; Conservative 250; Mismatches 910; Indels 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SM00395; SANT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       666 YFNYKRRHNLDNLLQQHKQKTSRKPREERDVSQCESVAS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00249; myb_DNA-binding; 1.
Pfam; PF01448; ELM2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 288:2185-2195(2000).
EMBL, AE003555, AAF50413.1; -Flyamase; FR00020427; Gug.
InterPro; IPR0001949; -InterPro; IPR0001005; -InterPro; IPR0001005; -InterPro; IPR0001005; -InterPro; IPR0001005; -INTERPRO; IPR0001005; -INTERPRO; IPR0001005; -INTERPRO; -INTERPR
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Σ			QQ
NAPPHEDS - MINITONIONS NIETKNEDA			Qy
930 LOHKAAVIPPMYSCIPCNIPIGIPYSGIALYORHIKAMHESALLEEDRQRQEGIDLECRS    -			qq
		_	οy
990 SISANSTARSMEVLOJARAFH-ULLININEGVKLPTYKPTKPPPPLIESK 			QQ
1042 TTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQE			δλ
691AAGGVSGAPPGAPTTPOKYPPEMPMKFAPODLKXPPPPDDDLDALKYS			QQ
			δλ
737 QEMQAAAAAAAAGKXDMKXMMEQQGKXNVELSAAHO		<u>ц</u>	Dp
1145 TRGTPTSKISVESIPSLEGSITOGTPALBOTGIPTEALVEGSISPMPIEDSSPEEGE			δy
774PPSKPGYQDSLKIPDIKPGFGHLPHNVGSP-			qq
1205 ASKGHVIYEGKSGHILSYDNIKNAREG-TRSPR-TAHEISLKRSYEGVIKOGMSMRE			δλ
			Dβ
SPVSAPLEGLICRALPRGSPHSDLKERTVLSG	T CIMOGTDRATTEGEDGIKV 1314		δy
PPGATPPPGIAMPKPHYQHDVQTPPLGRPFE		<b>—</b>	qa
1315 PKOIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHEIPRODIIJAGESRKTDEVVOST			οy
			q
1375 RPTIEGSTSOGTPIKEDNNSGOSATKHNVKSLITCPSKLSBCMPDLEIVDENIKVVVERCK	ETVDENIKAMERCK 1434		δy
934OGSNSQPPSMPPQPQQFQSPHMDSPAGGGLPP-GMHPQNLIHGP			qq
1435 YEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSR 	ARRIPVSYONTMSR 1494       ::		γο d
983 PPGAAGGSGPQPPPPPTSLHQPTPTSAGPPSLQHGLHP	тѕасрругонстир 1020		3
1495 GSPMMNRTSDVTIPPNKSTNHERKSTLTPTQRESIPAKSPVPGVDPVVSHSPFDPHHRGS	VVSHSPFDPHHRGS 1554	щ.	RESULT
1021 GHQHSQLSVASSIPPSSIGIPPTLSTMAPSH	МНРНГНРН 1059		38;
1555 TAGEVYWSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMBNTR :	YPSQYQLYAMENTR 1610 :		DII G
1060AHLQCLHRPHDLPPSMHPHAPMPLSLQG	APMPLSLQGHPQHGHGLPPSHTS 1101		동
1611 QTILNDYITSQQMQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPPTILVPH	IDLTNMPPTILVPH 1666		NS
1102 QQQQQQQQQQQQQQGGPAGTVRTPSPAQQPPRSMHDPQSSREPPTSQPSTTWAGS	EPPTSQPSTTMAGS 1154		388
1667 PGGTSTPPMDRITYIPGTQITFPPRPYNSAS	YNSASMSPGHPTHLAAAAS 1711		388
1155 SGPGGPPPQQSPHAHRTSPLPGLAGSGPPPGLIGHPMAIHPHLAHLPPGHPAHAALAHP	. IIII   I   I   LPPGHPAHAALAHP 1214	——	RN G
1712 AERERERERERERERIAAASSDLYLRPGSEQPGRPGS	1750		2 2 2
1215 GHHLLSHSIAGLGPGGGPIALLAGPGGLGGIPESALSRRTPPSHL	PESALSRRTPPSHL 1259		2
1751 -HGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMPLPAGGPSISQGL	MPLPAGGPSISQGL 1809		5 <b>2</b> 2
1260 PHSHASSAPLTAHSVASMTSTSMSLTTSTVPSSAFSRASPSVQISSSGGGPSGPGSV	-SSSGGPSGPGSV 1316		S & &
1810 -PASRYNTAADALAALVDAAASAPQMDVSKTKES 	SKHEAARLEENĪRSR 1856     ::   :		R R
1317 GPGGMPNSSAAAAAAAAAAHRAASPASSVSSLSRQSPLHPVPQSPLSHHPSSSALSAA	HHPSSSALSAA 1373		RA RA
1857 SAAVSEOOOLEOKTLEVEKRSVOCLYTSSAFPSGKPOPHSSVVYSEAGKDKG	HSSVVYSEAGKDKG 1908	_	;

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STRAIN-BERKELEY;
Adams M.D., Cellniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Admanatides P.G., Scherer S.E., Hilt. W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
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Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nalson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchhan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
:|||:| : | : | : | : | : AAVAERDRHALMRQQSPHMTPPPVSNASLMASPLSKMY---APQP------GQRGLGTS 1424
                                                                                                                                                                     PHGL-----KPTSHMDALRAHAHSANSAGMGGGHHPTEPLPIDIEPDPEP-EIPSPTHN 1688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | : ::: :: :: 1802
| REERDRKLAEKERERROQQQQQQQQQQQQQAAAQQAAWWAELKPYADTPALRQLS 1802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 MSQPMGVVPGTANTSVVTSGETRREEGDPSPHSGGVCKPKLISKSNSRKSKSPIPGQGYL 2345
                                                                                                              PPPKSRYEEELRTRGKTTITAANFIDVIITRQIASDKDARERGSQSSDS-----SS 1959
                                                                                                                                                                                                                                                                               -----YETPSDAIEVISPASSPA------PPQEKLQTY 1992
                                                                                                                                                                                                                                                                                                                                                       FYSPHHHPFNSPYGYAPYGPEPAYMKPPPQPGQLDPAAVMAAHHAGLQGPPPQQMRQDE 1537
                                                                                                                                                                                                                                                                                                                                                                                                                                                QPEVVKANQAENDPTRQYEGPL---HHYRPQQESP-----SPQQQLPPSS 2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ONAAAAAAQAAAEKQHQAAAAAAQQHKAPQQQQPGGMPPNKPPTPKTPQGPGGGMPPGM 1597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSALVSTPVRTKTSNRYSPESQAQSVHHQRPGSRVSP-ENL-VDKSRGSRPGKSPERSHV 2142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSEPYEPISPPQVPVVHEKQDSLLLLS-QRGAEPAEQRNDARSPGSISYLPSFFTKL--- 2198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --ENTSPMVKSKKQEIFRKLNSSGGDSDMAAAQPGTEIFNL-----PAVTTSG----S 2246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSSRGHSFADPASNL-----GLEDIIRKALMGSFDDKVEDH-----GVV 2285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EYARPHVAFSPVEQMVPYHHPMGPMYRERELEEIKNAQAAAASQSRLDPHWMEYYRRGIH 1862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSQ----FPLYANPAI -- SQMERERLGIPPPHHVGL------DPGEHMVRMPQPPEA-- 1907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sophila melanogaster (Fruit fly).
sophila melanogaster (Fruit fly).
ryyota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
rygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
ydroidea; Drosophilidae; Drosophila.
I_TaxiD-727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QAEGM-----GQVPRTHRLITLADHICQIITQDFARNQVSSQTPQQPP-TSTF---QNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WAY-2000 (TrEMBLrel. 13, Created)
MAY-2000 (TrEMBLrel. 13, Last sequence update)
JUN-2000 (TrEMBLrel. 14, Last annotation update)
2864 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 3257 AA
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58

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cherry J.W., Cawley S., Dahlke C., Davenport L.B., Davies P.,

de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.W.,

Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

Durbin K.J., Evangelista C.C., Ferriera S., Fleischmann W.,

R. Durbin K.J., Evangelista C.C., Ferriera S., Fleischmann W.,

R. Cong F., Gorg F., Gorg N.S., Gelbart W.M., Glasser K.,

A clodek A., Gong F., Gorg N.S., Gelbart W.M., Glasser K.,

Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Harris N.L., Harvey D., Heiman T.J., Heiman T.J., Heiman T.J., Hough M. H., Ibegwam C.J.,

Anali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Kimmel B.E., McIntosh T.C., McLeod M.P., McPherson D.,

N. Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

A Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

Reinert K., Remington K., Sauders R.D.C., Scheeler F., Shen H.,

Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

Sylrskas R., Tector C., Stapleton M., Strong R., Sun E.,

Reiner K., Massarman D.A., Weinstock G.M., Weissenbach J.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQLRRRPSLLSEFHPGSDR-PQERRTSYEPFHPGPSPVDHDSLESKRPRLEQV-SDSHFQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QOVKH----ANEQSAASDKEANKKERDLEPPEASSSAKSSASKSSGSRKLYDVANNATLE 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RVSAAVLPLVHPLPEGLRASADAKKDPAFGGKHEAPSSPISGQPCGDDQNASPSKLSK-E 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         405 AVERMSLDLAEQIME----IDVERSYEFEKRSASKSRSLSRSKIPAD--SSTSQLGHVR 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KODELVSDLDNAKELTGSTNLPQDDIEMASNHQETDLKCAPDRVALDKSESTPKVEEEQL 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 NGLMEDPMKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNFGLIASYLERKSVPDCVLYYYL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 SSGYPPNQGAFSTEQSRYPPHSVQYTFPNTRHQQEFAVPDYRSSHLEVSQASQLLQQQQQ 62
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Matches 551; Conservative 392; Mismatches 1132; Indels
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SEQUENCE 3257 AA; 355970 MW; 7E9212C20A40810C CRC64;
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NKTVEDESKKQEILKDLEPDNAALEEDTASTAKAAEEMDLYIKEKSNVKSVLAEPETDVT
                                                                                DDE----ELAQSPIP----NSSETTSVTDDPEPSTSSVVKRSLRKREADSSQ-----P
                                                                                                                                                                                                                                                                                                                                                                       ----LQKPSTLD
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                                                                                                                                  LEIVP----ENIKVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGI
                                                                                                                                                                                                                                                                                                                                                                                                               PGYPSQYQLYAMENTRQT1LNDY1TSQQMQVNLRPDVARGLSPREQPLGLPYPATRG11D
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                                                                                                                                                                                                                             1476 YDDTSARRTPVSYQNTMSRGSPMMNRTSDVTIPPNKSTNHERKSTLTPTQRESIPAKSPV
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----VVTSGETRREEGDPSPHSGGVCKPKLISKSNSRKSKSPIPGQGYLGTERPSSVSS 2355
                                                 2763 PQFLVITTKFISKADKNMPSKVR---AKLELLDKSKERDSSKLTP-TATTPTADPTGPSS 2818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              873; Indels 698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Nyakatura G., Mewes H.W., Mannhaupt G.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        German Neurospora genome project;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL389901; CAB97476.1; -.
InterPro; IRRO1005; -.
PROSITE; PS50090; MYB_3; 1.
SEQUENCE 2649 AA; 294398 MW; 36FB50BF3917F2AB CRC64;
                                                                                                                                                      2356 VHSEGDYHRQTPGWAWEDRPSSTGSTQFPYNPLTMRMLSSTPPTP 2400
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Last sequence update)
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B7F21.40.
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456 1304 513 1364 567 1424	605 1544 1604 1604	692 1664 750 1717 799 1775	856 1819 916 1863 976 1910	1036 1950 1096 1962 1156 2001	1216 2045 1276 2082 1327 2132
	TANDOSCHENFEGVANGGERGARUJFRADAEFAVERFAGALARITFFAGSSGRUTINARSSGRUTI	WASATAKWOTKSEACKNYYENYKRRHNLDNLLQQHKQKTSRKPRE WASATAKWOTKSEACKNYYENYKRR	QQEHSAEEGSVCDPPPATKADSVDVEVRVPENHASKVEGDNTKERDLDRASEKVEPR	RQROEQIDLECRSSTSPCGTSKSPNREWEVLQPAPHQLITNLPEGVRLPTTRPTRPPPPL	SIPSLEGSTTQGTPALPQTGIPTEALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKS
401 1245 457 1305 514 1365 568	592 1485 1485 606 606	647 1605 693 1665 751 1718	800 1776 857 1820 917	977 1911 1037 1951 1097	1157 2002 1217 2046 1277 2083
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                                                                                                                                                                                                       1508 PPNKSTNHERKSTLTPTQRESIPAKSPVPGVDPVVSHSP---FDPHHRGSTAGEVY--WS 1562
                                                                                                                                                                                                                                                                           1563 HLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITSQQ 1622
                                                                                                                                                                                                                                                                                                         2305 ATPTQQPHALGLREPAPRGQAVFSAHEAQSPTGSVVSHQHHRSLDG------R 2351
                                                                                                                                                                                                                                                                                                                                           1623 MQVNLRPDVARGLSPREQ------PLGLPYPATRGIIDLTNMPPTILVPHPGGTST 1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1720 REKERERERIAAASSDLYLRPGSEQPGRPGSHGYV-RSPSPSVR-TQETMLQQRPSVFQG 1777
                                                                                      2176 YA-----TSQALAASPT-----PQYAAHPSSIS----GRRE----AQSAREE 2209
                                                                                                                                                                                                                                1778 TNGTSVITPLDPTAQLRIMPLPAGGPSISQGLPASRYNTAADALAALVDAAASAPQMDVS 1837
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1328 FEGAITKGKPYDGITTIKEMGRSIHEIPRQDILTQESRKTPEVVQSTRPIIEGSISQGTP 1387
                                                                  1388 IKFDNNSGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVKAGETVRSR 1447
                                                                                                                                    1448 HTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTSDVTI 1507
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                ---HOPGASNSPVPHQVHHYSOSAQHPQQHLQQPQMAYPSQQQYQP
                                                                                                                                                                      2452 IRDAQLREM-----GSRDLGR--DHRVMGRDPRELGRDPREVAAQQRE----
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Last sequence update)
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MEDLINE-99069613; PubMed-9851916;
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SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
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SEQUENCE FROM N.A.
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AC Q9N435;
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Wate. Subm. EMBL.	Waterston R., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL: ACO24760; ARF59460.1; - Interpro: IPR003599; -		
	SMART; SM00409; IG; 1. SEQUENCE 6677 AA; 742580 MW; 7AC6B0B47BA11987 CRC64;	_	
Query Ma Best Loc Matches	Query Match 3.4%; Score 429; DB 5; Length 6677; Best Local Similarity 18.8%; Pred. No. 4.9e-14; Matches 500; Conservative 374; Mismatches 1016; Indels 772; Gaps 119;		
168 642	DQNASPSKLSKEELIQSMDRVDREIAKVEQQILKLKKKQQQLEEEAAKPPEP 219  ::   ::  ::           DESKRPSEVQPAEIVEQKDVPVQETSAPTVEKLAPVESKETPEVQAAEIVEQKDVPVPET 701	-	
220	EKPVSPPPVEQKHRSIVQIIYDENRKKAEEAHKIFEGLGDRVVELPL 265		
266 756	YNQPSDTKVYHENIKTNQVMRKKLILFPKRRNHARKQREQKICQRYDQL 314 :		
315 808	MEAWEKKUDRIENNPRRAKESKTREYYEKQFPEIRKQREQQERFQRVGQRGAGLSATIA 374 		
375 865	RSEHEISEIIDGLSEQENNEKOMRQLSVIPPMMFDAEQRRVKFI 418		
419	NANGLMEDPMKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNFGLIASYLERKSVPDCVLYY 478  :      :		
479	YLTKKNENYKALVRRNYGKRRGRNQOIARPSQEEKVEEKEEDKAEKTEKKEEEK 532   : :                   TTSĮQKGSTAAPAQEPTVEKLAPVESKETSEVQQAEIIEQKDVPVPETSAPTVEPTVEKL 1035		
533 1036	KDEEEKDEKE-DSKENTKEKD-KIDGTAEETEEREQATPRGRKTANSQGRRKGRITRSMT 590		
591 1088	NEAAAAAAAAAATEEPPPPLPPPPEPISTEPVETSRWTE-EEMEVAKKGLVEH 643		
644 1138	GRNWAAIAKMYGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRKPREERDVSQC 699   :-  :-  :-    PETSAPTVEPTVEKLAPVESKETSEVQQAEIIEQKDVPVP 1177		
700	ESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSEDSPENATSRGNTEPAVE 752  :		
753 1234	SLAVPSTKPAEDESV 780  ESKETSEVQPAEIVEQKVVPVPETSAPTVEPTVEKLAPVESKETPEVQPAEILEQKDVTC 1293		
781	ETQVNDSISPETAEQMDVDQQEHSAEEGSVCDPP 814		
815 1354	PATKADSVDVEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQ 865   :::		
866 1413	INAQRPEPQSDNDSSATCSADEDVDGEPERQRNFPMDSKPSLLNPTGSILVSSPLKPNPL 925 :		
926	DLPQLQHRAAVIPPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEQRQRQEQIDL 985		_

qq	1447	
Š i	986	ECRSSTSPCGTSKSPNREWEVLQPAPHQLITNLPEGVRLPTTRPTRPPPPLIPSSKTT 104
g	1468	ELLFSQAEVFSGLELDLLMECSEYVTTSIQKGSTAAPAQEPTVEKLAPVESKE 1520
δλ	1044	VASEKPSFIMGGSISQGTPGTYLFSHNQASYTQETPKPSVGSISLGLPRQQESAKSATLP 1103 : : :  :   :    :
QQ	1521	ISEVEPAEIVEQKDVPPVPETSAPTVEPTVE 1550
δy	1104	GLLVRAQHEGVVRGTAGAIQEGSITRGTP :   :     :
qq	1551	KLKSVESKETSEVQQAEIIEQKDVPVPETSAPTVEPTVERHAPVESKETSEVQPAEI 1607
δλ	1159	PSLRGSITQGTPALPQTGIPTEALVKGSISRM-PIEDSSPEKGREEAASKGHVIYEGKSG 1217
qq	1608	VEKLAP
δy	1218	HILSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAP-LE 1270
g	1653	PVPETSAPTVEPTVEKLAPVESKETSEVEPAEIVEQKDVPVPETSAPTVE 1702
ογ	1271	GLICRALPRGSPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYPKQIKRESPPIRAFEG 1330
Ωp	1703	PTIEKLAPVESKETSEVEPAEIVEQKDVSVPETSAPTVEP 1742
δ	1331	AITKGKPYDGITIIKEMGRSIHEIPRQDILIQESRKIPEVVQSTRPIIEGSISQGTPIKF 1390
ΟP	1743	TIEKLAPVESKETSEVEPAEIVEQKDVSVPETSAPTVEPTVEKLAPVES 1791
ÓΫ	1391	DNNSGOSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVER 1432
QC	1792	KETSEVEPAEIVEQKDVPVPETSAPTVEPTVEKLAPVESKETSEVQPAEIV 1842
δλ	1433	GKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDD 1478
qq	1843	- EHKDVQVPETSSPTVEPTVEKLAPVESKETSEVEPAEIVEQKDVPVPETSAPTVEP 1898
οy	1479	TSARRIPVSYQNTMSRGSPMMNRTSDVTIPPNKSTNHERKSTL 1521
QQ	1899	TVEKLAPVESKETSEVEPAEIVEQKDVPVPETSAPTVEFTAPVEKLAPVESKETSEVQPAEI 1958
δλ	1522	TPTQRESIPAKSPVPGVDPVVSH-SPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRAL 1578
qq	1959	VEQKDVSVPETS-APTVEPTVEKLA
δλ	1579	DPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITSQQMQVNLRPDVA 1632
Dp	2014	EPTVEKLAPVESKETSEVQPAEIVEHKDVQVPETSSPTVEPTVE 2057
δy	1633	RGLSPRE-QPLGLPYPATRGIIDLTNMPPTILVPHPGG-TSTPPMDRITYIPGTQITFPP 1690
d	2058	K-LAPVESKETSEVEPAE1VEQKDVPVPETSAPTVEFTVEFTA 2099
οy	1691	RPYNSASMSPGHPTHLAAAASAERERERERERERERIAAASSDLYLRPGSE-QPGRPG 1749
q	2100	-PVESKETSEVQPAEIVEHKDVQVPETSAPTVEPTIEKLAPVESKETSEVEPAEIV 2154
δy	1750	SHCYVRSPSPSVRTQETMLQQRPSVFQCTNGTSVITPLDPTAQLRIMPLPAGGPSI 1805
QQ	2155	EQKDVSVPETSAPTVEPTIEKLAPVESKETSEVQPAEIVEHKDVQVPETSSPTVEPTV 2212
Qy	1806	SQGLPASRYNTAADALAALVDAAASAPOMDVSKTKESKHEAARLEENLRSRSAAVSEQQQ 1865
QQ	2213	EKLAPVESKETSEVQPAEIV
Qγ	1866	LEQKILEVEKRSVQCLYTSSAFPSGKPQPHS
තු	2267	LDLIMECSEYVTTSIQKGSTAAPAHEPTVEKLAPVESKETSEVEPAEIVEQKDVPVPETS 2326
δ	1898	VVYSEAGKDKGPPPKSRYEEELRIRGKTIITAANFIDVIITRQIASDKDARERGSQSSDS 1957

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Best Local Sim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-BRAIN;
Ishikawa K., Nagase T., Nakajima D., Seki N., Ohira M., Miyajima N.,
Tanaka A., Kotani H., Nomura N., Ohara O.;
                                                          2360 -- PVPETSAPTVEPTVEKLAPVESKKTSEVEPAEIVEQKDVPVFETSAPTVEPTVEKLAP
                                                                                                                                                                                                                                                                                           ----PQEKLQTYQPEVVKANQ
                                                                                       2002 AENDPTRQYEGPLHHYRPQQESPSPQQQLPPSSQAEGMGQVPRTHRLITLADHICQIITQ
                                                                                                                                                                                                               --PESQAQSVH-------RQRPGSRVSPENLVDKSRGS--------RPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHSGGV ---- CKPKLI --- SKSNSRKSKSPIPGQGYLGTERPSS ----- VSSVHSE
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                                                                                                                          -----PTVEKLAPVES-----
                                                                                                                                                   2062 DFARNQVSSQTPQQ------PPTSTFQNSPSALVSTPVRTKTSNRYS------
                                                                                                                                                                                                                                                                          SPERSHVSSEPYEPISPPQVPV-------VHEKQDSLLLLSQRGAEPAE-
                                                                                                                                                                                                                                                                                                                                   -QRNDARSPGSISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGGGDSDMAAAQ----
                                                                                                                                                                                                                                                                                                                                                                                              ---PGTEIFNL-PAVTTSGSVSSRGHSFADPASNLGLEDI-IRKALMGSFDDKVEDHGVV
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                       2418 VESKETSEVEPA--EIVEQKDVPVPETSAPTVE---
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01-AUG-1999 (TrEMBLrel. 11, Last sequ
01-OCT-2000 (TrEMBLrel. 15, Last anno
BASSON PROTEIN (KIAA0434) (FRAGMENT)
                               SSSLSSHRYETPSDAIEVISPASS----
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2327 APTVEPTVEKLAPVESKETSEVE-
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DE BASSOOI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 GLRASADAKKDPAFGGKHEAP----SSPISGQPCGDDQNASPSKLSKEELIQSMDRV--- 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPTSQQPPVGAP-HRAS-----GTSPLKQKGPQGLGQPSGPL----PAKASPLSTKASP 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----TAEQMDVDQQEHSAEEGSVCDPPPATKADSVDVEVRVPENHASKVEGDNTKE 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PNTRHQQEFAVPDYRSSHLEVSQASQLLQQQQQQLRRRPSLLSEFHPGSDRPQERRTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPSKASPQAKPL-RASEPSKTPSSVQEKKT---RVPTKAEPMPKPPPETTPTPATPKVKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVRRAEPA--TPVVKAVPEAPKGGEAEDLVGKPYSQDASRSPQSLS--DTGYSSDGISSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DREIAKVEQQILKLKKKQQQLEEEAAKPPEPEKPVSPPVEQKHRSIVQIIYDENRKKAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             453 IQHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         513 KVEEKEEDKAEKT--EKKEEEKKDEEEKDEKEDSKENTKEKDKIDGTAEETEEREQATPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEMEVAKKGLVEHGRNWAAIAKMVGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRKP
                                                                                                                                                                                                                                                                                                                                                                                             967;
                                                                                                                                                                                                                                                                                                                          Length 3851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VELEPTIET -- APSISPSLAVPSIKPAED ------ESVETQVNDSISAE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPFHPGP--SPVDHDSLESKRPRLEQVSDSHFQRVSAAVLPLVHPLPE----
                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                7CA91DB23284C161 CRC64;
(OCT-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                          3.4%; Score 425.5; DB 4; ilarity 18.8%; Pred. No. 3.6e-14; Conservative 355; Mismatches 1132;
                          EMBL, Y18448, CAA77176.1; EMBL, Y18449, CAA77176.1; JOINED EMBL, Y18450, CAA77176.1; JOINED EMBL, Y18451, CAA77176.1; JOINED
                                                                                                                                                                                                                             3851 AA; 410202 MW;
                                                                                                                                                             EMBL; AB007894; BAA23707.1; -.
                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
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<b>&gt;</b> (	1201	RDLDRASEKVEPRDEDLVVAQQINAQRP EPQSDNDSSATCSADEDVDGEPERQRMFPM 901
	1001	NULME AEURANDEN
<u>-</u>	1247	
~	937	E-i
0	1306	
_	997	SKSPNTEWEVLQPAPHQLITNLPEGVRLPTTRP 1029
0	1332	ы
~ 0	1030	TRPPPPLIPSSKTTVASEKPSFIMGGSISOGTPGTYLTSHNQASYTQETPKPS 1082
	1083	VGSISLGLPROOESAKSATLPYIKOEEFSPRSONSOPFGILLVEROHEGEVR
	1438	PASDMPRSPGAPTPSPWVAQGTQTPHRPSTPRLVWQESSQEAPFMVITL
~	1134	PQTGIPTEALVI
0	1487	SDASSQTRMVHASASTSPLCSFTETQPTTHG-YSQTTPPSVSQLP 1531
<b>~</b>	1192	IEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIKNAR
0	1532	PEPPGP-PGFPRVPSAGADGPLALYGWGALPAENISLCRISSVPGTSRVEPGPR 1584
~	1234	
	1585	TPGTA-VVDLRTAVKPTPIILTDQGMDLTSLAVEARKYGLALDPIPGRQSTAVQPLVINL 1643
. 👡	1279	RGSPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYPKQIK 1319
0	1644	NAQEHTFLATATTVSITMASSVFMAQQKQPVVYGDPYQSRLDFGQGGSPVCLAQVKQVE 1703
<u>~</u>	1320	
0	1704	OAV.
~	1361	TQESRKIPEVVQSINPIIEGSISQGTPIKFDNNSG 1395
0	1760	PEPGAEPHRATPAELRSHALPGARKPHTVVVQMGEG
_	1396	
0	1820	
_	1429	VVERGKYED 1457
0	1879	TYRAQGVVGPGPHEEQRPYPQGLPGRLYSSMSDINLAEAGLNYHAQRIGQLFQGPGRDSA 1938
_	1458	
0	1939	MDLSSLKHSYSLGFADGRYLGQGLQYGSVTDLRHPTDLLAHPLPMRRYSSVSNIYSDHRY 1998
~	1508	PPNKSTNHERKSTLTPTQRESIPAKSPVPGVDPVVS
•	1999	GPRGDAVGFQEASLAQYSATTAREISRMCAALNSMDQYGGRHGSGGGFDLVQY 2052
~	1564	- F
_	2053	QP-QHGPGLSAPQSLVPLRPGLLGNPTFP
ν.	1618	
_	2112	VRAADGMIYSTINTPIAATLPITTQPASV-LRPWVRGGMYRPYASGGITAVPLTSLTRVP 2170

oy Db	1635	-LSPREQPLGLPYPATRGIIDLINMPPTILVPHEGGTSTPPMD 1 	1676 2229
δy	1677	ITFPPRPYNSASMSPGHPTHLA-	
o Q	2230	:	
λ δ	1713	EREREREREKERERERIAAASSDLYLRP	1740
2 20	1741	SVITPLDPTAQLRI	1795
qq	2348		2399
δy	1796	MPLPAGGPSISQGLPASRYNTAADALAALVDAAASAPQ	1833
q	2400	APFPAACEAPGRGPPLAAAELAQNGQYWPPLTHAAFIAMAGPEGLGQPREPVLHRGLPSS 2	2459
δy	1834	-MDVSKTKESKHEAARLEENLKSRSAAVSEQQQLEQKTLEVEKRSVQC	1880
qq	2460	ASDMSLQTEEGWEASRSGIKKRHSMPRLRDACELESGTEPCVVRRIADSSVQTDDEDGES 2	2519
ΟŊ	1881	AGKDKGPPPKSRYEEELRTRGKTTITAANFIDVIITRO	1940
g	2520	RYLLSRRRRARRSADCSVQTDDEDSAEWEQPVRRRSRLPRH 2	2561
δλ	1941	SSPAPP	1985
qq	2562	AATVRAMSSVGIQTISDCSVQTEPDQLPRVSPAIHITAATDP	2621
٥y	1986		2019
g	2622	KVEIVRYISAPEKTGRGESLACQTEPDGQAQGVAGPQLVGPTAISPYLPGIQIVTPGPLG	2681
δλ	2020	TLADHICQIITQDFARN	2066
QQ	2682	HLPPESLSQLVSRQPPKSPQVLYSPVSPLSPHRLLDTSFASS	2739
ΟŊ	2067	SALVSTPVRTKTSNRYSPESQAQS	2109
qq	2740	: :: : : : : : : : : : : : : : : : : :	2795
Øχ	2110	SSEPYEPISPPOVPVVHEKODSL	2165
qq	2796	SQVSALPPNSLVRKVKRTLPSPPPEEAHLPLAGQASPQLYAAS	2846
δλ	2166	LENTSPMVKSKKQEIFRKLNSSG	2220
QQ	2847	LLQRGLTGPTTVPATKASLLKELDRDLRLVEHESTKLRKKQAEL	2890
Qy	2221	DIIRKALMGSFDDKV	2279
QQ	2891	DEEEKEIDAKLKYLELGITQRKESLAKDRGGRDYPPLRGLGEHRDYLSDSELNQL 2	2945
οy	2280	SVVTSGETRREE GDPSPHSGGVCKPKL	2326
Dp	2946	RFQPPAPQYSAGSGGPTQNGFPAH	3003
ΟŊ	2327	GWAWEDRPSSTGSTO	2382
Dp	3004	:: OAPTYPGPSTYPAPAFPPGASYPAEPGLPNQAFRPTGHYAGQTPMPTTQSTL	3056
Qy	2383	PLTMRMLSSTPPTPIACAPSAVNQAAPHQ	2415
Dp	3057	FPVPADSRAPLQKPRQTSLADLEQKVPTNYEVIAS-PVVPMSSAPSETSYSGPAVSSGYE	3115
δλ	2416	ONRIWEREPAP 2426	
5	3116	OCKVIDENDE ACTION CONTRACTOR OF STATE	

RESULT	17 40		
1090P	.5 Q9UPAS PRELIMINARY; PRT; 3926 AA.	δy	631 EEMEVAKKGLVEH
A S		qq	1108 ELRQAAE
8888	OI-MAY-2000 (TEMBLrel. 13, Created) 01-MAY-2000 (TEMBLrel. 13, Last sequence update) 01-CCT-2000 (TEMBLrel. 15, Last annotation update) NEURONAL DOUBLE ZINC FINGER PROTEIN.	Qy	691 REERDVSQCESVA 
s s s s s	ZNF231. Homo sapiens (Human). Eukarusi, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutharia; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;	QY Db	751 VELEPTTETAP :       1159 MSLYSPTETPSGS
RA RP R	[1] SEQUENCE FROM N.A. MEDLINE-99026125; PubMed-9806829; Hashida H., Goto J., Zhao N., Takahashi N., Hirai M., Kanazawa I.,	Oy	792TAEQM :   1218 PTGPRGLGSFEYQ
RT RT	Sakaki Y.; "Cloning and mapping of ZNF231, a novel brain-specific gene encoding neuronal double zinc finger profer whose expression is enhanced in a neurodecenerative disorder, militials extrem arronty (Mss) ".	da .	844 RDLDRASEKVEPR       :  :  276 RDLAFAEDKKKEK
RL DR SQ	Genomics 54:50-58(1998).  EMBL; AF052224; AAC83555.1; - SEQUENCE 3926 AA; 416462 MW; 75CD56EADD437343 CRC64;	Qy Dp	902 D-SKPSLLNPTGS    : :  1322 SFSTPTSSDSSGG
M Bei	Query Match Best Local Similarity 18.8%; Pred. No. 3.7e-14; Matches 568; Conservative 355; Mismatches 1132; Indels 967; Gaps 134;	Qy	937 IPPMVSCTPCNIP 
oy O	30 PNTRHQQEFAVPDYRSSHLEVSQASQLLQQQQQQLRRRPSLLSEFHPGSDRPQERRTSY 89 1	Qy Db	997 SKSPN :  : 1407 ERSPSPSSTAHSY
Qy Dp		oy g	1030 TRPPPP :1 1467 SRAYSYFASSSPP
Qy Dp	136 GLRASADAKKDPAFGGKHEAPSPISGQPCGDDQNASPSKLSKEELIQSMDRV 188  :  :	oy Db	1083 VGSISLGLPRQQE   :    1513 PASDMPRSPG
Oy Op	189 DREIAKVEQOILKIKKKQQQLEEEAAKPPEPEKPVSPPPVEQKHRSIVQIIYDENRKKAE 248	oy Oy	
Qy Db	249 EAHKIFEGLGPKVELPLYNQPSDTKVYHENIKTNQVMRKKLILFFKRRNHARKQREQKIC 308 : :	Qy Dp	1192 IEDSSPEKGREEA 
oy Oy		oy Bb	1234 SPRTAHEISLKRS :     :  : 1660 TPGTA-VVDLRTA
Oy Dp		Ογ Dp	1279 RGSPHSDLKERTV 
o do		Qy Dp	1320 RESPPIRAFEG : ::    : 1779 QAVQTAPYRSG
<u>ک</u> د	IQHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEE	Qy	1361TQESRKTPE :      1835 PEPGAEPHRATPA
3 6 8	908 1GSPEGKSKGERSSILFPSTISGISFISLSSLEEDSDSSPSKRQRLEEAKQQR 1023 513 KVEEKEEDRAEKTEKKEEEKKDEEEKDEKEDSKENTKEKDKIDGTAEETEBREQATPR 570 1024 KARRESHGDIIDTTRACSPEPTIPPEPTI IDPOPTITE DEPTATE OF THE STOCKED STANDEND TO THE STANDEND T	ky es	1396QSAIKHNVKSL             1895 ESQLACCDMVYKL
	GENTANSGGERKGETITESMINEAAASAAAAATEEPPPPLPPPPEPTSTEVETSRWIE  GENTANSGGERKGETITESMINEAAASAAAAATEEPPPPLPPPPPPFPTSTEVETSRWIE  DKGELRAQRRRERSKIPPSNLSPIEDASPFE	oy Op	1429VVERGKY      : 1954 TYRAQGVVGPGPH

δλ	631 EEMEVAKKGLVEHGRNWAA	IAKMVGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRKP	069
QQ	1108 ELRQAAE		1114
Qy	1 REERDVSQCESVASTV	//SAQEDEDIEASNEEENPEDSEVEAVKPSEDSPENATSRGNTEPA	750
qq	1115 MEELHRSSCSEYSPSPSL	DSEAEALDGGPSRLYKSGSEYNLPTF	1158
ΟY	751 VELEPTTETAPSTSPS : {	SLAVPSTKPAED	791
qq	1159 MSLYSPTETPSGSSTTPSSGRP	-LKSAEEAYEEMMRKAELLQRQQQQAAGARGPHGGPSQ	1217
Qy	792TAEQMDVDQQ		843
qq	1218 PTGPRGLGSFEYQDTTDR	PTGPRGLGSFEYQDTTDREYGQAAQPAAEGTPASLGAAVYEEILQTSGSIVRMRQASS 1	1275
οy	844 RDLDRASEKVEPRDEDLVVAQQINAQRP	EPQSDNDSSATCSADEDVDGEPERQRMFPM	106
qq	1276 RDLAFAEDKKKEK	OFLNAESAYMDPMKQNGGPLTPGTSPTQLAAPV	1321
οy	902 D-SKPSLLNPTGSILV	>	936
qq	1322 SFSTPTSSDSSGGRVIPD		1380
QY	937 IPPMVSCTPCNIPIGTPV	PIGTPVSGYALYQRHIKAMHESALLEEQRQRQRQGQIDLECRSSTSPCGT 9	966
QQ	1381 -PATTAVAPCPAGLP-		1406
Οy	997 SKSPN	-REWEVLQPAPHQLITNLPEGVRLP	1029
QQ	1407 ERSPSPSSTAHSYGHSPTTANY	:	1466
οy	1030 TRPPPPLIPSS	IMGGSISQGTPGTYL	1082
g	1467 SRAYSYFASSSPPLSPSS	PSESPTFSPGKMGPRATAEFSTQTPSPA 1	1512
δ	IS	ILPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVR 1	1133
qq	1513 PASDMPRSPGAPTPS	: PWVAQGTQTPHRPSTPRLVWQESSQEAPFWVITL 1	1561
δλ	1134 GTAGAIQEGSITRGTPTSKI	SVESIPSLRGSITQGTPALPQTGIPTEALVKG	1191
QQ	1562 ASDASSQTRWVHASASTSPLC	SPTETQPTTHG-YSQTTPSPACQLP	1606
ΟŸ	1192 IEDSSPEKGREEAASKGHVIYEGKSGHILSY	DNIKNAREGTR	1233
g	1607 PEPPGP-PGFPRVPS	AGADGPLALYGWGALPAENISLCRISSVPGTSRVEPGPR 1	1659
ογ	1234 SPRTAHEISLKRSYESVE	3NI-KQGMSMRESPVSAPLEGLICRALP1	1278
QQ	1660 TPGTA-VVDLRTAVKPTP	TPGTA-VVDLRTAVKPTPIILTDQGMDLTSLAVEARKYGLALDPIPGRQSTAVQPLVINL 1	1718
Óγ	1279 RGSPHSDLKERTVLS	GSIMQGTPRATTESFEDGLKYPKQIK 1	1319
qq	1719 NAQEHTFLATATTVSITM	:	1778
Oy	1320 RESPPIRAFEGAITKG	AITKGKPYDGITTIKEMGRSIHEIPRQDIL	1360
qq	: ::   :: :   ::   1719 QAVQTAPYRSGPRGRPR	: EAKFARYNLPNQVAPLARRDVLITQMGTAQSIGLKPGPV	1834
Qy	1361TQESRKTPEVVQS-	TRPILEGSISQGTPIKFDNNSG1	1395
QQ	1835 PEPGAEPHRATPAELRSH	PEPGAEPHRATPAELRSHALPGARKPHTVVVQMGEGTAGTVTTLLPEEPAGALDLTGMRP 1	1894
δλ	1396 QSAIKHNVKSLITGPSI	KLSRGMPPLEIVPENIK1	1428
QQ	1895 ESQLACCDMVYKLPFG-S	SCTGTFHPAPSVPEKSMADAAPPGQSSSPFYGPRDPEPPPP 1	1953
ΟŊ	1429VVERGKYED		1457
qq	1954 TVDACCOURTED	ORPVEORINGSBLYSSMENTARAGINVHANALORICOLISASA 2	5113

6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	RESUL O9N3Y ID AC DT DT DE DE OC OC	O N A R R R R R R R R R R R R R R R R R R	8	Maese Maese Oy Oy Oy Oy
		·		
-VLRSTLHEAPKAQLSPGI-YDDTSARRTPVSYQNTMSRGSPMANRTSDVTI 1507   1	SPREQPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPMD  1   1   1   1   1   1   1   1   1   1	GSEQPGRPGSHGYVRSPSFSVRTQETMLQQRPSVPQGTNGTSVITPLDPTAQLRI 1795	SQSSDSSSSLSSHRYETPSDAIEVISPASSPAPP	2067 OVSSQTPQOPPISTFQNSPSALVSTPVRTKTSNRYSPESQAGS 2109 2815 ERLNKAHVSPQKHFTADSALRQQTLPRPMKTLQRSLSDPKPLSPTAEESARERFSL 2870 2110 VHHQRP-GSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEPISPQVPVVHEKQDSL 2165 2871 VQHQGGLGSQVSALPPNSLVRKVRTLPSPPPEBAHLPLAGQASPQLYAAS 2921 2106 LLLSQRGAEPAEQRNDARSPGSISYLPSFFTKLENTSPWVKSKKQEIFRKLNSG 2220 2107 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
2014   1508   1508   1564   1564   1518 ( 2128 ( 2128 ( 2128 ( 2128 ( 2128 ( 2128 ( 2187 ) 2187 ) 2187 ) 2187 )		2423 E 1796 N 1834 - 2535 P 1881 1 1881 1 2595 E 1		2067 C 2815 F 2110 V 2871 Y 2166 I 2922 - 2221 G 2966 -
0 O O O O O O O O O O O O O O O O O O O			0	8 8 8 8 8 8 8 8

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Gaps 109;
3021 RLGG--CTTPAGQEYDFPATAAAPATPSGPTAFQQPRFQPPAPQYSAGSGGPTQNGFPAH 3078
                                                                                                                                                                                                     2383 FPYN-----HQ 2415
                                                                                                                                                                                                                                      3079 QAPTYPGPSTYPAPAFPPGASYPAEPGLPNQQAFRPTGHYAGQTP------MPTTQSTL 3131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 DGDSTSTAEIVLVTTTEEITTTSETTTSATTTEETTTEPSTTE---PSTTEEFTTEETT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      555 DGTAEETEE-----REQATPRGRKTANSQGRRKGRITRSMINEAAAAAAAAAAATEEP- 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 TVSTNPPTTPELSDDPTDGNDATDIDDKIVKKEVSSYTAETPVAPPFFENTVTSVFEEPD 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       631 ----EEMEVAKKGLVEHGRNWAAIAKWVGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQ-- 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 DDAFEDSKPVKKSTLPNG-----INSKRST-----SYANPLTVDNAAAESRNTK 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   685 ------KTSRKPREER--DVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKP 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                   2327 ISKSNSRKSKSPI----PGQGYLGTERPSSVSSVHSEGDYHRQTPGWAWEDRPSSTGSTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ery Match 3.4%; Score 424; DB 5; Length 2344; st Local Similarity 19.8%; Pred. No. 2.2e-14; tches 457; Conservative 241; Mismatches 807; Indels 806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 None; "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Kalicki J., Randall J.;
"The sequence of C. elegans cosmid Y40C5A.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [3]
SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Waterston R.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
BMBL; ACO24772; ARF60538.1;
InterPro; IPR000194;
InterPro; IPR002965;
InterPro; IPR002965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO11217; PRICHEXTENSN.
PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
SEQUENCE 2344 AA; 245901 MW; 7D8696D48D0ADDBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last annotation update)
Y40C5A.3 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 2344 AA
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SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                           2416 QNRIWE------REPAP 2426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9N3Y8
Q9N3Y8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41
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:   VTITLSAPAKSPATYGPAPEPSR 452	EEGSVCDPPPATRADSVDVEV 826 	QQINAQRPEPQSDND 878   :	VSSPLKPNPLDLPQLQHRAAVIP 938  -   - :   :  - :     RAPPSPSSPNAIPEGPPFGPDVP 625	HESALLEEGROROEGIDLECRSSTSPCGTSK 998 :    : :  :  :  YNSGAGEDKGGEVDQEEVN 655	GVRLPTTRPT 1039  :	-LTSHNQASYTQETPKPSVGSIS 1087                     PIPPPRQESITGSTRHPTRGSSPSI 774	SSPRSONSOPEGLLVRA 1126 	SVESIPSLRGSITGGTPALPQTGIPTEALVK 1184 	IVEGKSGHILSYDNIKNAREGTRSPRTAHEIS 1242 	GLICRALPRGSPHSDLKERTVLSGSIMQGT 1300 	IRAFEGAITKGKPYDGITTIKEMG 1348 :    :     ::  : PNVVVDAFENS-SPAAPAVSTMEEVT 1036	EVVQSTRPIIEGSISQGTPIKF 1390   :	KGMPPLEIVPENIKVVERGKYEDVRAGE 1442 :   : :   : :   QTQEPTQASSNVVEISEESSSPIVSSVS 1143	DDTSARRTPVSYQNTMSRGSPMMNRT 1502 :       -TAKSRPTPG 1170	TORESIPAKSPVPGVDPVVSHSPFDPHHRGSTA 1556 	RALDPAAAAYLFQRQLSPTPGYPSQYQLYAMBNTRQTILND 1616 :  :	
	VETQVNDSISAETAEQMDVDQQEHSAEEGSVCDPPPATKADSVDVE	RVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPO- 	SSATCSADEDVDGEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVIP :	PMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEGRORQEQIDLECRSST   :     :   :   :   WMIALPPPKSPYNSGAGEDKGGEVDQEEV	SPNREWEVLQPAPHQLITNLPEGVRLPTTRPT	SKITVASEKPSFIMGSISQGTPGTYLTSHNQASYTQETPKPSVGSIS	LGLPRQCESAKSATLPYIKQEEFSPRSQNSQPEGLLVR	QHEGVVRGTAGAIQEGSITRGTPTSKISVESIPSLRC 	GSISRMPIEDSSPEKGREEA-ASKGH-VIYEGKSGH:  : :             :       : :  GTPSSIPSMEPTRSTANSSKNHPVSSKISNSNI	LKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIMQGT ::	PRATTESFEDGLKYPKQIKRESPP	RSIHEIPRQDILTQESRKTPEVVQSTRPIIEGSISQGTPIKF	DNNSGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVRAG :: :: :	TVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRT  :	SDVTIPPNKSTNHERKSTLTPTQRESIPAKSPVP- :            :        PQGIVPPYALFPRPHETLSTASP-PASSLSASAKLPR	GEVYWSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILND	I I
394	780	827 513	879	939	939	1040	1088	1127 835	1185	1243 933	1301	1349	1391	1443	1503	1557	1617
QQ	O <sub>Y</sub>	Oy Db	Qy Db	. Q	QY Db	Qy Db	Oy Db	oy do	Oy Dp	oy Dp	Oy Dp	QY Dp	Qy	Oy Dp	Qy Dp	ογ Db	οy

셤	1285	IISSGKPATIPDWIMAMYTSQSSSKFSKSTAFPTLITKQTEIKPTTVSSFAPKVPETKI 1344
δy	1639	EQPLGLP 1645
qq	1345	
δy	1646	
ф	1405	:   1   : KPKTKLGLTSHPSAIPPWAISSKTLAPPVAPPTVTVPSNIAPSTTGHQSQQTRPTPTT 1462
δλ	1666	-HPGGTSTPPMDRITYIPGTQITFPPRPYNSASMSPGHPTHLAAAASAE- 1713
qq	1463	HRPGITPPLAPKTIYPSSLQTGSSSPTPPGTSSIIVVAGSRASSNYPTTASIET 1516
δy	1714	RERERERERERERIAAASSDLYLR
Dp	1517	DGSSEEQEEENTRILPEETLSPASARLWTPDMISKYISSKAISTESVSSAEQPSYLSSNL 1576
οy	1747	RIME
qq	1577	P. C.
Οy	1805	ADALAAL
qq	1633	PSSSSBSSSG
ΟŊ	1854	RSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKS 1913
Ор	1681	-GPYEPLSPPQPAEPNHVEEYQNTVDTIIEKSATPAPAPVTQPAVQPAPGP 1730
οy	1914	RYEEELRTRGKTTITAANFIDVIITRQIASDKDARERGSQSSDSSSSLSSHRYETPSDAI 1973
οp	1731	1740
δy	1974	EVISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGPLHHYRPQQESPSPQQQLP 2031
qq	1741	GPAPGPALEPAPAPTSAPQIVEPLPPVQPLPOPOPTEPEEPLPIA 1785
Qy	2032	-PSSQAEGMGQVPRTHRLITLADHICQIITQDFARNQVSSQTPQQPPT-STFQ 2082
QQ	1786	TPAPQPTEHTYGAQGPNIVPVVTAAPYVPQETQAPIAPSNPEPVQ 1830
δŏ	2083	RTKTSNRYSPESQAQSVHHQRPGSRVSPENLVD
qq	1831	PNPSQIVSIPEPTGNIEEAEHVD-AKPSYPGQSSYNNLE 1868
δλ	2138	VPVVHEKQDSLLLLSQRG
qq	1869	EDHEEGHIAELPALEPVSVPT1900
Οy	2194	FFTKLENTSPMVKSKKQEIFRKLNSSGGGDSDMAAAQPGTEIFNLPAVTTSGSVSSRGHS 2253
qq	1901	SNLEEDHDDKHHLVEGPSVPSTPTQTSSGSSYSILEE 1937
δy	2254	EDIIRKALMGSFDDKVEDHGVVMS
QΩ	1938	DNQETNNSGGPSYSSFDKEQVPQVVVPTKPAGGYRDGGWVENTAPQPTTYQRPH 1991
δλ	2298	NTSVVTSGETRREEGDPSPHSGGVCKPKLISKSNSRKSKSP 2338
qq	1992	PIKVQVRPATKPYRPRPSPAPRIQPRPYNDQPVVVQRPQFRPQPQPRPQPPQPQPQPQPQP
δλ	2339	STERPSSVSSVHSEGDYHRQTPGWA
QQ	2052	QPQQPYIQRP-ALTLPFQQPQYPPPIPFQPRPAPFIPFQPMVQRP 2095
δ <sub>λ</sub>	2399	241
Q C	2036	SPAGCCGGQLFSQQGGLCMPISFNPCQQQQQ 2126

RESULT 42 Q9PU36

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Gaps 144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Aczonin, a 550-kd putative scaffolding protein of presynaptic active profilin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         864 CNLCGENPMPHIVEVQEWLCLNCQTQRAMSGQLGD--MGKV------PLPK-LGPSQ 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 IFEGLGPKVELPLYNQPSDTKVYH----ENIKTNQVMRKKLILFFKRRNHARKQREQKIC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QRYDQLMEAWEKKUDRIENNPRRKAKESKTREYYEKQFPEIRKQ--REQQERFQRVG--- 363
                                                                                                                                                                                                                        Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSLAKDSKHQTAEAKKPAELSEQEKASQPKVSCPLCKTGLNIGSKDPPNFNTCTECKKVV 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----PFHPGPSPVDHD-----SLESKRPRLEQVSDSHFQRVSAAVLPLVHPLPEGLRASA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 DAKKDPAFGGKHEAPSSPISGQPCGDDQNASPSKLSKEELIQSMDRVDREIAKVEQ---- 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QILKLKKKKQQQLEEEAAKPPEPEKPVSPPP----VEQKHRSIVQIIYDENRKKAEEAHK 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -- QRGAGLSATIARSEHEISEIIDGLSEQENNEKQMRQLSVIPPMMFDAEQRRVKFINMN 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---VPDYRSSHLEVSQASQLLQQQQQQLR-RRPSLLSEFHPGSDRPQERRTSYE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang X., Kibschull M., Laue M.M., Lichte B., Petrasch-Parwez E., Kilimann M.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 3.3%; Score 415.5; DB 13; Length 5120; Best Local Similarity 18.6%; Pred. No. 1.8e-13; Matches 596; Conservative 380; Mismatches 1053; Indels 1183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           560760 MW; A658D9891B65B412 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1011 -----QTKLTKTPSSDKILHGVQKEDIKFQEAKLAKI----
                                                               Created)
Last sequence update)
Last annotation update)
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      PRT; 5120 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0360; C2DOMAIN.
PRINTS; PR01217; PRICHEXTENSN.
PRNTS; PR01399; SYNAPTOTAGMN.
PROSITE; PS00499; C2_DOMAIN_1; UNKNOWN_1.
PROSITE; PS50004; C2_DOMAIN_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99439764; PubMed-10508862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Cell Biol. 147:151-162(1999).
EMBL: Y19187; CAB60725.1; -.
HSSP; P04410; 1A25.
                                                                  13,
16,
Q9PU36 PRELIMINARY;
Q9PU36;
01-MAY-2000 (TFEMBLrel. 1
01-MAX-2000 (TFEMBLrel. 1
01-MAR-2001 (TFEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001565; -.
InterPro; IPR002965; -.
Pfam; PF00168; C2; 2.
Pfam; PF00595; PDZ; 1.
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NON_TER 1
SEQUENCE 5120 AA;
                                                                                                                                                            ACZONIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
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   ID DAC CONTRACTOR OF THE PROPERTY OF THE PROPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSHIPSDEKDLPREPSQKDIISQESPPSPSDLAKLESIVLSILEAQASTLIDEKSVKRKE 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1569 GEELAISGGGGLRRFKTIELNSTITSKYSETPEQQKGILYFDEEPELEMESLTDSPEDRS 1628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :| | :| | : | | : | | : | | : | | TPGSSPTQPTSDLAPTSDMKV--SSIGEIADSTSLTSSTTSAISDVSSLSSIALSI---- 2049
                                                                                                                                                                                                                                                                                                                                    1176 PKDKKEQITAETTGHITEQKVEVEAPCDKLHEKKQEDVKKEDLTTGIPQMVSKPEKAEEE 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1356 LYETYSEQTKDQHKTKPLPVTPESYSSD------EEDLEA-----1QEGERTIAADSK 1402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1403 GGASSQT-----DYKEEDGGNDTPARRQRYDSVEDSSESENSPVPRRKRR-----A 1448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | |: || | : | :| || SVGSSSDEYKRDDSQGSGDEEDFIRKQIIEMSADEDASGSEDDEFIRNQLKEISVTESQ 1508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1509 KKEEVKSKAKGTVGKHRRMARKSSAGYDEDAGRRHSWHDDDDETFDESPEPKYRETKSQD 1568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----SALLEEQRQRQEQIDLECRSSTSPCGTSKSPNREWEV 1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQPAPHQLITNLPEGVRLPTTRPTRPPPPLIPSSKTTVASEKPSF-----IMGGSISQ-- 1059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----SAKSATLPYIKQE--EF 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1936 VEPLCSIVPQEDIVSSSYIIPESHEIVVLDSTVTSTTEEKQLLDAEAAYEELMKKQRMQL 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPRSQNSQPEGLLVRAQHEGVVRGTAGAIQEGSITRGTPTSKIS-VESIPSLRGSITQGT 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1170 PALPQTGIPTEALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIKNAR 1229
                                                                                                                                                                                                                                                              531
                                                                                                         GLMED -- PMKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNFGLIASYLERKSVPDCVLYYY 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -------PPPPLPPPPEPISTEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAKM 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    654 VGTKSEAQCKNFYFNYK------RRHNLDNLLQQHKQKTSRKPREERDVSQCESVA 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KPSEDSPE----SPSLAVPSTRGNTEPAVELEPTTETAPST---SPSLAVPSTKPAE 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      777 DESV-----ETQVNDSIS---AETAEQMD---VDQQEHSAEEGSVCDPP--- 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDRASEKVEPRDEDLYVAQQINAQRPEPQSDNDSSATCSADEDYDGEPERQRMFPMDSKP 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SILINPTGSILVSSPLKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTPVSGYALYQRHIK 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STVSAQEDE----DIEASNEEEN-----VEAV 731
                                                                                                                                                                                                                                                          LTKKNENYKALVRRNYGKRRGRNQQIARPSQEEKVEE-KEED-----KAEKTEKKEEE
                                                                                                                                                                                                                                                                                                                                                                                                              K------IDGTAEETEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      565 EQATPRGRKTANSQGRRKGRITRSM------TNEAAAAAAAAAAATEE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----GIPGIYLISHNQAS--YIQE-----
1097 KIQHGIQKDLNLQHVKIEKTSSVEKIQEAQKESK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----TPKPSVGSISLGLPRQQE-----
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qq	2050	PDVKITQHFTAEEIEDEYLTDYAREIQEIISHETSMLTYSEVS 2092	
δλ	1230	EGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKER 1289	
QY	1290	TVLSGSIMOGTPRATTESFEDGLKYPKQIKRESPPIRAFEGAITKGKFYDGITTIKEMGR	
qq	2139	LVDSEDIIAQVPFTSTEEXSEVSMPYESVAGATTKPAIASDMDTVHQAAV 2188	
Qy Db	1350	SIHEIPRQDILTQESRKTPEVVQSTRPIIEGSISQGTPIKFDNNSGOSAIKHNVKSLI-T 1408 	
٥y	1409		
QQ	2235	:   GIIKIHHEDSHKELSLDMTRINLTGATSEQPPLCVASVSVREPASETPAVP 2285	
δò	1444	VRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGI	
a :	2286	TPRVVSKTSTVSMPSSAPALTSKVFSLFRSSSLDSP-AQPSPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP	
g 8	2345	LPKPAIYPKKKSQIQAPMATAPTAVPLVTSVATLESAAVLKNHVVPVTKTYTPT 2398	
ογ	1532	ррник	
QQ	2399	PPPVPPKPSSIPAGLVF-SHRPTEVTKPPIAPRPAPPLPIAVHKPAE 2445	
ογ		ENTROTILNDYITSQQMQVNLRPDVARGLSPREOPLGLP	
g	2446	TQPKPIGLSLTSSMTLN-LVSSAEYKIASPTSPLSPHSNKS-SPRLTKP 2492	
δλ	1646	YPATRGIIDLTNMPPTILVPHPGGTSTPPM	
qq	2493	SOETYVVITLPSEPGTPTEAITSQAVTSWPLEAPSKEQIPQPMQPIFTSSMKAVEIQSMA 2552	
δò	1676	DRITYIPGTQITFPPRPYNSASMSPGHPTHLAAAASAERERE	
2	2003		
δŏ	1718	REREKERERERIAAASSDLYLR-P ::	
<b>Q</b>	2610	ITIPPEPIYISDQPRYRENGRFHPLGDVIDLRTLTKVDIEMRDSCMDLSAVSMDARRQMP	
60 04	1741	GSEQPGRPGGHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTS 1782  :	
ò	1783		
g 2	2730	VPPV	
δλ	1833	QMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEV 1873	
QQ	2788	SVINGWIDLSTSQEPMEIGAVDLSTIK-SHRIVVIMDETISGIIITIVIEDDE-KPVDLTA 2845	
οy	1874	EKKSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSR 1914	
g	2846	GRRAVCCDMYKLPFGRSCTAQQPPTTLPEDRFGYRDDHYQYDRSGSYGYRGWGMKPSM 2905	
δλ	1915	YEEELRTRGKTTITAANFIDVIITRQIASDKDARERGSQSSDSSSSLSSHRYETPSDAIE 1974	
QQ	2906	SDINLSEAGLFAYKSKNSFDYQVGATDAAVDLTSGRV-TSGEVMD 2949	
δy	1975	VISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGPLHHYRPQQESPSPQQQLPPSS 2034	
Op	2950	YSSKTTGPYPETRQVISGIGISTPQYSQARMVSSLS 2985	
ΟŸ	2035	ICQIITQDFAR	
qq	2986	2986 SPEGAGSVLRSSNGVVYSSVATPIPSTFAITTQPGSIFSTTVR 3028	_

δ	2095TKTSNRYSPESQAQSVHHQRPGSRVS 2120	
q	:     : ::     3029 DLPTLQTIDSVPSLSTLQQNQPLPRSYSFLTTWAAEKDASTTLDIETGLPPLTLESIATE 3088	
Qy	2121 PENLVDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVHEKQDSLL 2166	
qa	3089 PTNLIPATASEVYTDVIEDEVALIIAPEEGKQQQLDLERELLELEK 3134	
Qy	2167 LLSQRGAEPAE-QRNDARSPGSISYLPSFFTKLENTSPMVKSKKQEI 2212 :          :	
Q C	QEIQRFREQEKFMVQKKL	
Ολ	2213 SSGGG 2222	
q	3183 ERQAQYMMRQETLAQQQLQLEQFQQLQQQLHQQLEEQKIRQIYQYGYDPSGTGSPQTTTD 3242	
δy	2223DSDMARAQPGTEIFNLPAVTTSGSVSSRGHSFAD 2256	
q	3243 QALLEGQYATAENG-ÇFWPTDDATTTASGVLGIEISQSQTWYTVQSDGITQYIPRSGILS 3301	
δλ	2257 PASNLGLEDIIRKALMGSFDDKVEDHGVVMSQPMG 2291	
οg	3302 SVSEMSLKDIDVREEKQLKKRSSMPKLRGPYEELEESLEEEPRCYKKIVDSGVQTDDEDG 3361	
δy	2292 VVPGTANTSVVTSGETRREEGDPSPHSGGVCKPKLISKSNSRKSKS- 2337	
qq	3362 ADRGYTNRRRRTKKSVDTSVQIDDED-QDEWDLSSRSGRKPRVGKYSESTTEADKAKQ 3418	
δλ	2338 PGOGYLG 2346	
qq	3419 FSKVSSIAVQTVAEISVQTEPVGTIRTPSIRARLDAKVEIIKHISAPEKTYKGESLGCQT 3478	
Qy	2347TERPSSVSSVHSEGDYHRQTPGWAWEDRPSSTGSTGFPYNPLIMRMLSSTPP 2398	
QQ	3479 ETESDTQSPQYLSASSPQKDKKRPTPLEIGYSSHLRPDSTLQV-VPSPPKSPKVLYS-PI 3536	
οy	4	
qa	3537 SPVSPSKVIESAFVPYEKSITDDISPOKML 3566	
RESULT	LT 43	
Q9H4 TD	R4 OGHARA PRELIMINARY DRT. 102 AA	
AC		
턴	(TrEMBLrel. 16, Creat	
45	(Trembliel 16, Last annotation update)	
DE E	BB329D4.2 (NOVEL PROTEIN SIMILAR TO A TRUNCATED NUCLEAR RECEPTOR CO- REDRESCOR 1 (NOOR) (RETINOTH Y PROPERTOR INTERACTING DECEPTOR 13))	
GN	John T. (Modical) (Marinette & Machinette Committee Committee of the Commi	
s ဝ	(Human). etazoa: Chordata: Craniata:	
88	ia; Primates; Catarrhini; Hominidae;	
R C	NCBL_TAXID=9000;	
RP	SEQUENCE FROM N.A.	
R R	CT-2000)	
DR W	<u>ŏ</u> .	
SO	SEQUENCE 102 AA; 11336 MW; 462EC7C4AE382014 CRC64;	
no	Score	
Be	Local Similarity 43.7%; Pred. No. 1e-15; ss 90; Conservative 3; Mismatches 4;	
ογ	1 MSSSGYPPNQGAFSTEQSRYPPHSVQYTFPNTRHQQEFAVPDYRSSHLEVSQASQLLQQQ 60	
QQ	1 MSSSGYPPNQGAFSTEQSHYPPHSVKYTFPSTHHQQ36	

5	O. COUCLANDS FOR THE STANKING THE TRIBLE STANKING TOOLS OF THE TOOLS O	,		
Op	37 36	δλ	552 DF	
ò	121 RVSAAVLPLVHPLPEGLRASADAKKDPARGGKHEAPSSPTSGOPGGDDONASPSKTSKRE 180	đ	1165 Y	
. <u>8</u>		Qy	597 SF	
è	I.IOSMDRVDRETAKVEOOTEKEKKO 206	QQ	1225 PS	
5 B	LISCADRYDREIARVEOOILKLKKKO	Qy	643 НС	
}		qq	1280 -	
RESULT	JT 44	Qy	703 AS	
202	7970039 PRELIMINARY; PRT; 2829 AA.	qa	1326 NE	
828	01-FEB-1997; (TrEMBLrel. 02, Created)	QY	756 TJ	
3 5 5	O1-MAR-109) (ILEMBLIEL. 03, Last Sequence update) 01-MAR-2001 (TIEMBLIEL. 16, Last annotation update)	qa	1374 TE	
388	Augmorations Foliated Clawed frog).  Xenopus lactic (clawed frog).	Qy	807 EC	
388	Eukaiyota; metazoa; Unordatu; Craniata; Verrebiata; Eureleoscomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Yanonodiaa: Yanonis	qa	1427 PS	
X	nempromise, amples.	οy	867 NZ	
RP	VIOUENCE FROM N.A.	qa	1474 -	
7 2	Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.	QY	925 LI	
2 2 2	HSSP Q02442; AD410/1.1; HSSP Q02483 3BCT.	QΩ	1515 LE	
5 8 8 B	INCERTO, IFROUGES; F. Prouds PROBLEM P	QY	977 RG	
S S	SEQUENCE 2829 AA; 310879 MW; 8A2BABDB7706E496 CRC64;	qa	1558 RS	
å	900	Qy	1026 TJ	
B B C	Josef March Best Local Similarity 18.6%; Pred. No. 1.35-13; Marches 480; Conservative 320; Mismatches 880; Takala 680; Cana 116.	qq	1597 QE	
į	TORUNDAMBERANTEOCTICES 000, INGELS 000, Caps	Qy	1069 н	
<u> </u>	103 GANGSCONLONDELLIGORUMY DEGLIANDANNIQUEEEA	qa	1657 TS	
3 8	WATER THE TAXABLE DATE OF THE REPORT OF THE PROPERTY OF THE PR	οy	1122 LI	
;	214 217 218 219 219 210 DETENT WIT EDVILLED TO COCCUDENT CONTRACTOR CONTRACTO	qa	1693 -	
3 8	FOTGREIT VESTITRIT VERGOOOF VETROOOF FERNOREKI ROUGRI 1651 I ESSGROOF I	οy	1182 LN	
<u> </u>	254 FEGLGFRVEL-PLINGESDIRVYHENIKINQVMKKKILLEFEKRNHARKQREQRICQRYD 312 	qa	1718 AE	
3 8	OT LEARING TOWNING TOW	δy	1242 SI	
5 A	928	qq	1769 DR	
غ ا	THE TENTON TO THE TENTON THE TENT	Οy	1285 -	
i é		qq	1823 EF	
3 8	QVARSVESI SEUDESARFSIGQI FAGLAHATIQSANHMUDUNI ELIDIRINI SUKI SUEQLA	Oy	1325 IF	
5 6	DGLDSEQERNEROMENGLES VEFRME DAEGKKVAR I NANGLÆEDFMKVI KURGEMVWIDHE	QO	:1878 LF	
3	SGRUSFIQNERWSRFAHIIDSEMRUSEQRUFRTTKTTISSYTENK	Qy	1373 -	
à á	VRRNYGKRRGRNQQ	qa	1934 AK	
3 8	ELANDA ARTERIA EL TERRITORIO E	Qy	1419 PI	
S 8	303 1ARFSQEEKVEEKEEDAAEKTEKKEEEKKREEEKDEKEDSKUTKEK 551 1112 VIDGREVSSNI.SNINSKASKPHOLVIDYDDIDARTHINFSERVSEEFOORDEREPON	qa	1988	
3				

QY DP	552 DKIDGTAEETEEREQATPRGRK	SSAQKPSFPYSNUSSKQKPKKEQVSSNSNTPT 1224
Oy Dp	597 SAAAAAATEEPPPPLPFPPEFI: : :     :	STEPVETSRWTEEEMEVA-KKGLVE 642 :   ::  :   :   : NOETIOTYCVEDTPICFSRG 1279
Οÿ	643	702
qa .	1280SSLSSL	TEPKEISAVSKDGAV 13
oy G	703 ASTVSAQEDEDIEASNEENPEDSEVEA 	VKPSEDSPENAT SRGNTEPAVELEP 755 :   :   :       ISPSDSSRHKSVEFSSGAKSPSKSGAQ 1373
οy	756 TTETAPSTSPSLAVPSTKPAEDESVET	-QVNDSISAETAEQMDVDQQEHSAE 806
οp	Db 1374 TPKSPPEHYVQETPLMFSRCTSGSSLDSFESHSIASSIASSVA	SIASSVASEHMISGIIS 1426
ΟŊ	807	ERDLDRASEKVEPRDEDLVVAQQI 866
Д	1427 PSDLPDSPGQTMPPSRSKTPPPPPQTVQAKK	SKPIVPDEERGKVAK 1473
Qy	867 NAQRPEPQSDNDSSATCSADEDVDGEPERQRM	FPMDSKPSLLNPTGSILVSSPLKPNP 924
q	Db 1474TAVHSAIQRVQVLQEADTLLHFATESTPD	TESTPDGFSCASSLSALS 1514
QY Dp	QY 925 LDLPQLQHRAAVIPPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALL 	LYQRHIKAMHESALLEEQ 976
δy	977 ROROEOIDL-	-ECRSSTSPCGTSKSPNREWEVLQPAPHQLITNLPEGVRLP 1025
qq	DD 1558 RSEQERDMLDDTDDDIDILEECIISAMPRKPSR	::   RKNKKVP 1596
Qy	1026	-PSFIMGGSISQGTPGTYLTS 1068
qq	DD 1597 QPTPGKPPPPVARKPSQLPVYKLLSSQNRLQTQKHVNFTHSDDMPRVYCVEGTPINF	NFTHSDDMPRVYCVEGTPINFSTA 1656
ΟŊ	1069 HNQASYTQETPKPSVGS	ISLGLPRQQESAKSATLPYIKQEEFSPRSQNSQPEG 1121
qq	Db 1657 TSLSDLTIESPPSEPTNDQPNTDSLSTDLEKRD	Tip 1692
οy	QY 1122 LLVRAQHEGVVRGTAGAIQEGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGIPTEA	IPSLRGSITQGTPALPQTGIPTEA 1181
QΩ	Db 1693TEGRSTDDTDASK	PLNPTTVLDEDK 1717
ΟŸ	1182 LVKGSISRMPIEDSSP	HILSYDNIKNAREGTRSPRTAHEI 1241
Q	Db 1718 AEEGDILAECHSAMPKGKSHKPYRVKK	-IMDQINHTSAATSSGNSRSMQET 1768
Qy	QY 1242 SLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHS	LEGLICRALPRGSPHS 1284
qq	Db 1769 DKNKPTSPVKPMPQSIGFKERLKKNTELKLNPNS	-ENQYCDPR-KPSSKKPSKVAN 1822
δy	Qy 1285DLKERTVLSGSIMQGTPRATTES	FEDGLKYPKQIKRESPP 1324
QQ	Db 1823 EKIPNNEERTKGFAFDSPHHYTPIEGTPYCFSRNDSLSSLDFEDD-	DSLSSLDFEDDDIDLSKEKAE 1877
Οy	1325 IRAFEGAITKG	TQESRTPE-VVQ 1372
Q	Db 1878 LRKEKGTKDTDQKVKYKHENRAINPMGKQDQTGPKSLGGRDQPKALVQKPTSFSSA	GPKSLGGRDQPKALVQKPTSFSSA 1933
δλ	1373	KHNVKSLITGPSKLSRGMP 1418
QQ	Db 1934 AKGTQDRGGATDEKMENFAIENTPVCFSRNSSLSSLSDIDQENNNKE-	SDIDQENNNKETEPLKQT 1987
δλ	1419 PLEIVPENIKVVERGKYEDVKAGETVRSRH	-TSVVSSGPSVLRSTLHEAPKAQLSPGI 1475
Dp	DD 1988GISETQLGLRRPQTSGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQECI	CFSRNSLSLSIDSEDDLLQECI 2040

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1619
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                                                                                                        | : : | | : : | | 2100 WKAIQEGANSIVSRL----HQAAAAGSLSRQGSSDSDSILSLKSGISLGSPFHITLDKE 2154
                                                                                                                                                                                                                                                                                                                                                                                                      1729 IAAASSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLD 1788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1789 PTAQLRIMPLPAGGPSISQGLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAAR 1848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2251 GHSFADPASNLGLEDIIRKALMGSFDDKVEDHGV----VMSQPMGVVPGTANTSVVTSG 2305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2680 VLDQQQKEEAAKDCHTRHNSGNGNVPLL---ENRQKSFIKVDGLDTKGTD-PKSLINNQQ 2735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2736 ETNENTVAERTAFSSSSSKHSSPSGIVAARVIPFNYNPSPRKSNGENSTSRPSQIPIPV 2795
1476 YDDTSARRTPVSYQNTMSRG----SPMMNRTSDVTIPPNKSTNHERKSTLTPTQRESIP 1530
                                                                                                                                                                                                                                                                                                                       1669 GTSTPPMDRITYIPGTQITFPPRPYNSASMSPGHPTHLAAAASAERERERERERERER 1728
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                                                                                                                                                                                                                                                                   ---PAAAAYLFQRQLSPTP----GYPSQYQLYAMENTRQTILNDYIT--
                                                                                                                                                                                                                                                                                                                                                                                                                                -----KSLNQNVNTGSN------ELSRMSSTKSSGSESDRSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2432 PA-----EAPSPTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALVSTPVRTKTSNRYSPESQAQSVHH-QRPGSRVSPENLVDKSRGSRPGKSPERSHVSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2146 PYEPISPPQVPVV-----HEKQDSLLLLSQRGAEPAEQRNDARSPGSISYLPSFFTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2306 ---ETRREEGDPSPH----SGGVCKPKLISKSNSRKSKSPIPGQGYLGTERPSSVSSVHS
                                   2041 SSAMPKKRKPSKIKNEVGKSRSNSVGGILAEEPDLTLDLRDIQSPDSENAFSP-DSENFD
                                                                                                                                                                                                  2155 EKTITSNKGPKILKPAEKSALENKKTEEEPKGIKGGKKVYKSLITGKSRSS--SDFSSHC
                                                                                                                                                                                                                                            -----LSPREQPLGLPYPATRGIIDLTNMPPTILVPHPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----SGRMSYISPGRQLSQPNLSKQ------SGLPKTHSSIPRSESAS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2198 LENTSPMVKSKKQEIFRKLNSSGGDSDMAAAQPGT-----EIFNLPAVTTSGSVSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---TQFPYNPLTMRM----LSSTP---PTPI
                                                                               ---HLPTQLDPAMPFHRALD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1909 PPPKSRYEEELRTRGKTTITTAANFIDVIITRQIASDKDARERGSQSSDSSSSLSSHRYET
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                                                                               AKSPVPGVDPVVSHSPFDPHHRGSTAGEVYWS---
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Wilson R., Ainscoun R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
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"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

to the EMBL/GenBank/DDBJ databases

Submitted (OCT-1996) [3] SEQUENCE FROM N.A. STRAIN=BRISTOL N2;

SEQUENCE FROM N.A. STRAIN-BRISTOL N2;

Nature 368:32-38(1994)

elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. NCBL\_TaxID=6239;

STRAIN=BRISTOL N2; MEDLINE=94150718; PubMed=7906398;

[1] SEQUENCE FROM N.A

(TrEMBLrel. 02, Created) (TrEMBLrel. 02, Last sequence update) (TrEMBLrel. 14, Last annotation update)

01-FEB-1997 (TIEMBLIE) 01-FEB-1997 (TIEMBLIE) 01-JUN-2000 (TIEMBLIE)

SIMILARITY TO SALMO GAIRDNER.

Caenorhabditis elegans

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Gaps 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     434 RQFMNVWIDHEKEIFKDKFIQHPKN-FGLIASYLERKSVPDCVLYYYLIKKNENYKALVR 492
                                                                                                                                                                                                                SDRPQERRISYEPFHPGPSPVDHDSLESKRPRLEQVSD - SHFQRVSAAVLPLVHPLPEG 136
                                                                                                                                                                                                                                                                                                 LRASADAK----KDPAFGGKHEAPSSPISGQPCGDDQNASP-----SKLSKEELIQSM 185
                                                                                                                                                                                                                                                                                                                                         SRASNDSSASRLPDTALVGLSEAEKQHIMSVMSRSNRNTSPMTSRRCSSALQMLPEVDNL 125
                                                                                                                                                                                                                                                                                                                                                                                    DRVDRE-----IAKVEQQ---ILKLKKKQQ------QLEEEAAKPPEPEKP 222
                                                                                                                                                                                                                                                                                                                                                                                                            223 VSPPPVEQKHRSIVQIIYDENRKKAEEAHKIFEGLGPKVEL----PLYNQPSDTKVYHEN 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----IKTNQVMRKKLILFFKRRNHARKQREQKICQRYDQLMEAWEKKVDRIENNP 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 GSSAHSQFGFSTPSISGFK--IFFDK--AKTATETLVKEIKDEVIVEVDK--DKTETKP 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RRKAKESKTREYYEKQFPEIRKQREQQERFQRVGQRGAGLSATI----ARSEHEISEIID 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GL-----SEQENNEKQ-MRQLSVIPPMMFDAEQRRVKFINMNGLMEDPMKVYKD 433
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IEEPIVEIPSRAVT----PRNNLRV-----IPPPIAISHPTPPHSAKTDTGSRHSS
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                                                                                                                                                                                                                                                        SDRPRSALAMF --- TNPSPSASPSL -- LRKESEDRGDILNLLRRSSGA---
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Waterston R.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U70852; AAB09135.1; -
SEODENCE 2361 AA; 261579 WW; 75F7106658D38E3B CRC64;
                                                                                                                           Query Match 3.2%; Score 409.5; DB 5; Best Local Similarity 18.6%; Pred. No. 1.4e-13; Matches 523; Conservative 374; Mismatches 975;
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                                                                                                                               Query Match
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2361 AA

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RESULT 45 Q94226 ID Q94226 AC Q94226;

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384	539	599	659	711	762	819 667	879	937	997	1057	1109	1167 928	1227 968	1281	1315	1363	1391	1445
::   ::   :     ::   :     ::   :   :	3 RNYGKRRGRNQQIARPSQEEKVEEKEEDKAEKTEKKEEEKKDEEEKD :	DEKEDSKENTKEKDKIDGTABETEEREQATPRGRKTANSQGRRKGRITRSMTNEAAASAA   :	AAAATEEPPPPLPPPPEPISTEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAKWVGTKSE	AQCKNFYFNYKRRHNLDNLLQQHKQKTSRKPREERDVSQCESVASTVSAQED ::	EDIEASNEEENPEDSEVEAV               E-IELS-EEEREHISRIAAM	TSPSLAVPSTKPAEDESVETQVNDS	DSVDVEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDS	SATCSADEDVDGEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVI	PPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEQRQRQEQIDLECRSSTSPCGTS :: :: :: :: :: :: :: :: :: :: :: :: ::	KSPNREWEVLQPAPHQLITNLPEGVRLPTTRPTRPPPPLIPSSKTTVASEKPSFIMGGSI	SQGTPGTYLLSHNQASYTQETPKPSVGSISLGLPRQQESAKSATLPYIKQEE	) FSPRSQNSQPEGLLVRAQHEGVVRGTAGAIQEGSITRGTPTSKISVESIPSLRGSITQ 	GTPALPQTGIPTEALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIKN	) AREGTRSPRTAHEIS-LKRSYESVEGNIKOGMSMRESPVSAPLEGLICRALPRGS	PHSDLKERTVLSGSIMQG	KQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIH-EIPRQDILTQE	SRKTPEVVQSTRPIIEGSISQGTPIK	NNSCQSAIKHNVKSLITGPSKLSRGMPLEIVPENIKVVERGKYEDVKAGETVR 
365	493	540	600	660	712	763	820 668	880	938	966	1058 831	1110	1168	1228 969	1282	1316	1364	1392
අ	Oy Pp	9 Pb	Q D	9 9	oy D	S S	Q P	ç P	g Pp	5 A	O. Db	Oy Dp	ç G	g G	Qy Dp	Q D	Qy Db	ογ

<b>Q</b>	1203	DSVNNVKPSTSGSSNIPAGMEDLSEAEREKIMSVMANAEMEMGARFP 12	249
Qy	1446	TLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRG 1	495
qq	1250	PPSSQIPTRSPSVWSSSIMSELPPGLDDLSDDERMKIMAVMAEADMQNVRKPIARG 1	305
δŽ	1496	TLTPTORE 15	527
qq	1306	PPPMPPSTSM-IPPGMEGLSEEERQKIMSVMANAETDSSSSVITSRQPSRSPSVARMQPQ 13	364
Qy	1528	STAGEVYWSHLPTQLDPAM 1	572
qq	1365	LMPPQQAIPIIPPGLEGLSDEERHTIMSVMAEAEFEESRSQVPSRQPSRSPSFVNPQQ 14	1422
δy	1573	ALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITSQQMQVNL	1627
qq	1423		1456
δy	1628	RGIIDLINMPPTILVPHPGGTSTPPMDRITYIPGT	1684
qq	1457	RQKIMSVMAEA	1509
οy	1685	ы	1738
QQ	1510	ILSVMAEAEIDSAKIPSRSTSSYS	1569
δλ	1739		1778
QQ	1570	MPPPLPQMSQPEITTGLEHSSEADMEFGRDSSRSHQVIPPGLENLSEEERQQIMSVMAHA 16	1629
Οÿ	1779	PPLDPTAQL-RIMPLPAGGPSISQGLPASRYNTAADALAALVDAAASAPQMDVS 1	837
qq	1630		1675
οy	1838	SKHBAARLEENLRSR	1856
QQ	1676		1735
Qy	1857	SAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFP 18	1888
QQ	1736	VYTDVPSVSPVTENVPEKQTDDFDFTYSDSRFAEIVQMQEEEEAGSLQKQKV	1795
οχ	1889	SSVVYSEAGKDKGPPPKSRYEEELRTRGK	1924
QQ	1796	DEKPRAWETVFDGDESELPHQDFVFNEPTTKKTSDFDFPKETDEVFEKPSEIQRIKV 18	1855
Qy	1925		1961
QQ	1856	H. H	912
٥y	1968	LQTYQPEVVKANQAENDPTRQYEGPL	2014
qq	1913		1954
οy	2015	PSSQAEGMGQVPRTHRLITLADHICQIITQDFARNQVSSQTPQ	2074
q	1955	:: : : : : : : : : : : : : : : : : : :	1987
٥y	2075	RTKTSNRYSPESQAQSVHHQRPGSRVSPENLVDKSRGS	2131
qq	1988	T	2037
οy	2132	LLLLSQRGAEPAEQRNDARS	2184
qq	2038		092
οy	2185	7	241
qq	2093	SNSESRLVAREKRIMDKKTADSIMAKYQKMKKVQAKQTTTASSTSVTATPAYAIINFSDL 21:	2152
οy	2242		2288
qq	2153	KTS-TRTTDSNSYFETTKNIPALEIKDPKKDIPPEISASIDKTMAEVDALLGQVYTNEKA 22	2211

Search completed: September 8, 2001, 14:46:21 Job time: 453 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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protein search, using sw model OM protein

8, 2001, 14:39:33; Search time 19.61 Seconds (without alignments) 4262.284 Million cell updates/sec September Run on:

Title: Perfect score: Sequence:

US-09-522-753-11 12643 1 MSSSGYPPNQGAFSTEQSRY.....EREPAPLLSAQYETLSDSDD 2440

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	075376 homo sapien 060974 mus musculu 0999618 h nuclear r 099402 mus musculu 0994018 rattus norv P46821 homo sapien P34926 rattus norv P14873 mus musculu 0761315 mus musculu 0761315 mus musculu 0761315 homo sapien P76478 rattus norv P46013 homo sapien P25357 saccharcomyc 080953 gallus gall P25054 homo sapien P12270 homo sapien P12270 homo sapien P25504 homo sapien P25506 mus musculu 0713428 homo sapien P55200 mus musculu 0713428 homo sapien P55201 mus musculu 071428 homo sapien P55201 mus musculu 071428 homo sapien P55204 homo sapien P36457 rattus norv 060559 mus musculu 071447 homo sapien P3774 homo sapien P3774 homo sapien P3774 homo sapien P48611 mus musculu 092794 homo sapien P48611 homo sapien
SUMMARIES	NCRI_HUMAN NCRI_MOUSE NCR2_MOUSE NCR2_MOUSE NCR1_RAT MAPB_HUMAN MAPB_RAT MAPB_ROUSE APC_MOUSE APC_MOUSE APC_HUMAN YCS3_YEAST APC_HUMAN YCS3_YEAST APC_HUMAN TPR_HUMAN TPR_HUMAN TPR_HUMAN TPR_HUMAN TPR_HUMAN TPR_HUMAN TPR_HUMAN TPR_HUMAN TPR_HUMAN TPR_HUMAN TPR_HUMAN TPR_HUMAN TPR_HUMAN TPR_HUMAN TPS_EXT MAPP_SCHPO XKSC_CAEEL ARAC_HUMAN HRX_MOUSE SMF1_HUMAN HRX_HUMAN HRX_HUMAN HRX_HUMAN MAPP_RAT PCC_HUMAN HRX_HUMAN MAPP_RAT PCC_HUMAN RAT_HUMAN RAT_HUMAN RAT_HUMAN RAT_HUMAN MOZ_HUMAN CBP_MOUSE SMF1_HUMAN MOZ_HUMAN MOZ_HUMAN MOZ_HUMAN RES_MOUSE SMF1_HUMAN RES_MOUSE SMF1_HUMAN MOZ_HUMAN RES_MOUSE CBP_HUMAN RES_MOUSE
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HFC1_MESAU TRX2_HUMAN CALD_CHICK SC16_YEAST MAP2_MOUSE HFC1_HUMAN ZEP1_HUMAN ZEP1_HUMAN MAP2_HUMAN MAP2_HUMAN MRSP_STAAU
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## ALIGNMENTS

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                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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              SPECIFICITY.
SIMILARITY: CONTAINS 1 SANT DOMAIN (COMPOSED OF SANT-A+SANT-B).
SIMILARITY: CONTAINS 2 CORNR BOX.
SIMILARITY: BELONGS TO THE N-COR NUCLEAR RECEPTOR COREPRESSORS FAMILY.
                                                                                                                                                                                                        Repressor;
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        THE CORNR BOX DETERMINE NUCLEAR HORMONE RECEPTOR
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PROSITE; PS50090; MYB_3; 1.
Nuclear protein; Transcription regulation; DNA-binding;
Coiled coil.
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INTERACTION WITH SINJA/B.
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SANT-A (POTENTIAL).
SANT-B (POTENTIAL).
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EMBL; AB019524; BAA75814.1; -.
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          GGPSISQGLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAV
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                                         RTSDVIIPPNKSTNHERKSTLTPTQRESIPAKSPVPGVDPVVSHSPFDPHHRGSTAGEVY
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1- SUBCELLULAR LOCATION: NUCLEAR.

1- DOMAIN: THE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

1- DOMAIN: THE N-TERMINAL REGION CONTAINS REPRESSION FUNCTIONS THAT ARE DIVIDED INTO THREE INDEPENDANT REPRESSION DOMAINS (RD1, RD2, INTERACTING DOMAINS (RD1, ND2).

1- DOMAIN: THE TWO INTERACTION DOMAINS (ID) CONTAIN A CONSERVED CONTAINS (ID) CONTAIN A CONSERVED

2- SEQUENCE REFERRED TO AS THE CORNR BOX. THIS MOTIF IS REQUIRED AND SUPPLICIENT TO PERMIT BINDING TO UNLICANDED TR AND RARS. SEQUENCES CONTAINS (ID) C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor: two novel orphan receptors.";
Mol. Endocrinol. 9:72-85(1995).
-1-ENUCTION: MEDIATES THE TRANSCRIPTIONAL REPRESSION ACTIVITY OF SOME
NUCLEAR RECEPTORS BY PROMOTING CHROMATIN CONDENSATION, THUS
PREVENTING ACCESS OF THE BASAL TRANSCRIPTION.
-1-SUBUNIT: FORMS A LARGE COREPRESSOR COMPLEX THAT CONTAINS SINJA/B
AND HISTONE DEACETYLASE HDACI AND HDACZ. THIS COMPLEX ASSOCIATES
WITH THE THYROID (TR) AND THE RETINOID ACID RECEPTORS (RAR) IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COLDS:
COLD COIL (POTENTIAL).
INTERACTION WITH SIN3A/B (BY SIMILARITY).
                           01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
NUCLEAR RECEPTOR CO-REPRESSOR 1 (N-COR1) (N-COR) (RETINOID X RECEPTOR INTERACTING PROTEIN 13) (RIP13).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seci W., Chol H.S., Moore D.D.; "Isolation of proteins that interact specifically with the retinoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 1 SANT DOMAIN (COMPOSED OF SANT-A+SANT-B). SIMILARITY: CONTAINS 2 CORNR BOX. SIMILARITY: BELONGS TO THE N-COR NUCLEAR RECEPTOR COREPRESSORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00249; myb_DNA-binding; 2.
PROSITE; PS50090; MYB_3; 1.
Nuclear protein; Transcription regulation; DNA-binding; Repressor;
Colled coil; Alternative splicing.
DOMAIN 174 216 COLLED COLL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoerlein A.J., Naeaer A.M., Heinzel T., Torchia J., Gloss B.,
Kurokawa R., Ryan A., Kamei Y., Soederstroem M., Glass C.K.,
Rosenfeld M.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Ligand-independent repression by the thyroid hormone mediated by a nuclear receptor co-repressor."; Nature 377:397-404(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2] SEQUENCE OF 1792-2453 FROM N.A. (ISOFORM LONG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Pituitary;
MEDLINE=96008539; PubMed=7566114;
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InterPro; IPR001005;
                                                                                                                                                                                                                                                                                                             musculus (Mouse)
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                                                                                                                                                                                                                                                               NCOR1 OR RXRIP13
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th 2453;	### ATTIVE	241 DENRKKAEEAHKIFEGLGPKVELPLYNOPSDTKVYHENIKTNOVMRKKLILLFFKRRNHAR	541 KEDSKENTKEKDKIDGTAEETEREGATPREKTANSOGRRKGRITRSATINEAAASAAA

COROROZOIDLECRSSTSPCGTSKSPNREW 1004 PLIPSSKTTVASEKPSFIMGGSISOGTPGT 1064 AALPRGSPHSDLKERTVLSGSIMOGTPRAT 1304 KRPYDGITTIKEMGRSIHEIPRQDILTQES 1364 SOSAIKHNVKSLITGPSKLSRGMPPLEIVP 1424 PSVLRSTLHEAPKAQLSPGIYDDTSARRT 1484 HRALDPAAAAYLFQRQLSPTPGYPSQYQLY 1604 LSPREQPLGLPYPATRGIIDLTNMPPTILV 1664 GGRPGSHGYVRSPSPSVRTQETMLQQRPSV 1774 SAKSATLPYIKQEEFSPRSQNSQPEGLLV 1124 TESIPSLRGSITQGTPALPQTGIPTEALVK 1184 SGHILSYDNIKNAREGTRSPRTAHEISLK 1244 ERKSTLTPTQRESIPAKSPVPGVDPVVSH 1544 ASMSPGHPTHLAAAASAEREREREREK-- 1722 896 VSSPLKPNPLDLPQLQHRAAVIPPMVSCT 944 824 884 MDVDQQEHSAEEGSVCDPPPATKADSVDV 

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EMBL; AF113003; AAD20946.1; -. EMBL; AF125672; AAD22973.1; -. EMBL; S137146; AAC50236.1; -. EMBL; S83390; AAB91446.1; -. EMBL; U80750; AAB91446.1; -.
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DVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQP 1894
                                                                                                                                                                                                                                                                                                                                                                                                                                           NCR2_HUMAN STANDARD; PRT; 2517 AA.
097618: 097500 (13354; 000613; 015416;
01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last sequence update)
NUCLEAR RECEPTOR C-FEPRESSOR 2 (N-COR2) (SILENCING MEDIATOR OF RETINOIC ACID AND THYROID HORMONE RECEPTOR) (SMRT) (SMRTE) (THYROID-, RETINOIC-ACID-FECEPTOR-ASSOCIATING CO-REPRESSOR) (T3 RECEPTOR-ASSOCIATING FACTOR) (TARAC) (CTG26).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ordentlich P., Downes M., Xie W., Genin A., Spinner N.B., Evans R.M.; "Unique forms of human and mouse nuclear receptor corepressor SMRT."; Proc. Natl. Acad. Sci. U.S.A. 96:2639-2644(1999).
          2031 HHYRSQQESPSPQQQPPLPPSSQSEGMGQVPRTHRLITLADHICQIITQDFARNQV----
                                                                                  SDSSSSLSSHRYETPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGPL
                                                                                                                                                                                                                            SFFTKLENTSPMVKSKKQEIFRKLNSSGGGDSDMAAAQPGTEIFNLPAVTTSGSVSSRGH
                                     HSSVVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVIITRQIASDKDARERGSQS
                                                                                                              HHYRPQQESPSPQQQ---LPPSSQAEGMGQVPRTHRLITLADHICQIITQDFARNQVSSQT
                                                                                                                                                                                       PGKSPERSHVSSEPYEPISPPQVPVVHEKQDSLLLLSQRGAEPAEQRNDARSPGSISYLP
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Park E.J., Schroen D.J., Yang M., Li H., Li L., Chen J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Pituitary;
MEDLINE-99178941; PubMed-10077563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM SMRT).
TISSUE-Cervix adenocarcinoma;
MEDLINE-99199215; Pubmed=10097068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM SMRT).
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ID NCR2_H
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TISSUE-Brain cortex;

MEDLINE-97369492; PubMed-9225980;

MEDLINE-97369492;

MEDLINE-97369493;

MEDLINE-97369493;

MEDLINE-973694999;

MEDLINE-973694999;

MEDLINE-973694999;

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INDUCTRON. REGULATED DURING CELL CYCLE PROGRESSION.
DOMAIN: THE N-TERMINAL REGION CONTAINS REPRESSION FUNCTIONS THAT
ARE DIVIDED INTO THREE INDEPENDANT REPRESSION DOMAINS (RD1, RD2
ARD DRD3; THE C-TERMINAL REGION CONTAINS THE NUCLEAR RECEPTOR-
INTERACTING DOMAINS THAT ARE DIVIDED IN TWO SEPARATE INTERACTION
DOMAINS (ID1 AND ID2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen J.D., Evans R.M.; "A transcriptional co-repressor that interacts with nuclear hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS 1 SANT DOMAIN (COMPOSED OF SANT-A+SANT-B). SIMILARITY: CONTAINS 2 CORNR BOX. SIMILARITY: BELONGS TO THE N-COR NUCLEAR RECEPTOR COREPRESSORS FAMILY.
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TISSUE SPECIFICITY: UBIQUITOUS. HIGH LEVELS OF EXPRESSION ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96408715; PubMed-8813722; Sande S., Privalsky M.L.; Sande S., Privalsky M.L.; Tdentfilation of TRACS (T3 receptor-associating cofactors), a indentfilation of TRACS (T3 receptor-associate the activity of, nuclear hormone receptors.";
thyroid hormone of to the nuclear
"SMRTe, a silencing mediator for retinoid and thyro receptors-extended isoform that is more related to
                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 96:3519-3524(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM TRAC-1).
TISSUE=Fetal liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Endocrinol. 10:813-825(1996)
                                                                                                                                                                                                                                                                                                                                                            TISSUE=Cervix adenocarcinoma;
MEDLINE=96008552; PubMed=7566127
                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1023-2517 FROM N.A.
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                                                                                                                                  corepressor
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                       TKE---KDKIDGTA-EETEEREQATPRGRKTANSQGRRKGRITRSMTNEAAAAAAAAA 603
                                                                                                                                                                                                                                                  NFYFNYKRRHNLDNLLQQHKQKTSRKPREERDVSQCESVASTVSA----QEDEDIEAS-- 717
                                                                                                                                                                                                                                                                                                                                            NFYFNYKKRONLDEILQQHKLKMEKERNARRKKKKAPAAASEEAAFPPVVEDEEMEASGV 710
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                                                                              LVRRNYGKRRGRNQQIARPSQEEKVEEKEE--DKAEKTEKKEEEKKDEEEKDEKEDSKEN
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PGNERSQELHLRPESHSYLPELGKSEMEFIESKRPRLELLPD------PLLRPSP 122
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                                                              Repressor;
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MISSING (IN ISOFORM TRAC-1).
L -> P (IN REF. 2).
L -> W (IN REF. 2).
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SS -> EF (IN REF. 5).
SS -> P (IN REF. 5).
SS -> T (IN REF. 5).
SS -> T (IN REF. 2).
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S -> T (IN REF. 2).
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S -> F (IN REF. 2).
A -> S (IN REF. 2).
SSSPAPPA -> MEAWDAHP (IN REF. 3).
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                                                          DNA-binding;
                                                                                                                 INTERACTION WITH SIN3A/B
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785;
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Matches 1099; Conservative 341; Mismatches 7
                 Pfam; PF00249; myb_DNA-binding; 2. PR05TE; PS50090; MTB_3; 1. Nuclear protein; Transcription regulation; Colled coll; Alternative splicing.
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VNL-----RPDVARGLSPREQPLGLPYPA-TRGIIDLTNMPP-TILVPHPGGTSTPPMD 1676
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                                                                                                       --LHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTSDVTIP----PNKSTNHE 1516
                                                                                                                                   VIVPELGKPRQSPLTYEDHGA----PFAGHLPRGSPVTMREPTPRLQEGSLSSSKASQD 1582
                                                                                                                                                                 RKSTLTPTQRESIPAKSPVPGVDPVVSH--SPFDPHHRGSTAGEVYWSHLPTQLDP-AMP 1573
                                                                                                                                                                                     RITYIPGTQITFPPRPYNSASMSPGHPTHL---AAAASAERERERERERERERER---IA 1730
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                                                                         RSLIGSPGRIFPPVHPLDVMAD-ARALERACYE-----ESLKSRPGTASSSGGSIARGAP 1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1891 KP----QPHSSVVYSEAGKDKGP--PPKSRYEEELRTRGKTTITAANFIDVIITRQIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1998 KANQAENDPTRQYEGP-----LHHYRP---QOESPSPQQQLPPSSQAEGMGQVPRT
                                                                                                                                                                                                                                                                                                                                                                                                              1731 AASSDL----YLRPGSEQ------PGRPGSHGYVRSPSP-SVRTQETMLQQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2078 DKSHLEGELRPKQPGPVKLGGEAAHLPHLRPLPESQPSSSPLLQTAPG-----VKGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RYSPESQAQSVHHQRPGSRVSPENLVDKSRGSRPGKSPERSHV---SSEPYEPISPPQ--
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                                          1404 KSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRST-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VPVVHEKQDSLLLLSQRGAEPAEQRNDARSPGSISYLPSFFTKL-ENTSPMVKSKKQEIF
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Proc. Natl. Acad. Sci. U.S.A. 96:3519-3524(1999).

-I FUNCTION: MEDIATES THE TRANSCRIPTIONAL REPRESSION ACTIVITY OF SOME NUCLEAR RECEPTORS BY PROMOTING CHROMATIN CONDENSATION, THUS PREVENTING ACCESS OF THE BASAL TRANSCRIPTION.

-I SUBUNIT: FORMS A LARGE COREPRESSOR COMPLEX THAT CONTAINS SIN3A/B AND HISTONE DEACETYLASES HDAC1 AND HDAC2. THIS COMPLEX ASSOCIATES MITH THE THYROID (TR) AND THE RETINOID ACID RECEPTORS (RAR) IN THE ABSENCE OF LIGAND, AND MAY STABILLIZE THEIR INTERACTION WITH TFIIB.
-I SUBCELLULAR LOCATION: NUCLEAR.
-I ALTERNATIVE PRODUCTS: 2 ISOFOMS; ALPHA (SHOWN HERE) AND BETA; ARE PRODUCED BY ALTERNATIVE SPLICING.
-I SSUE SPECIFICITY: UBIQUITOUS. ALSO WIDELY EXPRESSED IN EARLY
2404 KVSGRPSSRKAKSPAP--GLASGDRPPSVSSVHSEGDCNRRTPLTNRVWEDRPSSAGSTP 2461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBRYOS.

DOMAIN: THE N-TERMINAL REGION CONTAINS REPRESSION FUNCTIONS THAT ARE DIVIDED INTO THREE INDEPENDANT REPRESSION DOMAINS (RDJ, RD2 AND RD3). THE C-TERMINAL REGION CONTAINS THE NUCLEAR RECEPPORINTERACTING DOMAINS THAT ARE DIVIDED IN TWO SEPARATE INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCES
                                                                                                                                                                                                   01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
NUCLEAR RECEPTOR (CREEXSOR 2 (N-COR2) (SILENCING MEDIATOR OF RETINOIC ACID AND THYROID HORMONE RECEPTOR) (SMRTE) (THYROID --
ASSOCIATING FACTOR) (TRAC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIFICITY.
SIMILARITY: CONTAINS 1 SANT DOMAIN (COMPOSED OF SANT-A+SANT-B).
SIMILARITY: CONTAINS 2 CORNR BOX.
SIMILARITY: BELONGS TO THE N-COR NUCLEAR RECEPTOR COREPRESSORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99178941; PubMed-10077563; Ordentlich P., Downes M., Xie W., Genin A., Spinner N.B., Evans R.M. "Unique forms of human and mouse nuclear receptor corepressor SMRT. Proc. Natl. Acad. Sci. U.S.A. 96:2639-2644(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAINS (ID1 AND ID2).

DOMAINS (ID1 AND ID2).

DOMAINS (ID1 COUTERACTION DOMAINS (ID) CONTAIN A CONSERVED
SEQUENCE REPERRED TO AS THE CORNE BOX. THIS MOTIF IS REQUIRED SUFFICIENT TO PERMIT BINDING TO UNLIGANIBED TR AND RARS. SEQUENCE FLANKING THE CORNE BOX DETERMINE NUCLEAR HORMONE RECEPTOR
                                                            2462 FPYNPLIMRLQAGVMASPPPPGLPAGSG-PLAGPH---HAWDEEPKPLLCSQYETLSDSE
                                         FPYNPLTMRM---LSSTPPTPIACAPSAVNQAAPHQQNRIWEREPAPLLSAQYETLSDSD
                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Park E.J., Schroen D.J., Yang M., Li H., Li L., Chen J.D.; "SMRTe, a silencing mediator for retinoid and thyroid hormone receptors-extended isoform that is more related to the nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A. (ISOFORM ALPHA AND ISOFORM BETA)
                                                                                                                                                                                      2472 AA
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SEQUENCE FROM N.A. (ISOFORM ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Embryo;
MEDLINE=99199215; PubMed=10097068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Spleen, and Brain;
                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor corepressor.";
                                                                                                                                                                                                                                                                                                                                                                           NCOR2 OR SMRT
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                                                                                                                                               RESULT 4
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1007 GDVSQQSGGSPRGKSRSPVPPAEKEAEKPAFFPAFPTEGPKLPTEPPRWSSGLPFPIPPR 1066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1050 SFIMGGSISQGTPGTYLTSHNQASYTQETPKPSVGSISLGLPRQQESAKSATLPYIKQEE 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAAAIPPIVTKVHEPPREDTVPPKPVPPVPPT-----QHL------QPE 1006
 VASTVS----AQEDEDIEAS----NEEENPEDSEVEAVKPSE-----DSPENATSRGN 746
                                                                                                                                                                                                                                                                                                                                                                                                                                 -----TQVND-----SISAETAEQMDVDQQEHSAEEGSVCDPPPA 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKADSVDVEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSD 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NDSSATCSADEDVDGEPE---RQRMFPMDSKPSLLNPTGSILVS-SPLKPNPLDLPQLQH 932
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                                                                                                                                                                                                                                                                                                                                  KGRITRSMINEAAAAAAAAAATEEPPPPLPPPPEPISTEPVETSRWTEEEMEVAKKGLV 641
                                DDQNASPSKLSKEELIQSMDRVDREIAKVEQQILKLKKKQQQLEEEAAKPPEPEKPVSPP
                                           PVEQKHRSIVQIIYDENRKKAEEAHKIFEGLGPKVELPLYNQPSDTKVYHENIKTNQVMR
                                                                                     KKLILFFKRRNHARKQREQKICQRYDQLMEAWEKKVDRIENNPRRKAKESKTREYYEKQF
                                                                                                                               PEIRKQREQQERFQ-RVGQRGAGLSATIARSEHEISEIIDGLSEQENNEKOMRQLSVIPP
                                                                                                                                                                                                      MMFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNFGLIASY
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DVG (IN REF. 2).
E -> K (IN AAD20945).
I -> IQ (IN AAD20944).
I -> IQ (IN AAD20944).
PKLEPEPRAKSGLPFPI -> QSYRLSPHAGHRLPSH
PHAADPSA -> TRADPL (IN REF. 2).
PHAADPSA -> TRADPL (IN REF. 2).
                                                                                                                                                                                                                                                                            PPMLYDA -> RHVYRR (IN REF. 2).
D -> H (IN AAD20944).
T -> M (IN AAD20944).
V -> A (IN REF. 2).
HHLPHPRLLWTRMNKKPRLLQLPRQRMPRSRSLRPRRSMWE
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                                                                                                                    SIMILARITY)
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                                                            Pfam: PF00249; myb_DNA-binding; 2.
PROSITE; PS50090; MXB_3; 1.
Nuclear protein: Transcription regulation; DNA-binding; Repressor;
Colled coil; Alternative splicing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 1069; Conservative 354; Mismatches 766; Indels 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G-> E (IN REF. 2),
GSATSGSITKGLPSTRAADGPSYRGSITHG -
SPRASQYPGCRRPQLQRLYHPR (IN REF.
                                                                                                                    (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . A (IN REF. 2).
2A58F4DF7B79285B CRC64:
                                                                                                                                                                                                                                                         MISSING (IN ISOFORM BETA).
M -> RL (IN REF. 2).
                                                                                                      COLLED COIL (POTENTIAL).
INTERACTION WITH SIN3A/B
                                                                                                                                                COILED COIL (POTENTIAL).
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1 -> G (IN REF. 2).
2 -> A (IN REF. 2).
1 -> S (IN REF. 2).
1 -> G (IN REF. 2).
                                                                                                                             SANT-A (POTENTIAL).
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MISSING (IN REF. 2)
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PRO-RICH.
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EMBL; AF113002; AAD20945.1;
EMBL; AF125671; AAD22972.1;
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                    EMBL; AF113002; AAD20945
EMBL; AF125671; AAD22972
MGD; MGI:1337080; Ncor2.
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1357
2098
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507
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TISSUE=Skeletal muscle;

XX MEDLINE=99421707; PubMed=10491148;

AMEDLINE=99421707; PubMed=10491148;

AMEDLINE=99421707; PubMed=10491148;

AS Caller M.J., Buchler S., Pette D.;

Schuler M.J., Buchler S., Pette D.;

In Edge to contractile activity and hypothyroidism on nuclear hormone receptor mRNA isoforms in rat skeletal muscle.";

Eur J. Blochem. 264:982-988(1999).

C. I. SUBULTION: MEDIATES THE TRANSCRIPTIONL REPRESSION ACTIVITY OF SOME NUCLEAR RECEPTORS BY PROMOTING CHROMATIN CONDENSATION, THUS NUCLEAR RECESS OF THE BASAL TRANSCRIPTION.

C. I. SUBUNIT: FORMS A LARGE COREPRESSOR COMPLEX THAT CONTAINS SIN3A/B AND HISTONE DEACETYLASE HADCI AND HADC2. THIS COMPLEX ASSOCIATES AND HISTONE OF LIGAND (BY SIMILARITY).

C. I. SUBCELLULAR LOCAPIION: NUCLEAR (BY SIMILARITY).

C. I. SUBCELLULAR LOCAPIION: NUCLEAR (BY SIMILARITY).

C. I. DOMAIN: THE N-TERMINAL REGION CONTAINS REPRESSION FUNCTIONS THAT ARE DIVIDED IN TWO SEPARATE INTERACTION COMMAINS (IDI AND ID2).
                                                                                             2120 SFPGA--SCPVLDLRRPPSDLYLPPPD-----HGTP-ARGSPH----SEGGKRSPEPSK 2166
                                                                                                                                              2195 FTKL-ENTSPMVKSKKQEIFRKLNSSGGDSDMAAAQPGTEIFNLPAVTTSGSVSSRGHS 2253
                                                                                                                                                                                                                          2254 FADPAS-NLGLEDIIRKALMGSFDDKVEDHGVVMSQPMGV---VPGTANTSV-----VT 2303
                                                                                                                                                                                                                                                                                                  2304 SGETRREEGDPSPHSGGVCKPKLISKSNSRKSKSPIPGQGYLGTERPSSVSSVHSEGDYH 2363
NSPSALVSTPV---RTKTSNRYSPESQAQSVHHQRPGSRVSPENLVDKSRGSRPGKSPER 2139
                                                                                                                                                                                                                                                                                                                                                                          2364 RQTP--GWAWEDRPSSTGSTQFPYNPLTMRM----LSSTPPTFIACAPSAVNQAAPHQQN 2417
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"Aberrant interactions of transcriptional repressor proteins with the Huutington's disease gene product, huntingtin.";
Hum. Mol. Genet. 8:1647-1655(1999).
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID-10116;
                                                                        SHV---SSEPYEPISPPQ--VPVVHEKQDSLLLLSQRGAEPAEQRNDARSPGSISYLPSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O9WUB5; O70463; PRT; 533 AA. 01-OCT-2000 (Rel. 40, Last sequence update) 01-OCT-2000 (Rel. 40, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) NUCLEAR RECEPTOR CO-REPRESSOR 1 (N-COR1) (N-COR1).
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MEDLINE-99371771; PubMed-10441327;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
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DOMAIN: THE TWO INTERACTION DOMAINS (ID) CONTAIN A CONSERVED SEQUENCE REPERRED TO AS THE CORNE BOX. THIS MOTHER IS REQUIRED AND SUFFICIENT TO PERMIT BINDING TO UNLIGANDED IR AND RARS. SEQUENCES FLANKING THE CORNR BOX DETERMINE NUCLEAR HORMONE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      415
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                                                                                                                                SIMILARITY: CONTAINS 2 CORNR BOX.
SIMILARITY: BELONGS TO THE N-COR NUCLEAR RECEPTOR COREPRESSORS
FAMILY.
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EMBL; AF059311; AAC14567.1; -.
ROSSITE; PS50090; MYB_3; PARTIAL.
NUCLEAR Protein: Transcription regulation; DNA-binding; Repressor.
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A -> V (IN REF. 2).
7DF60F8228227EC2 CRC64;
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90.0%; Pred. No. 4e-86;
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The Lieb L. Feener C., Fischbach N., Kunkel L.M.;

"Cloning of human microtubule-associated protein 1B and the identification of a related gene on chromosome 15.";

"Cloning of human microtubule-associated protein 1B and the identification of a related gene on chromosome 15.";

"Genomics 22:273-280(1944).

"C -!- FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.

"C -!- FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.

"C -!- FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.

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"C -!- SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE WITH MAPIA AND MAPIB PROTEINS.

"ITH MAPIA AND MAPIA PROTEINS.

"ITH MAPIA AND 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PTM: LC1 IS COEXPRESSED WITH MAP1B. IT IS A POLYPEPTIDE GENERATED FROM MAP1B BY PROTEDLYTIC PROCESSING, IT IS FREE TO ASSOCIATE WITH BOTH MAP1A AND MAP1B.
-!- SIMILARITY: TO NEURAXIN.
                                                                   01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: MAP1 LIGHT CHAIN LC1].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prosite; Pro014; MAPIB_neuraxin; 10.
PROSITE; PS00230; MAPIB_neuraxin; 6.
Maicrtubules; Repeat; Phosphorylation.
CHAIN 7468 MAPI LIGHT CHAIN LC1.
DOMAIN 589 790 LYS-RICH (HIGHLY BASIC, CONTAINS MANY KEE AND KKEE AND KKEE AND KKEEIV REPEATS).
DOMAIN 1869 2074 12 x 17 AA TANDEM REPEATS.
                                                                                                                                                                                         Euteleostomi;
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                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                540839CBDF09D461 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                             MEDLINE=95104835; PubMed=7806212;
                                               (Rel. 32, Created)
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2072
AA; 270618 N
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1885
1902
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1953
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                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                                          01-NOV-1995 (
01-NOV-1995 (
01-OCT-2000 (
MAPB_HUMAN
P46821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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REPEAT
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113;

Gaps

762;

Indels

71 LLSEFHPGSDRPQERRISYEPFHPGPSPVDHDSLESKRPRLEQVSDSHFQRV---SAAVL 127

Match 3.8%; Score 480; DB 1; L. Local Similarity 18.7%; Pred. No. 8.8e-11; es 492; Conservative 375; Mismatches 1009;

Query Match

Matches

οχ

MAPB\_HUMAN

174	**************************************
P	PLVHPLPEGLRASADAKKDPAFGGKHEAPSSPISGOPCGDD 168   :
NG!	QNASPSKLSKEELIQSMDRVDREIAKVEQQILKLKKKQQ 207 
요그림	QLEEEAAKPEKPVSPPPVEQKHRSIVQIIYDENR 244 
X - X	KKAEEAHKIFEGLGPKVE-LPLYNQPSDTKVYHENIKTNQVMRKKLILFFKRR-NHARKQ 302     : :   :   :   :   :
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<b>≈</b> ⊐	
-1 ·· ⊳	
H &	IFKDKFIQHPKNFGLIASYLERKSVPDCVLYYYLIKKNENYKALVRRNYGKRRGRNQQIA 506
₩ ₩	RPSQE-EKVEEKEEDKAEKTEKKEEEKKDEESKDEKEDSKENTKEKDKIDGTAEETE 562 :  :
⊠ >	EREQATPRGRKTANSQGRRKGRITRSMTNEAAAASAAAAATEEPPPPLPPPEPIST 620 ::: :  :  :  :  :  :  :  :  :     :  :
ш П	EPVETSRWTEE-EMEVAKKGLVEHGRNWAAIAKMYGTKSEAQCKNFYFNYKRRHNLDNLL 679 
0 '	QQHKQKTSRKPREERDVSQCESVASTVSAQE
ন ∙ ×	EAVKPSEDSPENATSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAE 776 ::   :  :    :
Δ –	DESVETQVNDSISAET
C4 E	
O: EI	EEOYGELTTPTKOLGAOS 107
₽ —	PLKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEGRQ 978   :-
- Ճ-	
₩	RQEQIDLECRSSTSPCGTSKSPNREWEV-LQPAPHQLITNLPEGVRLPTTRPTRPPPPLI 1037

QΩ	1106	REDQPEEFTATSGYTQSTIEISSEPTPMDEMSTPRDVM 1143
οy	1038	PSSKTTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQETPKPSVGSI 1086
Ob	1144	SDETNNEETESPSQEFVNITKYESSLYSQEYSKRADVTPLNGFSEGSK 1191
Oy	1087	SLGLPRQQESAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVRGTAGAIQEGSI 1144
qq	1192	TDATDGKDYNASASTISPPSSMEEDKFSRSALRDAYCSEVKASTTLDIKDSISAVS 1247
8	1145	ALPQTGIPTEALVKGSISRMPIED
G &	1195	SENVSFSASFSUSFSFESFLERIF-LGEKSVRFSLIFNEIKVSAEAEVAFVSFEV 1301 SSPEKGREEAASKGHVIYEGKSGHILSYDNIKNAREGTRSPRTAH 1239
οqα	1302	SSHLPTEVIEKP-PAV 13
δλ	1240	EISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLS 1293
ΟD	1360	PYSFEFS-DAKDENERASVSPMDEPVPDSESPIEKVLSPLRSPPLIGSESAYESFLS 1415
δλ	1294	GSIMQCTPRATTESFEDGLKYPKQIRRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHE 1353
qq	1416	AD-DKASGRGAESPFEEKSGRQGSPDQVSPVSEMTSTSLYQDKQEGKSTDF 1465
Οy	1354	IPRQDILTQESRKTPEV-VQSTRPIIEGSISQGTPIKFDNNSGQSAIKHNVKSLITG 1409
QQ	1466	APIKEDFGQE-KKTDDVEAMSSQPALALDERKIGDVSPTQID-VSQFGSFKEDTKMSISE 1523
δλ	1410	PSKLSRGMPPLEIVPENIKVVERGKYEDVKAG-ETVRSRHTSVVSSGPSVLRSTLHEAPK 1468
qq	1524	GTVSDKSATPVDEGVAEDTYSHMEGVASVSTASVATSSFPEPTT 1567
Qy	1469	AQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTSDVTIPPNKSTN 1514
qq	1568	DDVSPSLHAEVGSPHSTEVDDSLSVSVVQTPTTFQETEMSPSKE-E 1612
δλ	1515	HERKSTLTPTQRESIPAKSPVPGVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPF 1574
qq	1613	CPRPMSISPPDFSPKTAKSRTPVQDHRSEQSSMSIEF 1649
Qy	1575	HRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITSQQMQVNLRPDVA 1632
qq	1650	GOESPEQSLAMDFSRQSPDHPTVGAGVLHITENGPTEVDYSPSDMQDSSLS 1700
Qy	1633	RGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRITYIPGTQITFPPRP 1692
qq	1701	HKIPPMEEDSYTQDNDLSELISVSQVEASPSTSSAHTPSQIASPLQE 1747
δŏ	1693	YNSASMSPGHPTHLAAAASAERERERERERERERIAAASSDLYLRPGSEQPGRPGSHG 1752
q	1748	DTLSDVAPPRDMSLYASLTSEKVQSLEGEK
δy	1753	YVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMPLPAGGPSISGGLPAS 1812
Dp	1784	SPLYSPTFSDSTSAV 1807
δy	1813	RYNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLE 1872
QQ	1808	KEKTATCHSSSSPPIDAASAEPYGFRASVLFDTWQHHLALNRDLSTPG 1855
ΟŊ	1873	VEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANF 1932
Dp	1856	LEKDSGGKTPGDFSYAYQKPEETTRSPDEEDXDYESYEKTTRTSDVGGY 1904
δλ	1933	IDVIITRQIASDKDARERGSQSSDSSSSLSSHRYETPSDAIEVISPASSPAPP 1985
.qq	1905	YYEKIERTTKSPSD SGYSYETIGKTTKTPEDG 1936
Qy	1986	QAENDPTRQYEGPLHHYRPQQESPSPQQQ
qq	1937	DYSYEIIEKTTRIPEEGGYSYDISEKTTSPPEVSGYSYEKTERS 1980

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one messenger RNA.";
J. Biol. Chem. 267:16566(1992).

-! FUNCTION: STRUCTURAL PROTEIN INVOLVED IN THE FILAMENTOUS
-ROSS-BRIDGING BEWWEEN MICROTUBULES AND OTHER SKELETAL ELEMENTS.
-! SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE WITH MAPLA AND MAPLE PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: BRAIN, HEART AND MUSCLE.
DEVELOPMENTAL STAGE: EXPRESSED LATE DURING NEURONAL DEVELOPMENT
APPEARING WHEN AXONS AND DENDRITES BEGIN TO SOLIDIFY AND STABILIZE
                                                                                                                                                                                                                                                                                                                                                                                                               ---KPGTKTKS---SSPVKKSDGKSKPLAASP-KPAGLKESSDKVSRVASPKKKESVEKA 2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN: THE BASIC REGION CONTAINING THE REPEATS MAY BE RESPONSIBLE FOR THE BINDING OF MAPIA TO MICROTUBULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIOUS SERINE RESIDUES MAY BE PHOSPHORYLATED BY CAMP KINASE. LC2 IS COEXPRESSED WITH MAPLA. IT IS A POLYPEPTIDE GENERATED MAPLA BY PROFEOLYTIC PROCESSING. IT IS FREE TO ASSOCIATE WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Langkopf A., Hammarback J.A., Mueller R., Vallee R.B., Garner C.C.; "Microtubule-associated proteins 1A and LC2. Two proteins encoded in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2348 ERPSSVSSVHS----EGDYHRQTPGWAWEDRPSSTGSTOFPYNPLTMRMLSSTPPTPI 2401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1994 (Rel. 28, Created)
1-FEB-1994 (Rel. 28, Last sequence update)
15-JUL-1999 (Rel. 38, Last anotation update)
MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
                                                                                                     2041 CYETAEKITRTPQASTYSYETSDLCYTAEKKSPSEARQDVDLCLVSSCEYKHPKTELSPS
---TLAD-----HICQIITQDFARNQVSSQTPQQPPTSTF
                       -QNSPSALVSTPVRTK-----TSNRYSPESQAQSV-----HHQRPGSRVSPE
                                                                                                                                                                                         2101 FI-----LTQSGGAPPPGGKO
                                                                                                                                                                                                                                 --QRNDARSPGSISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGGGDSDMAAAQPGTEI
                                                                                                                                                                                                                                                           2138 QGRQCDETPPTSVS--ESAPSQIDSDVPPETEECPSITADANIDSEDESETIPTDKTVTY
                                                                                                                                                                                                                                                                                                             FNL---PAVTISGSVSSRGH---SFADPASNIGLEDIIRKALMGSFDDKVEDHGVVMSQP
                                                                                                                                                                                                                                                                                                                                                                                     MGVVPGTANTSVVTSGETRREEGDPSPHSGGVCKPKLISKSNSRKSK--SPIPGQGYLGT
                                                                                                                                                   NLVDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVHEKQDSLLLLSQRGAEPAE----
                                                                                                                                                                                                                                                                                                                                               2196 KHMDPPPAPVQDRSPSPR-HPDVSMVDPEA-LAIEQNLGKALKKDLKEKTKTK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2774 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-92355629; PubMed-1379599;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
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2046 HRLI----
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P34926;
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140;
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             156 PSSPISGQPCGDDQNASPSKLSKEELIQSMDRVDRE-IAKVEQQILK-----LKKKQQQL 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEEAAK------PEKPVSPPPVEQKHRSIVQIIYDENRKKAE 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EA----HKIFEGLGPKVELPLYNQPSDT----KVYH-----ENIKTNQVMRKKLILF 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAKE--SKTREYYEKQFP--------EIRKQREQQERFQRVGQRGAGLS 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | ; ; ; | ; ; ; | ; | ; | KILEGLEKLRHLDFLRYPVATQKDLAAGAVPANLKPSKIKHRADSKESLKAAPKTAV--- 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        371 ATIARSEHEISEIIDGLSEQEN-----NEKQMRQLSVIPPMMFDAEQRRVKFINMNG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKLAKREEVLEE---GAKEARSELAKELAKTEKKAKEPSEKPP-----EKPSKSERVRG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            483 KNENYKALVRRNYGKRRGRNQQIARPSQEEKVEEKEEDKAEKTEKKEEEKKDEEEKDEKE 542
                                                                                                                                                                                                                                                                                                                                                                                   96 PSPVDHDSLESKRPRLEQVSDSHFQRVSAAVLPLVHPLPEGLRASADAKKDPAFGGKHEA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215 LMQKWAGNSKAKTGIVLANGKEAEISVPYLTSITALVVWLPANPTEKIVRVLFPGNAPON 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  423 LMEDPMKVYKDRQFMNVWIDHEKEIFKDKFIQHPKNFGLIASYLERKSVPDCVLYYYLTK 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              558 PLPADATEQGHPSAAIQVTQPSGPVLEGE-----HVEREKEVVPDSPGDKGSTNRGPDS 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----EHGRNWAAI--AKMYGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRKPR- 691
                                                                                                                                                                                                                                                                                                                                                                                                               PSPFD------LLEPPTSGGFLKLSK---PCCYIFP-------GGRGDS 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EACLTLOH--LNRLGIQAE-PLYRVVSNTIEPLTLFHKMGVGRLDMYVLNPVKDSKEMOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FKRR---NHARKQ------REQKICQRYDQLMEA---W----EKKVDRI---ENNPRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               383 ESSEALKAEKRR------LIKDK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSK-ENTKEKDKIDGTAEETEEREQATPRGRKT---ANSQGR---RKGRITR---SMTNE
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                                                                                                                                                                                                                                                                                                                                                        Indels 1053;
                                                                                                                                                                                                                                                                                                                         Length 2774;
                                                                                    LYS-RICH (BASIC).
11 X 3 AA REPEATS OF K-K-[DE]
                                                                                                                                                                                                                                                                                3DEF74427BA9D7D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             593 AAAASAAAAATEEPPPPLPPPEPISTEPVETSRWTEEEMEVAKKGLV-
                                                                      MAP1 LIGHT CHAIN LC2
                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                        Conservative 350; Mismatches 1012;
                                                                                                                                                                                                                                                                                                                                     Pred. No. 3.5e-
                                                                                                                                                                                                                                                                                                                         3.7%; Score 465.5;
19.1%; Pred. No. 3.5
send an email to license@isb-sib.ch)
                                                     t; Phosphorylation
                           EMBL; M83196; AAB48069.1; -.
                                                                                                                                                                                                                                                                                299526
                                                                                                                                                                                                                                                                              2774 AA;
                                                           Repea
                                          A43359; A43359
                                                                                                                                                                                                                                                                                                                                          Similarity
                                                        Microtubules;
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                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                          Local
                                                                                    DOMAIN
                                                                                                                 REPEAT
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ò	692 C	EERDVSOCESVASTVSAOEDEDIEASNEE-ENPEDSEVEAVKPSENSPE 7	39
og q	12	<b>—</b> ы	7
ογ	740 NA	NATSRGNTEPAVELEPTT7	771
g	672 ETI	ETKAESFYQKHTQEALKASPKSREALGGRDLGFQGKAPEKETASFLS-SLATPAGATEHV 7	730
ογ		SVCDPPPAT	817
qq	731 SY	SYIQDETIPGYSETEQTISDEEIHDEPDERPAPPRFPTSTYDLSGPEGPGPFEASQ 7	786
οý	818 KAI	KADSVDVEVRVPBNHASKVEGDNTKERDLDRASEKVEP 8	855
Q	787 AAI	AADSAVPASSSKTYGAPETELTYPPNMVAAPLAEEEHVSSATSITECDKLSSFATS 8	842
οy			888
qq	843 VAI	_	902
ογ		LLNPTGSILVSSP	919
g	903 KG	KGFKSPPCEDFSVTGESEKKGETVGRGLSGEKAVGKEEKYVVTSEKLSGQYAAVFGAP 9	. 096
οy	920	-LKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTPVSGYALYQRHIKAM	296
QQ	961 GH	GHTLPPGEPALGEVEERCLSPDDSTVKMASPPPSGPPSAAHTPF 1	1004
yo 4	968 HE		1027
2		-GVSKEDSEE-QTVKPGPEEGTSEEGKGPPTK	1000
QY Db	1028 RP	RPTRPPPPLIPSSKTIVASEKPSFIMGGSISQGT-PGTYLTSHNQAS 1	1073
		Tibudouno	
<u> </u>		DWQ	1123
δý	1124		1152
g	1178 SP	AEDDSCH	1237
οy	1153 IS	VESIPS-LRGSITQGTPALPQTGIPTEALVKGSIS	1188
QQ	1238 LA		1297
οy	1189	HILSYDNIK	1226
QQ	1298 LT	LIKSPESLSSPAMEDLAVEWEGKAPGKEREPELKSETRQQKGQILPEKVAVVEQDLII 1	355
οχ	1227 NA	NAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRAL 1	1277
qq	1356 но	HQKDGALDEENKPGRQQDKTPEQKGRDLDEKDTAAELDKGPEPKEKDLDREDQG 1	1409
οý	1278 PR	PRGSPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYPKQIK-RESPPIRAFEGAI 1	1332
Op	1410 OR	QRAGPPAEKDKASEQRDTDLQQTEPRDRAQERRDSEEKDKSLELRDRTP 1	1461
οy	1333 TK	TKGKPYDGITTIKEMGRSIHEIPRQDILTQESRKTPEVVQSTRPIIEGSISQGTPI 1	1388
a	1462	:	496
οy	1389 KFI	LSRGMPPLEIVPENIKVVERGKYEDVKAGETVR	1445
qq	1497 K-1	-EQKEEASEEKEQVLEQKDWALGKEGETLDQEARTAEQ-KDETLKEDKT-Q 1	1545
οy	1446 SR	PMMNRT	1502
g	1546 GOF	GOKSSFVEDKTTTSKETVIDOKSAFKADSVEOODGAALEKTRALSLEATRALSL	1599

δλ	1503 SDV	DVTIPPNKSTNHERKSTLTPTQRESIPAK-SPVPG-VDPVVSHSPFDPHHRG 1553
qq	1600	:   :   : YWKEQDVVQGWRETSPTRGE
QY	1554	P
QQ	1652 RDR	RDRDITLQQDAYWRELSCDRKVWFPHELDGQGARPRYCEERESTFLDEGPDEQEITPL 1709
Qy	1607 ENT	-RQTILNDYITSQQMQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMP 1659
Op	1710 QHT	OHTPRSPWISDFKDFQEPLPQKGLEVERWIAESPVGLPPEEEDKLTRSPFEIISPPAS 1767
οy	1660	PTILVPHPGGISTPPMDRITYIPGTQITFPPRPYNSASMSPG- 1701
qa	1768 PPE	PPEMTGQRVPSAPGQESPVPDTESTAPMRNEPTTPSWLAEIPPWVPKDRPLPPAPLSPAP 1827
Qy	1702	
QQ	1828 APP	APPTPAPEPHTPVPFSWGLAEYDSVVAAVQEGAAELEGGPYSPLGKDYRKAEGEREGEGG 1887
Qy	1730 AAA	AAASSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDP 1789
qq	1888 AGA	AGAPDSSSFSPKVPEAGESLATRDTEQTEPEQREPTPYPDERSFQYADIYEQMMLTGLGF 1947
ΟY	1790 TAQ	TAQLRIMPLPAGGPSISQGLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEA 1846
q	1948 ACP	otreppigasgdwpphistreeaaggntsaerreppigasgdwpphistreeaaggntsae
Qy	1847 ARL	RLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYS- 1901
Ωp	1988 S	
ογ	1902	EAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVIITRQI 1941
g Q	2026 TPP	PPAVPPRAPISLSKDLSPPLNGSTVSCSPDRRTPSPKETGRGHWDDGTNDSDL 2079
Qy	1942 ASD	ASDKDARERGSQETPSDAI 1973
QQ	2080Ë	EKGAREQPEKETRSPSPHHPMPMGHSSLWPETEAYSSLSSDSHLGSVRPSLDFPASAF 2137
Qy	1974 EVI	EVISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGPLHHY 2017
QQ	2138 GFS	SSLQPAPPQLPSPAEPRSAPCGSLAFSGDRALALVPGTPTRTRHDEY 2186
δλ	2018 RPQ	RPQQESPSPQQQLPPSSQAEGMGQVPRTHRLITLADHICQIITQDFARNQVSSQT 2072
qq	2187 LEV	LEVIKAPSIDSSIPQIPSPSSPGGPILSNIPR
δ	2073 PQ0	POOPPISTEQNSPSALVSTPVRIKTSNRYSPESQAQSVHHQRPG 2116
QQ	2219	PASPALSEGSSSEATTPVISSVAERFPPGLEAAEQSAEGLGSGKESAAHSLWDLTPL 2275
δy	2117 SRV	/SPENLYDKSRGSRPGKSPERSHVSS 2144
q	2276 SPA	SPAPSASLDLAPAPAPAPAPAPGLPGDLGDGTLPCRPECTGELTKKPSPFLSPSGDHEAN 2335
Qy	2145 EPY	EPYE-PISPPQ-VPVVHEKQDSLLLLS-QRGAEPAEQRNDARSPGSISYLPSFFTKLENT 2201
QQ	2336 GPG	WERG
Qy	2202 SPM	SPWVKSKKQEIFRKLNSSGGDSDMAAAQPGTEIFNLPAVTTSGSVSSRGHSFA-DPASN 2260
οp	2386 QPL	QPLRPGKSSGGPPCSLSSEVEAGPQGCATDPRPH 2419
οy	2261 LGL	DKVEDHGVVMSQPMGV
q	2420 cg-	ELSPSFLNPPLPPSTDDSDLSTEEARLAGKGGRRKVGR 2459
οy	2314 PSP	PSPHSGGVCGYKLISKSNSRKSKSPIPGQGYLGTE 2348
<b>අ</b> ධ .	2460 PGA	PGA-TGGPCPMADETPPTSASDSGSSQSDSDVPPETEECPSITAEAALDSDEDGDFLPVD 2518
QY	2349 RPS	RPSSVSSVHSEGDYHRQTPGWAWEDRPSSTGSTQFPYNPLTMRMLSSTPPTPIAC 2403

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       ---PPRPDVCMADPE 2558
                                                                                                          01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
MICROTUBULE-ASSOCIATED PROTEIN IB (MAPI.2) (MAPI.X)) [CONTAINS: MAPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEGNITE; PS00230; MAPIB_neuraxin; 10.
PROSITE; PS00230; MAPIB_NEURAXIN; 7.
Microtubules; Repeat; Phosphorylation.
CHAIN 7.2464 MAPI LIGHT CHAIN LC1.
DOMAIN 589 787 LXS-RICH (HIGHLY BASIC, CONTAINS MANY KEE AND KKEI,VV REPEATS).

DOMAIN 1865 2068 12 X 17 AA TANDEM REPEATS.
                                                                                                                                                                                                                                     Noble M., Lewis S.A., Cowan N.J.,
"The microtubule binding domain of microtubule-associated protein
MAP1B contains a repeated sequence motif unrelated to that of MAP2
and tau.";
                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                           2559 GLSSESGRVERLREKGRPGRRAPGRAKPASPARRLDIRGKRSPTP
                          ---APSAVNQAAPHQQNRI-WEREPAP
                                                                                           Ā
                                                                                          2464
                                                                                                                                                                                                                        STRAIN-SWISS WEBSTER; TISSUE-Brain;
MEDLINE-90094539; PubMed-2480963;
      2519 KAGGVSGTHHPRPGHDPPPTPLPDPRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, X51396; CAA35761.1; -. PIR; S07549; ORMSP1. MG1:97179; Mtap5. InterPro; IPR000102; -.
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                                                                                          STANDARD;
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                                                                        RASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDVDGEPERQRMFPM----D 902
2.----AEQMDVDQQEHSAEEGSVCDPPPATKADSVDVEVRVPENHASKVEGDNTKERDLD
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MEDLINE=97001161; Pubmed=8812494;
Fink J.K., Jones S.M., Esposito C., Wilkowski J.;
Human microtubule-associated protein la (WAPIA) gene: genomic organization, cDNA sequence, and developmental- and tissue-specific -----PQQQLPPS----SQAEGM-GQVPRTHRLITLADHICQIITQD-----FAR 1822 TAE-----PYGFRS-----SMLFDTMQHHL------ALNRDLTTSSVEKDSGGKT 1817 AAD---ALAALVDAAASAPQMDVSKTKESK----HEAAR-----LEENLRSRSAAVSEQQ QLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRGK RLLD------DISNGYDDTEDGGHTLGD----CSYSYETTEKITSFPESESYSYE 2066 NQVSSQTPQQPPTSTFQNSPSALVS-TPVRTKTSNRYSPESQAQSVHHQR--PGSRVSPE 2123 NLVDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVHEKQDSLLL---LSQRGAEPAEQR NDARSPGSISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGGGDSDMAAAQPGTEIFNLP 1921 TIEKTTKTPEDGGYTCEITEKTTRTPEEGGYS---YEISEKTTRTPEVSGYTYEKTERSR SPASSPAPPQEKLQTYQ--PEVVKANQAENDPTRQYEGPLHHYRPQQESPS----2080 LVSSCEFKHPKTELSPSFINPNPLEWFAGEEP-----TEESEKPLTQSGGAPPPSGG KHMDPPPAPMODRSPSPRH------PDVSMV--DPDALAVDQNLGKAVKKDLKEK : : | | | | : |: | : | 2300 TIPEVKATRGEEKDKETKNAA-----NASASKSAKTATTGPGTTKTAKSSTV 2346 2300 SVVTSGETRREEGDPSPHSGGVCKPKLISKSNSRKSKSPIPGQGYLGTERPSSV 2353 CHAIN Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. MAPA\_HUMAN STANDARD; PRT; 2805 AA.
P78559; 015882; 012973;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
MICROTUBULE-ASSOCIATED PROTEIN IA [CONTAINS: MAPI LIGHT TISSUE-Fetal muscle; Chiannikulchai N., Pasturaud P., Richard I., Auffray C. Beckmann J.S.; Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases. [2] SEQUENCE OF 134-419 FROM N.A. Genomics 35:577-585(1996) NCBI\_TaxID=9606; expression RESULT 9
MAPA\_HUMAN MAP1A. 2180 1763 1861 1865 1978 1977 2023 2192 2026 g ÓΥ Ω ŏ a ò q g g ò g В Qγ g δy ŏ 셤 ŏ δ δy

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                                                                                                                                          TISSUE SPECIFICITY: BRAIN.
DOMAIN: THE BASIC REGION CONTAINING THE REPEATS MAY BE RESPONSIBLE FOR THE BINDING OF MAPIA TO MICROTUBULES.
PTH: VARIOUS SERINE RESIDUES MAY BE PHOSPHORYLATED BY CAMP KINASE.
PTH: LC2 IS CORARRESSED WITH MAPIA. IT IS A POLYPEPTIDE GENERATED FROM MAPIA BY PROTEOLYTIC PROCESSING. IT IS FREE TO ASSOCIATE WITH
                                                                                 CROSS-BRIDGING BETWEEN MICROTUBDILES AND OTHER SKELETAL ELEMENTS.
SUBUNT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE
WITH MAPIA AND MAPIB PROTEINS.
                                       Fukuyama R., Rapoport S.I.,
"Brain-specific expression of human microtubule-associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat; Phosphorylation.
90 2805 MAPI LIGHT CHAIN LC2.
93 496 LXS-RICH (BASIC).
15 541 9 X 3 AA REPEATS OF K-K-[DE].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                              (MAP1A) gene and its assignment to human chromosome 15.", J. Neurosci. Res. 40:820-825(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y -> AHSRV (IN REF. 3). 9027AF693EFFBE3A CRC64;
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ST -> AK (IN REF. 2).

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C -> K (IN REF. 2).

C -> K (IN REF. 2).

C -> W (IN REF. 3).

Y -> G (IN REF. 3).

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C -> A (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.5%; Score 437.5;
19.8%; Pred. No. 3.8
                          MEDLINE=95356255; PubMed=7629894;
SEQUENCE OF 1607-1883 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                          EMBL; U38291; AAB41132.1; -. EMBL; U38292; AAB41133.1; -. EMBL; Z47038; CAA87104.1; -. EMBL; U14577; AAA81362.1; -.
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Query Match

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LRASADAKKDPAFGGKHEAPSSPISGQPCGDDQNASPSKL----SKEEL---

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SPVEEKSEPQDFKEADSWGDTKRTPGVGKEDAAEETVKPGPEEGTLEKE--EKVPPPRSP 1070
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                                                                                                                                                                                                                                                                         ||| |: || :| || PLXVIPRSREAFG--GRELGLQGKAPEKETSLFSSLTTPAGATEHVSYIQDETIPGYSE 745
YDENRKKAEEAHKIFEGLGPKVELPLYNQPSDTKVYHENIKTNQVMRKKLILFFKRRNHA 299
                                                                                                                                                                      RKEEKKDX-------KKEEKRKDTKPELK-KISKPDLKPFTPEVRKTLYKAKVPGR 483
                                                                                                                                                                                                                                    -----EIRKQREQQERFQR-VGQRGAGLSATIA-RSEHEISEIIDGLSEQENNEKQMR 398
                                                                                                                                                                                                                                                                                                                                                      QLSVIPPMMFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHEKEIFKDKFIQHPKN 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDKAE----KTEKKEEE----KKDEEEKDEKEDSKE-NTKEKDKIDGTAEE-----TEE 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QREAERLPDRTEAREESXPXVKEDVIEKAELEEMEEVHPSDEEEEDATXXEGFYPXHMQE 687
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                                                    -----KAEKRKLIKDKVGKKHLKEKISKLEEKK--DKEXKEIPXERKEL----KKDEG
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                                                                                                                  RKQREQKICQRYDQLMEAWEKKVDRIENNPRRKAKESK------TREYYEKQFP--
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                                                                            1362 PKDEVLQQKDKTLEHKEVVEPKDTAIYQKDEALHVKN·-EAVKQQXKALE-QKGRDLEQX 1418
                                                                                                                            PGYPSQYQLYAMEN--TRQTILNDYITSQQMQVNLRPDVARGLSPREQPLGLP----YPA 1648
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                                                     KGREEAASKGHV----IYEGKSGHILSYD---NIKNAREGTRSPRTAHEISLKRSYESV 1250
                                                                                                                                                                    1311 GLKYPKQIKRESPPIRAFEGAITKGK-PYDGITTIKEMGRSI-HEIPRQDILTQESR--- 1365
                                                                                                                                                                                                                                                                                  PLEIVPENIKVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDD 1478
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                          1302 GKYLPGAITSPDEHILTXDSSFSKSPESLXGPALXDIAIKWEDKVPGLKDRTSEQKKEPE 1361
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EEVRLVGRGG------BSGSS 2509
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                                                                                                                                                                                                DSLLLLSQRGAEPAEQRNDARSPGSISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGGG 2222
                                                                                                                                                                                                                                                                                       GVVMSQPMGVVPGTANTSVVTSGETRREEGDPSPHSGGVC--RPKLISKSNSRKSKSPIP 2340
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2020 QOESPSPQQQLPPSSQAEGMGQVPRTHRLITLADHI--CQIITQDFARNQVSS-QTPQQP 2076
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STRAIN-C57B1/6J, AND CAST/EI: TISSUE-Brain;
MEDLINE-92263101; PubMed-1350108;
Su L.-K., Kinzler K.W., Vogelstein B., Preisinger A.C., Moser A.R.,
Luongo C., Gould K.A., Dove W.F.;
"Multiple intestinal neoplasia caused by a mutation in the murine
homolog of the APC gene.";
Science 256:668-670(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Su L.-K., Kinzler K.W., Vogelstein B., Preisinger A.C., Moser A.R., Luongo C., Gould K.A., Dove W.F.; Science 256:1114-1114(1992).
                                                                                     PEQPVCPXGGSGGPPSSASPEVEAGPQGCXTEPRPHRGELSPSFLNPPLPPSIDDRDLST
                               DLTPLSP---APPASLDLALAPAPSLPG--DMGDGILPCHLECSEAATEKPSPFQVPSED
                                                                -----PISTFQNSPSALVSTPVRTKTSNRYS------PESQAQSVHHQRPGSRVS
                                                                                                                                                                                                                                                                DSDMAAAQPGTEIFNLPAVTTSGSVSSRGHSFADPASNLGLEDIIRKALMGSFDDKVEDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathl; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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STRAIN-BALB/C; TISSUE-Liver;
Dicker F., Lambertz S., Reitmair A., Ballhausen W.G.;
"The murine APC gene: alternative splicing of 5' untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATIVE SPLICING.
MEDLINE-94061824; PubMed-8242607;
Osbitam M., Sugityama H., Kitagawa K., Taketo M.;
"APC gene messenger RNA: novel isoforms that lack exon 7.";
Cancer Res. 53:5589-5591(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APC_MOUSE STANDARD; PRT; 2845 AA.
061315; 062044;
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
ADENOMATOUS POLYPOSIS COLI PROTEIN (APC PROTEIN) (MAPC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----IACAP----SAVNQAAPHQQ 2416
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the FMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a licensee agreement (see http://www.isb-sib.ch/announce/or send an email to licenseelabrsib.ch).
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                                      SIMILARITY).
SUBDIT: PORMS HOMOOLIGOMERS AND ASSOCIATES WITH CATENINS (BY SIMILARITY).
ALTERNATIVE PRODUCTS: 4 ISOFORMS; 1 (SHOWN HERE), 2, 3 AND 4; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSVESYSEDDESKFCSYGOYPADLAHKIHSANHMDDNDGELDTPINYSLKYSDEQLNSGR 1038
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FUNCTION: TUMOR SUPPRESSOR. ALLOWS THE RAPID TURNOVER OF BETA-CATENIN. APC ACTIVITY CORRELATED WITH ITS PHOSPHORYLATION STATE ALLOWS THE DOWNREGULATION OF CYTOPLASMIC BETA-CATENIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISSING (IN ISOFORM 2 AND ISOFORM 4).
MISSING (IN ISOFORM 3 AND ISOFORM 4).
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                                                                                                       TISSUE SPECIFICITY: EXPRESSED IN LIVER, SPLEEN, KIDNEY, HEART, LUNG, BRAIN, STOMACH, INTESTINE, TESTIS AND OVARY.
PHOSPHORYLAFED BY GSK-3B (BY SIMILARITY).
SIMILARITY: CONTAINS 7 ARM REPEATS.
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                                                                                                                                                                                                                                                                                                                                        Pfan; PP00514; Armadillo_seg; 4.
PROSITE; PS50176; ARM_REPEAT; 1.
Anti-oncogene; Phosphorylation; Alternative splicing; Repeat;
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COILED COIL (POTENTIAL)
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ASP/GLU-RICH (ACIDIC).
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19.4%; Pred. No. 4
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492 RRNYGKRRGRNQQIARPSQEEKVEEKEEDKAEKTEKKEEEKKDEEEKDE-
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                                                                                                                                                                              GSTAGEVYWSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQT 1612
                                                                                                                                                                                                   2334 NGISPPNKLSQLPRTSSPSTASTKSSGSGKMSY----TSPG----RQLSQQNLTKQA 2382
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1319 KRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHEIPRQDILTQESRKTPEVVQSTRPII 1378
                                                                                                                                  GSPMMNRTSDVTIPPNKSTNHERKSTLTPTQRESIPAKSPV--PGVDPVVSHSPFDPHHR 1552
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                                                                                                    2229 TMIHIPGLRNSSSSTSPVSKKGPPLKTPASKSP----SEGPGATTSPRGTKPAGKSEL--
                                                                                                                                                                                                                                             2383 SLSKNASS------GNGSNKK
                                                                                                                                                                                                                                                                     1673 PPMDRITYIPGTQITFPPRPYNSASMSPGHPTHLAAAASAERERE--REREKERERIA
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                      -----HLTPDQEEKPFTSNKGPRILKPG----
                                           EGSISQCTPIKFDNNSCQSAIKHNVKSLITGP----SKLSRGMPPLEIVPENIKVVERGK
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                                                                                                                                                                                                                                                                                                                                                                                                                             2553 KHSSSLPRVSTWRRTGSSSSILSASSESSEKAKSEDERHVSSM--------
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Q01484; Q01485;
01-APR-1993 (Rel. 25, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID).
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Conomics 10.858-866(1991).

Conomics 10.868-866(1991).

Conomics 10.8
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                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                              TISSUE-Brain stem;
MEDLINE-94075409; PubMed-8253844;
Chan W., Kordell E., Bennett V.;
"440-ND ankyrinB: structure of the major developmentally domain and selective localization in unmyelinated axons."
J. Cell Biol. 123:1463-1473(1993).
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MEDLINE=91302466; PubMed=1830053;
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Pfam; PF00023; ank; 22.
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IPR002110;
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PIR, A39643, A39643.
PIR, B39643, B39643.
PIR, S14569, S14569.
HSSP, Q00420, IAWC.
sapiens (Human)
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SPFNTTFPLDYMKDEFLPALSLQSGALDGSSESLK------NEGVAGSPCGSL 2185
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                                                                                                                                         367 AGLSATIARSE------HEISEIIDGLSEQENNEKOMROLSVIPPMMFDAEORRV 415
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                                         --KQREQKICQRYDQLMEAWEKKVDRIEN- 327
                                                                                         -----BPRRAKESKTREYYEKQFPEIRKQREQQ-----ERFQRV-----GQRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q -> QFLGKLHLPTAPPPLNEGESLVSRILQLGPPGTK (IN ISOFCRM 2).
MISSING (IN ISOFCRM 2 AND ISOFCRM 3).
GQ -> PE (IN REF. 4).
I -> S (IN REF. 2).
QY -> HA (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QNASP----SKLSKEELIQSMDRVDREIAKVEQQILKLKKKQQQLEEEAAKPPEPEKPVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.3%; Score 411.5; DB 1; Length 3924; 18.7%; Pred. No. 5.2e-08;
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> Y (IN REF. 2).
52AC496C428E29D2 CRC64;
Pfam; PF00531; death; 1.
PROSITE; PS50088; ANK_REPEAT; 20.
PROSITE; PS50297; ANK_REP_REGION; 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
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13; Conservative 357; Mismatches 946;
                                                                                                                                                                                                                                                                                                                                                                     REPEAT-RICH REGION
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                                                               Phosphorylation; Multigene family
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                         3627 ----ISHSYAEIEQTITLDHSEGFSVLQEELCTAQHKQKEEQAVSKESETCDHPPIVSEE 3682
                                                                                                     ||| : | : | : | 3743 TPGT------SKIPEE 3767
2187 SISYLPSFFTKLENTSPMVKSKKQEIFR-KLNSSGGGDSDMAAAQPGTEIFNLPAVTTSG 2245
                                                                                                                                                            2293 VPGTANTSVVTSGETRREEGDPSPHSGGVCKPKLISKSNSRKSKSPIPGQGYLGTERPSS 2352
                                                                                                                                                                                                                                          2353 VSSVHSEGDYHRQTPGWAWEDRPSSTGST---QFPYNPLTMRMLSSTPPTPIACAPSAVN 2409
                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95148647; PubMed=7846077;
Rakiuchi H., Watanabe M., Ushijima T., Toyota M., Imai K.,
Rakiuchi H., Watanabe M., Ushijima T., Toyota M., Imai K.,
Weisburger J.H., Sugimura T., Magao M.;
"Specific 5'-GGGA-3'-->5'-GGA-3' mutation of the Apc gene in rat colo
tumors induced by 2-amino-1-methyl-6-phenylimidazo[4,5-b]pyridine.";
Proc. Natl. Acad. Sci. U.S.A. 92:910-914(1995).
-!- FUNCTION: TUMOR SUPPRESSOR: ALLOWS THE RAPID TURNOVER OF BETA-
CATENIN. APC ACTIVITY CORRELATED WITH ITS PHOSPHORYLATION STATE
ALLOWS THE DOWNREGULATION OF CYTOPLASMIC BETA-CATENIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=FISCHER 344/N; TISSUE-Brain; MEDLINE-96116966; PubMed-8563176; TOYOCA M., Ushljima T., Kakiuchi H., Watanabe M., Imai K., Yachi A., Sugimura T., Nagao M.; Sugimura T., Magao M.; Maranabe Genome 6:746-748(1995).
                                                                                ---PASNLGL----EDIIRKALMGSFDDKVEDHGVVMSQPMGV-
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SUBUNIT: FORMS HOMOOLIGOMERS AND ASSOCIATES WITH CATENINS (BY SIMILARITY).
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-!- PTM: PHOSPHORYLATED BY GSK-3B (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 7 ARM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
ADENOMATOUS POLYPOSIS COLI PROTEIN (APC PROTEIN).
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Pfam; PF00514; Armadillo_seg; 4.
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SEQUENCE FROM N.A.
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MUTAGENESIS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLP------QLQHRAAVIP 938
                                                                                                                                                                                                                                                                                                                   NHARKQREQKICQRYDQLMEAWEKKVDRIENNPRRKAKESKTREYYEKQFPEIRKQREQQ 356
                                                                                                                                                                                                                                                                                                                                            934 NFAKSESSNRTCS-----MPYAKVEYKRSSNDSLNSVTSSDGYGKRGOMKPSVESYSEDD 988
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                                                                                                                                                                                                           C->R: IN AN IQ-INDUCED COLON TUMOR. W; 3CBB2EA8A34E8F47 CRC64;
                                                                                                                                                                                                                                                              Query Match 3.2%; Score 406; DB 1; Length 2842; Best Local Similarity 19.4%; Pred. No. 5.7e-08; Matches 461; Conservative 293; Mismatches 844; Indels 780;
                                                             ARM 1.
ARM 3.
ARM 4.
ARM 4.
ARM 5.
ARM 6.
ARM 7.
SER-RICH.
ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
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ASP/GLU-RICH (ACIDIC).
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 ARM_REPEAT; 1.
             Phosphorylation;
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2842 AA;
PROSITE; PS50176;
            Anti-oncogene;
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qq	: 1579 SAMPTKS	:
Qy	939Б	PMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEE 975
qq	 1633 GDDVP	
٥y	916	-QRQRQEQIDLECRSSTSPCGTSKSPNREWEVLQPAPHQL 1014
qq	1693 RSTDE	STDEAGRGKVSSIAIPDLDGSKAEEGDILAECINSALPKGRSHKPFRVKKIMDQVQQAS 1752
οy	1015 ITNLP :  :	ITNLPEGVRLPTRPTRPPPLIPSSKTTVASERPSFIMGGSISQGTPGTYLTSHNQASY 1074 
qq	1753 MTSSG	MISSGINKNQIDIKKKKRPISPVKPMPQNTEYRIRVRKNTDSKVNVNTEETFSDNKDS- 1809
δy	1075 TQETP	GLLVRAC
QQ	1810	
δy	1134 GTAGA	GTAGAIQEGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGIPTEALVKGSISRMPIE 1193
qq	1834	GGFTFDSPHHYAPIEGTPYCFSRNDSLSSLDFD 1866
δy	1194 DSSPE	AASKGHVIYEGKSGHILSYDNIKNAREGTRSPRT
QQ	1867 DDDVD	DDDVDLSREKAELRKGKESKDSEAKVTCHTEPSSSQQSARKAQASTKHP 1915
δλ	1254 IKQGMS	ISSPINGER 1301
qq	1916 VNRGF	VNRGPSKPLLQEQPTFPQSSKDVPDRGAATDEKLQNFAIENTPVCFS 1962
δλ	1302 RATTE	RATTESFEDGLKYPRQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHEIPRQDILT 1361
QQ	1963 RNSSI	RDAEPANA
QY	1362 QESRK	QESKRTPEVVQSTRPIIEGSISQCTPIKFDNNSGQSAIKHNVKSLITG 1409
QQ	2002 QASGY	CFSRNSSLS
δλ	1410 PSKLSR	SRGMPPLEIVPENIKVVERGKYEDVKAGETVRSRHT 1449
qq	11:1 2052 PSRLK	
Qy	1450 SVVSS	SVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTWSRGSPMMNRTSDVTI 1507
qq	2103IQE	-Š
Qy	1508 PPNKS	PNKSINHERKSTLIPIQRESIPAKSPVPGVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQ 1567
qq	2149	HITPDQEE 2165
0y	1568 LDPAM	LDPAMPFHRALDPAAAAYLEQRQL-SPTEGYPSQYQLYAMENTRQTILNDYITSQOM 1623
QQ	2166	RILKPGEKSTLEAKKIESENKGIKGGKKVYKSLITGKIRSNSEISSQMKQPL 2217
δλ	1624 QVNLR	QVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRITYIPG 1683
qq	2218 QTNM-	SRGR
Οy	1684 TQITE	THLAAAASAEREREREKERERERIAAASSI
qq	2251 PPLKTP	PASKSPSEGPVATTSPRGTKPAVKSELSPITRQTSHISGSNK 2297
Qy	1744 QPGRP	QPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMPL 1798
qq	2298 GPSRSGS-	RDSTPSRPTQQPLSRPMQSPGRNSISPGRNGISTP-1
δy	1799 PAGGP	PAGGPSISQGLPASRYNTAADALAALVDAAASAPQMDVSKTK 1840
qq	2351 PSTAS	STASTKSSGSGKMSYTSPGRQLSQQNLSKQTGLSKNASSIPRSESASKGLNQMNNSNGS 2410
δλ	1841 ESKHE	ESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVY 1900

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...----ESDRSERPALVRQSTFIKEAPSPTLRRKL 2456
                                                                                                                                                                                                                 1961 LSSHRYETPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGPLHHYRPQ 2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2081 FQ--NSPSALVSTPVRTKTSNRYSPESQAQSVHHQRPGSRVSPENLVDKSRGSRPGKSPE 2138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
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                                                                      1901 SEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVIITRQIASDKDARERGSQSSDSSSS
                                                                                                                                             EESASFESLSPSSRPDSPTRSQAQTPVLSPSLPDM-----S
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                                                                                                                                                                                                                                                                                                                                                                                                           SESPS---RLP----SKHSSSLPRVST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FNLPAVTTSGSVSSRGHSFADPASNLGLEDIIRKALMGSFDDKVEDHGVVMSQPMGVVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2296 TANTSVVTSGETRREEGDPSP--HSGGVCKPKL--ISKSNSRKSKSP-----IPGQGY
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                    LSTH----PS----VQAGGWRKLPP----NLSPTI---EYSDGRPSKRHDIARSH----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-94043435; PubMed-8227122;
Schlueter C., Duchrow M., Wohlenberg C., Becker M.H.G., Key G.,
Flad H.-D., Gerdes J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     litted (MAR-1997) to the EMBL/GenBank/DDBJ databases. FUNCTION: THOUGHT TO BE REQUIRED FOR MAINTAINING CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2345 LGTERPSSVSSVHSEGDYHRQTPGWAWEDRPSSTGSTQ 2382
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2411 NKKVELSRMSSTKSSGS---
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MKI67.
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P46013;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEANLIVAKSWADVVKLGAKQTQTKVIKHGPQRSMNKRQRRPATPKKPVGEVHSQFSTGH 710
SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

BY SUPEROPARITYL STAGE: EXPRESSION OF THIS ANTIGEN OCCURS
PREFERENTIALLY DURING LATE G1, S, G2, AND M PHASES OF THE CELL
CYCLE, WHILE IN CELLS IN G0 PHASE THE ANTIGEN CANNOT BE DETECTED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               482 SSVDINNFGDSINESEGIPLKRRRVSFGGHLRPELFDENLPPN------TPLKRGE 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPVDHDSL------ESKRPRLEQVSDSHFQ-RVSAAVLPLVHPLPEGLRASA- 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       711 ANSPCTIIIGKAHTEKVHVPARPYRVLNNFISNOKMDFKED----LSGIAEMFKTPVKEQ 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      767 POLTSTCHIAISNSENLLGKQFQGTDSGEEPLLPTSESFGGNVFFSAQN-AAKQPSDK-C 824
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                                                                                                                                                                                                                                                                                                                                                        X 122 AA APPROXIMATE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3256;
                                                                                                                                                                                                                                                                                                             Cell cycle; Antigen; Nuclear protein; ATP-binding; Repeat;
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578F8C51BED42517 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                          SIMILARITY: CONTAINS 1 FHA DOMAIN.
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Pfam; PF00498; FHA; 1.
PROSITE; PS50006; FHA_DOMAIN; 1.
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EMBL; X6551; CAA46520.1; -.
EMBL; X94762; CAA64388.1; -.
                                                                                                                                                                                                                                                                                                                             Alternative splicing.
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ORYDQLMEAWEKKUDRIENNPRRKAKESKTREYYEKQFPEIRKQREQQERFQRVGQ 	RGAGLSATIARSEHEISEIIDGLSEQENNEKOMROLSVIPPMMFDAEORRVKFI   :  :: :        :  :  :  :           SGRSTEFRNIQKLPVESKSEETNTEIVECILKRGKATLLQQRR	NMNGLMEDPMKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNFGLIASYLERKSV 	PDCVLYYYLTKKNENYKALVRRNYGKRRGRNQOIARPSQEEKVEEKEEDKAEK	SKENTEEEKKDEEEKDEKEDSKENTKEKDKIDGTAEETE	EREGATPRGRKTANSGGRR	AATEEPPPPLPPPPEPISTEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAK	MVGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRKPREERDVSQCESVASTVSA	QEDEDIEASNEEENPEDSEVEAVKPSEDSPENATSRGNTEPAVELEPTTETAPST	SPSLAVPSTKPAEDESVETQVNDSISAETAEQMDV ::	DQQEHSAEEGSVCDPPPATKADSVDVEVRVPE	NHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATC	SADEDVDGEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQH	RHIKAMH :	ESAL		LPTTRPTRPPPPLIPSSKTTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQE-TPRPS	VGSISLGLPRQQESAKSATLPYIKQEEFSPRSONSQPEGLLVRAQHEGVVRG   :   :   :   :   :   :   :   :   :   :
309	365 875	419	472	525 1012	563	602	653 1178	709	764	799	831	884	933 1520	969	991	1024	1083 1737
Qy Dp	yo da	Oy Dp	oy Ob	Oy Dp	Qy Dp	Qy	Oy Dp	QY	Qy Db	Qy Db	Oy Dp	Oy Db	Oy Db	Oy Dp	Oy Ob	Qy Ob,	QY Dp

oy ep	1135 TAGA:	TAGAIQEGSITRGTPISKISVESIPSLRGSITQGTPALPQTG-IPTEALVKGSISRMPIE 1193
Qy	1194 DSSPI	YEGKSGHIL
a	1820	
οy	1254 IKQGN	GLICRALPRGSPHSDLKERTVLSGSIMOGTPRATTESFED
đQ ·	1858	LCKSPQSDPADTPTNTKQRPKRSLKKADVEEEFLAFRKLTPSAGK 1902
Qy	1311 GLKYI	GLKYPKQIKRESPPIRAFEGAIT
q	1903 AMHTI	AMHTPKAAVGEEKDINTFVGTPVEKLDLLGNLPGSKRRPQTPKEKAKALEDLAGFKELFQ 1962
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QQ	ТЪ	
Qy	X =	GMPPLEIVPENIKVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRST
q	00	RETAGDGKSIKA 2
δ d	1463 LHEAE   : 2042 FKESA	LHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTSDVTIPPNKSTNHERK 1518
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5 A		ST-TDDKTTKIACKSPPPESMDTPTSTRRRPKTPLGKRDIVEELSALKQLTQTTHTDKVP 2150
Qy	1566 TQLD	TQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQT-ILNDY 1617
qq	1 2151 GDEDF	:     :     :     :     :     :     :     :     :     :       :       :       :         :
δλ	1618 ITSOC	ITSQQMQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPPTI 1662
අ	2210 PTTHE	PTTHEKTTKIACRSPQPDPVGTPTIFKPQSKRSLRKADVEEESLALRKRTPSVGK 2264
QY	1663LVI	PRPYNSASMSPGHPTHLAAAASAERERERE
qq	2265 AMDTE	AMDIPRPAGGDEKDMKAFMGTPVQKLDLPGNLPGSKRWPQTPK 2307
Οy	1721 EKERI    :	EKERERERIAAASSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGT 1778
QQ	2308 EKAQ	EKAQALEDIAGFKELFQTPGTDKPTTDEKTTKIACKSPQPDPVDTPASTKQRPK 2361
Qy	1779 NGTSV	NGTSVITPLDPTAQLRIMPLPAGGPSISQGLPASRYNTAADALAALVDAAASAP 1832
qq	2362R	RINIRKADVEEEFLALRKRTPSAGKAMDTPKPAVSDEKNINTFVETPVQKLDLLGNLP 2418
Qy	1833 QMDV8	QMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAF 1887
qq	2419GSF	VGFKELFOTPGHTEESMTDDKITEVSCI
Qy	1888 PSGKI	SGKPQPHS-SVVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVIITR 1939
QQ	2467	PTG 2517
Óγ	1940 QIASI	QIASDKDARERGSQSSDSSSLSSHRYETPSDAIEVIS 1977
qq	2518 DSKS	DSKSIKAFKESPKQILDPAASVTGSRRQLRTRKEKARALEDLVDFKELFSAPGHTEESMT 2577
Qy	1978	PASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGPL 2014
qq	2578 IDKN	IDKNIKIPCKSPPPELIDIAISTKRCPKTRPRKEVKEELSAVERLIGISGQSTHIHKEPA 2637
Óγ	2015	HHYRPQQESPSPQQQLPPSSQAEGMGQVPRTHRLITLADHICQIIT 2060
qq	2638 SGDEC	SGDEGIKVLKQRAKKKPNPVEEEPSRRRPRAPKEKAQPLEDLAGFTELSETSGHTQESLT 2697
Οy	2061 QDFA	QDFARNQVSSQTPQQPPTSTFQNSPSALVSTPVRTKTSNR-YSPE 2104

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2698 ACKATKIPCESPPLEVVDTTASTKRHLRTRVQKVQVKEEPSAVKFTQTSGETTDADKEPA 2757
                                                                                                                                                                                                                                                                                                  -----LASFQE-----LSQTPGHTEELANGAADSFTSAPKQTPDSGKPLKISRRVL 2963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yeast 77.413-424(1991).
-1- MISCELLANEOUS: THIS PROTEIN IS ENCODED BY A NON-ESSENTIAL GENE.
-1- SIMILARITY: SOME, TO S.POMBE SPACZEL2.01.
                                                                     LLLLSQRGAEPAEQRNDARSPGSISYLPSFFTKLENTS-----PMVKSKKQEIFRKLNS
                                                                                                                                                                                         SG----GGDSDMAAAQP----GTEIFNLPA---VTTSGSVSSRGHSFADPASNLGLED
                                                                                                                                                                                                               IIRKALMGSFDDKVEDHGVVMSQPMGVVPGTAN---TSVVTSGETRREEGDPSPHSGGVC
                                                 SQAQSVHHQRPGSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVHEKQDS
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01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYPOTHETICAL 138.5 KDA PROTEIN IN RPS14A-GNS1 INTERGENIC REGION.
YCR033W OR YCR33W OR YCR592.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wicksteed B.L., Roberts A.B., Sagliocco F.A., Brown A.J.P.; "The complete sequence of a 7.5 kb region of chromosome III Saccharomyces cerevisiae that lies between CRY1 and MAT."; Yeast 7:761-772(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-91335897; PubMed-1872032; Jaha Y., Sloninski P.P., Herbert C.J.; Jrha Complete sequence of the unit YCR59, situated between MAT, reveals two long open reading frames, which cover 918, MAT, reveals two long open reading frames.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccl
Saccharomycetales; Saccharomycetaceae; Saccharomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00249; myb_DNA-binding; PROSITE; PS50909; MYB_3; 1. Hypothetical protein DOMAIN 594 599 POI
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ECEILTKLSENLRKEEIENKRKEH-----ELMEOKRREEGIETEKEKSLRHPSSSSSSR 600
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8D133A0918658E53 CRC64;
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ilarity 20.2%; Pred. No. 8.6e-08;
Conservative 181; Mismatches 368;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       990 VGQPTHGHNTSISSIDGSIRPFGPDFHRDTFSKISAPLTTLPPPRLPSIQFPRSEMAEPT 1049
                                                                                                                              1084
                                                                                                                                                                                           ------DIGRKSTTIS-----NLLNNSDRSMKSSFQSASRHEA 1116
                                                                                                                                                                                                                                                          1117 OLEDTPSMNNIVVQEIKPNITTPRSS-SISALLNPVNGNGQSNPDGRPLLPFQHAISQGT 1175
                                                                                             -----ESVETQVNDSISAETAEQMDVDQQEHSAEEGSVCDPPPATKADSVDVEVRV 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
----QQSQILIQPERPNINAYSNIPPQQRPALGYF 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEVELOPMENTAL STACE: DISAPPEARS AFTER THE CARTILAGE DEVELOPMENT (BY SIMILARITY).
SIMILARITY: CONTAINS 1 INMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
SIMILARITY: CONTAINS 2 LINK DOMAINS.
SIMILARITY: CONTAINS 1 CFTYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 SUSHI (SCR) REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYALURONIC ACID.
SUBCELLULAR LOCATION: SECRETED; EXTRACELLULAR MATRIX.
SUBCELLULAR LOCATION: SECRETED; EXTRACELLULAR MATRIX.
ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; V0 (SHOWN HERE) AND V1; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: PRECHONDROGENIC CONDENSATION AREA OF DEVELOPING LIMB BUDS.
                              ----NATSRGNTEPAVE------LEPTTETAPSTSPSLAVPSTKPAED-
                                                                                                              888 DVDGEPERQRMFPMDSKPSLLNPTGSILVSSPLKP-----NPLDLPQL--QHRAAVIP
                                                                                                                                                            829 PENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCSADE-
                                                                                                                                                                                                                                                                                                                                                                                                      PGCV_CHICK STANDARD, PRT; 3562 AA. 090953; 090945; 01.NOV-1997 (Rel. 35, Last sequence update) 01.NOV-1997 (Rel. 40, Last annotation update) 01.CCT-2000 (Rel. 40, Last annotation update) VERSICAN CORE PROTEIN PRECURSOR (LARGE FIBROBLAST PROTEOGLYCAN) (CHONDROITIN SULFATE PROTEOGLYCAN CORE PROTEIN 2) (PG-M).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X60226; CAA42787.1; -.
                                                                                                                                                                                                                                                                                                                           PTF---PLPAPRTSPIS 1189
                                                                                                                                                                                                                                                                                            939 PMVSCTPCNIPIGTPVS 955
----RDGTSSESV---
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NCBI_TaxID=9031;
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PGCV_CHICK
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CALCIUM-BINDING (POTENTIAL).
DR Pfam; PF00047; 1g; 1.

Pfam; PF00049; 1g; 1.

DR Pfam; PF00059; lectin_c; 1.

Pram; PF00084; sush; 1.

DR PROSITE; PS00010; ASX.HIPROXYL; 1.

PROSITE; PS01086; EGF_1; 2.

DR PROSITE; PS01187; EGF_2; 1.

DR PROSITE; PS01241; LINK; 2.

DR PROSITE; PS00141; LINK; 2.

DR PROSITE; PS00141; LINK; 2.

DR PROSITE; PS00151; CITYPE_LECTIN_1; 1.

R PROSITE; PS0041; C_TYPE_LECTIN_2; 1.

R Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi; signal; Repeat; EGF_11ke domain; Calcium; Immunoglobulin domain; W Hyaluronic acid; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
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EGF-LIKE 2, CA)
C-TYPE LECTIN.
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	ps 118;	56 840	26	668	139 959	199	1002	232 1062	289 1117	346	1177	406 1229	466	1264	526 1308	578	1352	638	1400	698	1445	718 1505	167	1565	821 1618	881
VARSPLIC 485 1411 MISSING (IN ISOFORM V1). SEQUENCE 3562 AA; 388078 MW; 9BC566E88C1602D2 CRC64;	/ Match 3.0%; Score 374.5; DB 1; Length 3562; Local Similarity 18.1%; Pred. No. 1.1e-06; les 511; Conservative 379; Mismatches 1102; Indels 833; Gap	NGGAFSTEQ-SRYPPHSVQYTFPNTRHQQEFAVPDXRSSHLEVSQASQL::	LOQQQQQQLRRRPSLLSEFHPGSDRPQERRTSYEPFHPGPS	:: : : :	PVDHDSLESKRPRLEQVSDSHFQRVSAAVLPLVHPLPEGLRA	SADAKKDPAFGCKHEAPSSPISGQPCGDDQNASPSKLSKEELLQSMDRVDREIAKVEQQI	KA-TEKSPATSAEDEVSTGTEISKYTMTEG-GQISSYTSAEKESY	LKLKKKKQQQ	RSIVQIIYDENRKKAEEAHKIFEGLGPKVELPLYNQPSDTKVYHENIKTNQVMRKKL 	ILFFKRRNHARKQREQKICQRYDQLMEAWEKKVDRIENNPRRKAKESKTREYYEKQF	TAGFESPQTTTQEKHDEMGSAYDEMYPATELSVPALMLTEYGQVSGPVETSTRSLHLTGT	PEIRKQREQOERFQRVGQRGAGLSATIARSEHEISEIIDGLSEQENNEKQMRQLSVIPPM   :   :   :   :	MFDAEQRRVKFINMNGLMEDPWKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNFGLIASYL	TMLSSPSTAGSISLLTLGASPS	ERKSVPDCVLYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEKVEEKEEDKAEKTE	KKEEEKKDEEEKDEKEDSKENTKEKDKIDGTAEETEEREQATPRGRKTANSQ	: :	GRRKGRITRSMINEAAAASAAAAAATEEPPPPLPPPPEPISTEPVETSRWTEEEMEVAKK	IDKEYFTSSTATAVARPTAPPTVMEATEALQPQEVSPTSHPDSGTDIR	GLVEHGRNWAAJAKWVGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRKPREERDVSQ	LYVIQITGNDTDHPVNEFLDLFSRHILPHAVDETHTDAESAQTEP	CESVASTVSA	EEENPEDSEVEAVKPSEDSPENATSRGNTEPAVELEPTTETAPSTSPSL	:   :: :   :	AVPSTKPAEDESVETQVNDSISAETAEQMDVDQQEHSAEEGSVCDPPPATKADS	VDVEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSA
VARS	Query Match Best Local Matches 51	9	57	841	98	140	960	200	233	290	1118	347	407	1230	467	527	1309	579	1353	639	1401	699	719	1506	768	822
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qa	: :   1619NLLLITNE	:     :
Qy Dp	882 TCSADEDVDG    :    1647 TMSSHED	TCSADEDVDGEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAV 936    :
o o	937 IPPMVSCTPCN    :      1695 IPKGGTATPGN	PCNIPIGTPVSGYALYQRHIKAMHESALLEEGRQROEGI 983 
S S	984DLECRSS'   :   :   1744 GSGDVEENST	104
δ		NQASYTQETPKPSVGSISLGLPRQQESAKSA ::       ::
g	1791 EITPALPGGT	EITPALPGGTRILYSTFDQSSEATVSTNFVSELIMEQVVGSSVATEKKVEDEKEV 1845
g g	1101 -TLPYIKQE-           1846 QTTVYSSQEI	IXQELVRAQHEGVVRGTA 1136
δò	_	TE 118
8 8	1181 ALV	IEFELKEKLE INEGSAEEFFALLERGSFIRK VOSIUSFFILSGSGUIDVITESATLISVESK 1905 ALVKGSISRMPIEDSSPEKGREBAASKAHVIVEGKSGHIISVDNIKNAREGTR 1233
원	SVIETOTVKH	-GIGGPVISVSSIGSD 201
δλ	1234 SPRTAHEISL	SPRTAHELSLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLS 1293
QQ	2013 GLTEESEVAIEMS	SMS-ENVFSTENÇGEPTQE2055
oy D	1294 GSIMQGTPRAT    :     2056 GSRREVTSHVT	GSIMQGTPRATTESFEDGLKYPKQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHE 1353 
Qy	1354 IPRQDILTQESRKTPEVVQ	SRKTPEVVQSTRPIIEGSISQGTPIKFDNNSGQSAIKHNVKSLITGPSKL 1413
q	: :  2072KDLETAE	KDLETAEVISSPESVVNNSTLDIMVHGTIRAVAESTES 2110
Oy	SRGMPPLEIV	-ENIKVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRS
qq	2111 KKGKGSFSAV	SLGKILMIEHGSGEELKVDSSTTKLMSNGPTEKLLGSHFSFFDQGS 2166
oy B	1462TLHEA-PKAQLSP     :    :   2167 GEAETLTESFTKASVSP	TLHEA-PKAQLSPGIYDDISARRIPVSY-ONTMSRGSPMANRTSDVTIPPNKS 1512     :    :
δy	1513 TNHERKST	-TLTPTORESIPAKSPVPGVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQL 1568
q	2219 TEHDITSLQT	
δλ	DPAMPEH: 	YLFQRQLSPTPGYPSQYQLYAMENTRQTIL
දු	2268 LPKAI	KAIESSGEATEDPFFISTQANHEHVEFLSVPTIRPHSEENKVEAESDEKILLP 2322
. Уо		SQQMQVNLRPDVAR-GLSPREQPLGLPYPATR 1
සි	2323 FNNDRVTESAVIERKYLS	/IERKYLSSPFTDTEQEEELVQNIFPTEDIPRLFLTPKEE 2372
δ i	1 GIIDLTNM	ILVPHPGGTSTPPMDRITYIPGTQITFPPRPYNSASMSP 170
8	!	FSGQGSGDEFTVIPSVESLAVKETTNTLSPWPFHPASVGP 242
oy B	1701GHPTHLA.   : 2425 KLSTDKTOVF	GHPTHLAAAASAERERE-REREKERERERIAAASSDLYLRPGSEOPGRPGSHGYVRS 1756
Qy	1757 PSPSVRTQET	-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---YNP-----LTMRMLSSTPPTPIACAPSAVNQAA--PHQQNRIWEREPAPLLSAQYE 2433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---RPLPTPG---DVSLEESSHML
                     1817 AADALAALVDAAASAPQMDVSK---TKESKHEAARLEENLRSRSA--AVSEQ-----Q
                                                                  QLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRGK
                                                                                                                                     2624 TVITGLASLFTEEKEIVANRTAADPKTGTSEELTSDTGMSLDIIPVVDDRRHVTLNVSVY
                                                                                                                                                                                   GDITLIEERLQIPSEKTTIIDMDHSKSMPEDIISVQTMPNLVIRSTQVSDDNMKAEEDKY
                                                                                                                                                                                                           2011 EGPLHHYRPQQES-----PSPQQQLPPSSQAEGMGQVPRTHRLITLADHICQIITQDFA
                                                                                                                                                                                                                                                                                                                                                 --DSLLLLSQRGAEPAE-QRNDARSPGSISYL--PSFFTKLENTSPMVKSKKQEIFRKLN
                                                                                                                                                                                                                                                                                                                                                                                              SSGGGDSDMAAAQPGTEIFNLPAVTTSGSVSSRGHSFADPASNLGLEDIIRKALMGSFDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3004 VSSDMAATYKPPTTDLDTTVSSLLVFSPEPESESISTESTPH-----FNKFVTERS
                                            2529 TTDDVTPVSVILSETPYLEMGKSLATSATKMPSRVLPESSGEGSGWDGVSDSFAPDTLTH
                                                                                         STAPSVMEVE-----LTASSHIPG------VYSEVMTTHVPGDGS------Q
                                                                                                                                                              ----SHRYETPSDAIEVISPASSPAPPQE--KLQTYQPEVVKANQAENDPTR----QY
                                                                                                                                                                                                                                                        ---NQVSSQTPQQPPTSTFQNSPSALVSTPVRTKTSNRYSPESQAQSV
                                                                                                                                                                                                                                                                           2804 TTVLNELGIFLPTVPSLVSPHMPHESKESEFEAKHIGRIST-----TDDVYEPYTSANN-
                                                                                                                                                                                                                                                                                                  2111 HHQRPGSRVSPENLVDKSR----GSRPGKSPERSHVSSEPYEPISPPQVPVVHEKQ----
                                                                                                                                                                                                                                                                                                                                                                       2906 TFDVSMVTTQSMSQHATVSSSSSEEKHSTVYMQTKSASTEYEETDSV-----SLN
                                                                                                                                                                                                                                                                                                                                                                                                                                           2278 KVEDHGVVMSQPMGVVPGTANTSVVTSGETRRE--EGDPSPHSGGVCKPKLISKSNSRKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSPIPGQGYLGTERPSSVS----SVHSEGDYHRQTPGWAWEDRPS----STGSTQFP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDILIDE-91335210; PubMed-1651562;
Kinzler K.W., Nilbert M.C., Su L.-K., Vogelstein B., Bryan T.M.,
Levy D.B., Smith K.J., Preisinger A.C., Hedge P., McKechnie D.,
                                                                                                                TTIT -- AANFID -- VIITRQIASDKDARERGSQSSDSSSSLS -- -
                                                                                                                                                                                                                                                                                                                                                                                                           2956 SVSQNPKSSVTVWLVNGVSKYPEVIIPSTSSAKDSDQSDHSSD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APC_HUMAN STANDARD; PRT; 2843 AA. P2504; 015162; 0151615; 015163; 01-M2Y-1992 (Rel. 22, Created) 01-MAY-1992 (Rel. 22, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) ADENOMATOUS POLYPOSIS COLI PROTEIN (APC PROTEIN) APC OR DP2.5.
2485 ITHYFLVIEDPYNKEMDHRRGENGTS---
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MEDLINE-95134544; PubMed-7833149;
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MEDLINE=91330307; PubMed=1678319;
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Fomlinson I.P.M.;
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THE ORDER OF SUPPRESSOR ALLOWS THE RAPID TURNOVER OF BETACATENIN. APC ACTIVITY CORRELATED WITH ITS PHOSPHORYLATION STATE
CATENIN. APC ACTIVITY CORRELATED WITH ITS PHOSPHORYLATION STATE
ALLOWS THE DOWNEGULATION OF CYTOPLASMIC BETA-CATENIN.

-1 SUBUNIT: FORMS HOMOOLIGOMERS AND ASSOCIATES WITH CATENINS.

SHORT FORM, ARE PRODUCED BY ALTERNATIVE SPLICING.
SHORT FORM, ARE PRODUCED BY ALTERNATIVE SPLICING.

-1 TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES TYPES.

-1 DISBASE: DEFECTS IN APC ARE A CAUSE OF FAMILIAL ADENOMATOUS
DOLYPOSIS (FAP) AND GANDINES SYNDOME (6S), THAT CONTRIBUTE TO
TUMON BUSTELORY. BUT ALSO OF UPPER GASTROINTESTING TRACT
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SIMILARITY: CONTAINS 7 ARM REPEATS. Query Match Matches 347 1311

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                                                                                                                                                                                                                                THE NUCLEAR PORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPONENTS, INCLUDING P62.
TISSUE SPECIFICITY: HIGHEST IN TESTIS, LUNG, THYMUS, SPLEEN AND BRAIN, LOWER LEVELS IN HEART, LIVER, AND KIDNEY.
DISEASE: INVOLVED IN TUMORIGENIC REARRANGEMENTS WITH THE MET, TRK OR RAF GENES.
                                                                                                                                                                                                        FUNCTION: COMPONENT OF THE CYTOPLASMIC FIBRILS OF THE NUCLEAR POR COMPLEX IMPLICATED IN NUCLEAR PROTEIN IMPORT. ITS AMINO TERMINUS IS INVOLVED IN ACTIVATION OF ONCOGRNIC KINASES.
SUBCELLULAR LOCATION: CYTOPLASMIC SUFFACE OF THE NUCLEAR PORE COMPLEX. THE ASSEMBLY OF THE NPC IS A STEPWISE PROCESS IN WHICH TRP-CONTAINING PERIPHERAL STRUCTURES ASSEMBLE AFTER OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Min; 10344) | Min; 10344 | Min; 10441 | Min; 1044
                                         King H.W.S., Tempest P.R., Merrifield K.R., Rance A.J.; "tpr homologues activate met and raf."; Oncogene 2:617-619(1988).
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MEDLINE-88262257; PubMed-3387099;
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                                                                                                     141 ADAKKDPAFGGKHEAPSSPISGQPCGDDQNASPSKLSKEELIQSMDRVDREIAK-VEQQI 199
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                                                                            24 SVQYTFPNTRHQQEFAVPDYRSSHLEVSQASQLLQQ----QQQQQLRRRPSLLSEFHPGSD 80
                                                                                                                                                                            2.8%; Score 360; DB 1; Length 2349; 18.3%; Pred. No. 2.3e-06; Live 394; Mismatches 966; Indels 800
                 Best Local Similarity 10.3%, ... Matches 484; Conservative 394;
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Š :		ESKTREYZEKÇFPELINGNEQÇERFQRYGQRGAGLSATIARSEHEISEIIDGLSEQENNE 3 : :    ::   :	394
<b>Q</b>		QEDTD	473
Qy			414
qq	474 KA	KANKQSSVLERDNRRMEIQVKDLSQQIRVLLMELEEARGNHVIRDEEVSSADISSSSEVI 5	533
δλ	415		467
đ	534 SQ	LVALRELGETREREEQETTSSKITELQLKLESALTELEQL	593
οy	468 RK	GRNQQIAR	207
q	594 RK	RKSRQHQMQLVDSIVRQRDMYRILLSQTTGVAIPLHASSLDDVSLASTPKRPSTSQTVST 6	653
δλ	508 PS		549
a	654 PA	PAPVPVIESTEAIEAKAALKQLQEIFENYKKEKAENEKIQNEQLEKLQEQVTDLRSQNTK 7	713
οy	550 EK	EKDKIDGTAEETEEREQATPRGRKTANSQGRRKGRITRSMINE 5	265
g	714 IS	NQKLTATTQKQEQIINTMTQD	992
Qy	593 A.A.	EVAKKGLVEHGRNWAAIAK	652
qa	767 LR	LRGANEKLAVAEVRAENLKKEK-EMLKLSEVRLSQQRESLLAEQRGQNLLLT 8	817
Qy	653 MVGT	KREAQCKNFYFNYKRRHNLDNLLQQHKQKTSRKPREERDVSQCESVAS	704
qq	818 NL	SETETKQRLSSQIEKLEHEISHLKKKLENEVEQRHTLTR	867
δλ	705 TV		761
q	868 NL		925
δλ	762 ST	STSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDVDQQEHSAEEGSVCDP 8	813
q	926 GQ	PSNKEDVDDLVSQLRQTEEQVNDLKERLKTSTSNVEQYQAMVTSLEESLNKE	616
φ	814 PP.		859
qq	980 KQ	KQVTEEVRKNIEVRLKESAEFQTQLEKKLMEVEKEKQELQDDKRRAIESMEQQLSELKKT 1	1039
Oy	860 LV	LVVAQQINAQRPEPQSDNDSSATCSADEDVDGEPERQRMFPMDSKPSLLNPTGSILV 9	916
q	1040 LS	LSSVQNEVQEALQRASTALSNEQQARRDCQEQAKIAVEAQNKYERE 1	1085
οy	917 SS	SSPLKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEQ 9	916
q	1086	-LMLHAADVEALQAAKEQVSKMASVRQHLEET	1116
Qy	977 RQ	Д	1029
qq	1117 TO	RERMIKDEVSKCVCRCEDLEKONRILHDO-	1162
Qy	1030 TR	PKPSVGSISLG	1089
q	1163	IEKLSDKVVASVKEGVQGPLNVSLSEEGKSQEQILEILRF 1	1202
δλ	1090 LP	ATLPY IKQEEFSPRSQNSQPEGLLVRAQHEGVVRGTAGA IQEGSITRGTP	1149
q	1203 IR	TELQE	1237
δλ	1150 TS		1208
ф	1238	LEDSLNAEREKVQVTAKT 1	1255
ογ	1209 HV	HVIYEGKSGHILSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAP 1	1268

Db 2155 PEDMPQTSSSHSDLG  Qy 2207 SKKQEIFRKLNSSGG		RT "Dense Alu clusterin family within a 90 k R. Nat. Genet. 3:137-14 CC -1- FUNCTION: UNKNOW CC -1- FUNCTION: UNKNOW CC This SWISS-PROT entroper bloom of the Swiss I CC the European Bloinfor Use by non-profit couse by non-prof
	1574 -FHRALDPAAAYLFOROLSPTPGYPSOYOLYAMENTROTILNDYITSOQMOVNLRPDVA 1  1612 RLEBELEREHÇERHLEGRDEPQEPS	1800 AGGPSISQGLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAA 1847
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                                                              GGDSDMAAAQPGTEIFNLPAVTTS-GSVSSRGHS-----FAD 2256
                                                                                                                          IIRKALMGSFDDKVEDHGVVMSQPMGVVPGT----ANTSVVTSGE 2306
                                                                                                                                                     GQLASQGGLGMYETPLFLAHEEESGG------RSVPTTPLQV 2204
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J., Strominger J.L., Spies T.;
The human major histocompatibility complex encodes proteins with multiple repeated motifs and a ke domain.";
Sci. U.S.A. 87:2374-2378(1990).
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hubmed=8499947;
sleret L., Prieur S., Caterina D., Primas G.,
Nodriguez-Tome P., Claverie J.-M., Dausset J.,
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Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
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    Created)
    Last sequence update)
    Last annotation update)
    PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2).

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Gaps 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 EPVGRPSILKEDNL------KEFDQLDQENDDGWAGAHEEVDYTEKLKFSDEE 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    761 APAMLRERGTPPVDPKLAWVGDVFTATPAEPRPLTSPLRQAADEDDKGMR-SETPPVPPP 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRKPREERDVSQCESVASTVSAQEDE 712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -EPPPPLPP------PPEPISTEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAK 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -------KRLDE 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PQSDNDSSATCSADEDVDGEPERQRMFPMDSKPSLLNPTGSILVSSPL-KPNPLDLPQLQ 931
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Qy Db	1034 P	PPLIPSSKTTVASEKPSFIMGGSISQGTPGTYLITSHNQASYTOETPKPSVGSISLGLPRQ 1093
oy Dp	1094 Q 859 D	QESAKSATLPYIKQEEFSPRSQNSQPE-GLLVRAQHEGVVRGTAGAIQEGS 1143 
oy Ob	1144 I	ITRGTPTSKISVESIPSLRGSITQGTPALPQTGIPTEALVKGSISRMPIEDSSPEKGREE 1203
QY Db	1204 A	AASKGHVIYEGKSGHILSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRES 1263 
Qy Db	1264 P	PVSAPLEGLICRALPRGSPHSDLKERTVLSGSIMQGTPRATTESFEDGLK 1313
0y		137
q è	1050 -	TRPITEGSTSOGTPITEDNNSGOSAIKHNVKSLITGESKLSRGMPPLETUPENIKVVRG 1433
g G		111
oy do	1434 K	KYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMS 1493
δ	4	PVPGVDPVVSHSPFDP 154
<u>අ</u>	ın d	PPQVCPGWSPPAKSLAPKKPPTGPLPPSKEPLKEKL-IPGPLSP 120
ž d	1206 V	HHKGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENT 1609    :
οy	0	TRGIIDLTNMPPTILVPHPGG 166
QO (	σ (	RENAARG-SEGKPSLTLPASAPG- 127
ନ୍ ବ	1670 T 1271 -	TSTPPMDRITYIPOTOITFPPRPYMSASMSPGHPTHLAAASAREREERR 1720 
Qy	~	RERERIAAASSDLYLRPGSEQPGRPGSHG 175
a ò	1322 D 1753 Y	DKEAPPPVLLTPKAVGTPGGGGGAVPGISAMSRGDLSQRAKDLSKRSFSSORPGMER 1379 YVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMPLPAGGPSISQC 1808
음	80	GSSGSSGGGGGGGGRTGPGRGDKRSWP 1
οy	1809 L	LPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQ 1868   :
QQ	1420 S	SPKNRSRPPEERPPGLPLPPPPPSSSAVFRLDQVIHSNPAGIQQALAQ 1467
Qy Dp	1869 K	KTLEVEKRSVQCLYTSSAFPSGKPQPHSSVYYSEAGKDKGPPPKSRYEEELRTRGKTTIT 1928
Qy	1929 A	AANFIDVIITRQIASDKDARERGSQSSDSSSSLSSHRYETPSDAIEVISPASSPAPPQEK 1988
qq	1512 -	::
ογ	1989 L	LQ-TYQPEVVKANQAENDPTRQYEGPLHHYRPQQESPSPQQQLPPSSQAEGMGQVPRTHR 2047
QQ	1547 E	ERPPRKPELLQEESLPPPHSSGFLGSRPEGPGPQAESRDTG 1587

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---NSPSALV 2089
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                                                                                                                                                                                                                                                                                                              1588 TEALTPHIWNRLHTATSRKSYRPTSMEPWMEPLSPFEDVAGTEMSQSDSGVDLSGDSQVS
                                                                                     SGP----CSORSSPDGGLKGAAEGPPKRPGGS-SPLNAVPCEGPPGSEPPRRPPPAPHDG
                                                                                                                  ERSHVSSEPYEPISPPQVPVVHEKQDSLLLLSQRGAEPAEQRNDARSPGSISYLPSFFTK
                                                                                                                                         DRKELPRE--QPLPPG--PIGTERSQR----TDRGTEPGPIRPSHR-PGP----PVQFGT
                                                                                                                                                                            LENTSPM------VKSKKQEIFRKLNSSGGDSDMAAAQPGTEIFN-LPAVTTSGSVSS
                                                                                                                                                                                             SDKDSDLRLVVGDSLKAEKE----LTAS-----VTEAIPVSRDWELLPSAAASAEPQS
                                                                                                                                                                                                                                                                KNLDSGHCVPEPSSSGQRLYPEVFYGSAGPSSSQISGGSHGLSITSKQWRLRPGTPSLHP
                                                                                                                                                                                                                                                                                             --SQPMGVVPGTANTSVVTSG-----ETRREEGDPSPHSGGVCKPKLISKSNSRK
                                                                                                                                                                                                                                                                                                                                                     SKSPIPGOGYLGTERPSSVSSVHSEGDYHRQ--TPGWAWEDRPSSTGSTQF-----
                                                         STPVRTKTSNRYSPESQAQSVHH---QRPGSRVSPENLV--DKSRGSRPGKSP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.M., Barrell B.G., Rajandream M.A., Walsh
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-972;
Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: SOME, TO YEAST YCR33W.
                                                                                                                                                                                                                                                                                                                                                                                                            -----PYNPLTMRMLSSTPPTPIACAPSAVNQAAPHQQNRIWEREPAP 2426
                                                                                                                                                                                                                                                                                                                                                                                                                                         1974 PVVNFGSLPPAPPPAPPLSLLPVGPALQPPSLAVRPPAPATRVL---PSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 protein.
661 Aa; 75096 MW; 59A15D8C990E2C45 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TDBJ_SCHPO STANDARD; PRT; 661 AA. 010256; 0110226; 011026; 011-027-1996 (Rel. 34, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) 15-JUL-1998 (Rel. 36, Last annotation update) SPAC22E12.19 OR SPAC2E12.01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                   R----GHSFADPASN---LGLEDIIRKALMGSFDDKVEDHGVVM-
2048 LITLADHICQIITQDFARN--QVSSQTPQQPPTSTFQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast)
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Papan; PF00249; myb_DNR-binding; 1.
Hypothetical protein
SEQUENCE 661 AA; 75096 MW; 59A
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Submitted (MAR-1996) to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                561 TEEREQATPR-GRKTANSQGRRKGRITRSMTNEAAAASAAAAAATEEPPPPLPPPPEPIS 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |: || : ::| | : || 418 IDMIDKSETVSGFKHDVDVYDTAENEGNNTLLQIKESVHEKTPTQDEPMDISQDTIKQED 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          617
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                        28 SEPPVGDMNNEDSDINTSITQSPINSEKLIDILQESQDIKALQ-EKYLQNIYALIQNQLF
                                                                                                                                                                                                                                  267 NQPSDTKVYHENIKTNQVMRKKLILFFKRRNHARKQREQKICQRYDQLMEAWEKKVDRIE
                                                                                                                                                                                                                                                                                                                                                    N-NPRRKAKESKTREYYEKQFPEIRKQREQQERFQRVGQRGAGLSATIARSEHEISEIID
                                                                                                                                                                                                                                                                                                                                                                                                        147 RLTEIDKTKNAKKSEPFIK-----RSTRKVMSNF-----TAGDIVRSEEFLEILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              386 GLSEQE---NNEKQMRQLSVIPPMMFDAEQRRVKFIN-MNGLMEDPMKVYKDRQFMNVWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 KLEQQEKEASNVSEASRIATIPPMILSEEEVKSQYFNDQSRLVTDCPKFYHFQSMPDIWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    832 HASKVEGDNT---KERDLDRAS-EKVEPRDEDLVVAQQINAQRPEPQSDND 878
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01-FEB-1994 (Rel. 28, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
HYPOTHETICAL 113.7 KDA PROTEIN C14B9.6 IN CHROMOSOME III.
Length
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STRALNE-BRISTOL N2;
MEDILINE-94150718; Pubmed-7906398;
Wilson R., Ainscough R., Anderson K., Baynes C., Berks
2.8%; Score 350; DB 1; 21.8%; Pred. No. 1.3e-06;
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                                                      Mismatches
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                                                         Conservative
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                           Similarity
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   Query Match
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Homo sapiens (Human)
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        Craxton M., Dear S., Du Z., Durbin, R., Favello A., Fraser A., Johnston L., Jones M., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N., Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen Islas M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R., Sulston J., Thlery Mag J., Thomas K., Vaudin M., Vaughan K., Watchson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
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                                                                                                                               Mb of contiguous nucleotide sequence from chromosome III of
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 Copsey T., Cooper J.,
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Bonfield J., Burton J., Connell M.,
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PROSITE; PS50090; MYB_3; 1.
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WormPep; C14B9.6; CE00077.
                                                                                                                                                         Nature 368:32-38(1994).
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SEQUENCE 1018 AA;
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MEDLINE-97250498; PubMed-9086354;
Wise C.A., Chiang L.C., Paznekas W.A., Sharma M., Musy M.M.,
Ashley J.A., Lovett M., Jabs E.W.;
"TCOFI gene encodes a putalive nucleolar phosphoprotein that exhibits
mutations in Treacher Collins syndrome throughout its coding
PMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAA----VIPPMVSCTPCNIPIGTPV 954
                                                                                                                                                                                                                                                                                                                                                                  PRIQKPS------TSSQPPPPEPMDTKENESDDGEEDNDILEIDVDEPPAKRPTPTSS 715
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                                                                                                                                                                                                    621 QDQDQDVDEEEEEVIVRDIDSPVKTLL-----SPKILSGGHKPDFFP----V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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-1- DISEASE: DEFECTS IN TCOF1 ARE THE CAUSE OF TREACHER COLLINS SYNDROME (TCS). TCS IS A AUTOSOMAL DOMINANT DISORDER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97195537; PubMed-9042910;
Edwards S.J., Gladwin A.J., Dixon M.J.;
"The mutational spectrum in Treacher Collins syndrome reveals
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCOE_HUMAN STANDARD; PRT; 1411 AA. 013428; 099408; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-COT-2000 (Rel. 40, Last annotation update) TREACLE PROTEIN (TREACHER COLLINS SYNDROME PROTEIN)
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---KPAEDESVET 782

VLGADLPSSMKEKAKAE-----TEKAGKTGNSMPHPATGKTVANLLSGKSPRKSAEP QVNDSISAETAEQMDVDQQEHSAEGSV-----CDPPPATKADSVDVEVRVPEN---SANTILVSETEEEGSVPAFGAAKPGMVSAGQADSSSEDTSSSSDETDVEVKASEKILQV

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732 KPSEDSPENATSRGNTEPAVELEPTTETAPSTSPSLAVPST-

EPERQRMFPMDSKPSLLNPTGSI-LVSSPLKPNPLDLPQLQHRAAVIPPMVSCTPCNIPI 950

à

HASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDVDG 891

164 832 224 RAASAPAKGTPGKGATPA----PPGKAGAVASQTKAGKPEEDSESSSEESSDSEEET--

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       LIVE BIRTHS. THE CLINICAL FEATURES OF TCS ARE BILATERALLY SYMMETRICAL AND INCLUDE: (1) ABNORMALITIES OF THE EXTERNAL EARS, ATRESTA OF THE EXTERNAL EAR CANALS, AND MALFORMATION OF THE MIDDLE EAR OSSICLES, WHICH MAY RESULT IN CONDUCTIVE HEARING LOSS; (2) LATERAL DOWNWARD SLOPING OF PALPEBRAL FISSURES, FREQUENTLY WITH COLOBOMAS OF THE LOWER EYELIDS; (3) HYPOPLASIA OF THE MANDIBLE AND ZYGOMATIC COMPLEX; (4) CLEFT PALATE.
 CRANIOFACIAL DEVELOPMENT THAT OCCURS WITH AN INCIDENCE OF 1/50,000
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W; 3880203D985C2699 CRC64;
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995 GTSKSPNREWEVLQPAPHQLITNLPE--------GVRLPTTRPTRPPPPL 1036
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                                                                                         --GKTGPAVAKAQAGKREEDSQSSSEESDSEEEAPAQAKPSGKAPQVRAASAPAKESPRK 372
                                                                                                                                                                                  373 GAAPAPPRK---TGPAAAQVQVGKQEEDSRSSSEESDSDREALAAMNAAQVKPLGKSPQV 429
                                                                                                                                                                                                                                                                         -----KPASTMGMGPLGKGAGPVPPGKVGPATPSAQVGKWEEDSESSSEESSDS 478
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                                                 RSSTSPC----
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Similarity

Query Match Local

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1714 RERERERERERERERIAAASSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPS 1773
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-1- FUNCTION: POSSIBLY ACTS AS A TRANSCRIPTIONAL REGULATORY FACTOR.
MAY REGULATE GENES INVOLVED IN SKELETAL FORMATION DURING
EMBRYONIC DEVELOPMENT.
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                                                                        ---CLTPGIR-----
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STAIN-C57BL/6J, AND B6/CBA; TISSUE-Spleen, and Lung;
MEDLINE-931376J, PubMed-8373517.
MA Q., Alder H., Nelson K.K., Chatterjee D., Gu Y., Nakamura T.,
Canaani E., Croce C.M., Siracusa L.D., Buchberg A.M.;
Analysis of the murine All-1 gene reveals conserved domains with
human ALL-1 and identifies a motif shared with DNA
methyltransferases:
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
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01-OCT-2000 (Rel. 40, Last annotation update)
ZINC FINGER PROTEIN HRX (ALL-1) (FRAGMENT).
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01-0CT-1996 (Rel. 34, Last sequ
01-0CT-2000 (Rel. 40, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps 140;
                                                                                                                                                                                                                                                                                                                                                                                       Proto-oncogene; Chromosomal translocation; DNA-binding;
Nuclear protein; Zinc-finger; Metal-binding; Transcription regulation;
Alternative splicing; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 QQQLRRRPSLLSEFHPGSDRPQERRTSYEPFHPGPSPVDHDSLESKRPRLEQVSDSHF-- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         566 SASGTAASARLFS-----PLHS-----GTRFDIHKRSPILRAPRFTPSEAHSRIFESV 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             614 TLPSNRTSSGASS--SGVSNRKRKRKVFSPIRSEPRSPSH----SMRTRSGRLSTSELSP 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----QRVSAAVLPLVHPL------PEGLRASADA-KKDPAFGGKHEAPSSPI-S 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        668 LTPPSSVSSSLSIPVSPLAASALNPTFTFPSHSLTQSGDSTEKNQRARKQTSAPAEPFSS 727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 GQPC------GDDQNASPSKLSKE-----ELIQSMDRVDREIAKVEQQILK 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------VQIIYDENRKKAEEAHKIFEGLGP-----KVELPLYNQPSDTKVYHENIKT 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSSGYPPNQGAFSTEQSRYPPHSVQYTFPNTRHQQEFAVPDYRSSHLEVSQASQLLQQQQ 61
ALTERNATIVE SPLICING. BELONGS TO THE TRITHORAX FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.7%; Score 343; DB 1; Length 3866; Best Local Similarity 19.0%; Pred. No. 1.8e-05; Matches 584; Conservative 381; Mismatches 1127; Indels 980;
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SIMILARITY).
SIMILARITY).
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                                          -!- SIMILARITY: CONTAINS 1 BROMODOMAIN.
-!- SIMILARITY: CONTAINS 1 SET DOMAIN.
-!- SIMILARITY: CONTAINS 3 PHD ZINC-FINGER DOMAINS.
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(BY
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                                                                                                                                                                                             or send an email to license@isb-sib.ch)
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3866 AA;
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               SIMILARITY:
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1773 RQCALCLMYGDDSANDAGRLLYIGQNEWTHVNCALWSAEVFEDDGSLKNVHMAVIRGKQ 1832 1135 -TAGAIQEGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGIPTEA---LVKGSISRM 1190 2034 SCYYHV-----ISKVPRIRTPSYSPIQRSPGCRPLPSAGSPT-PTTHEIVTVGDPL 2083 :::: 2260 KDTVSYPQLHLRGQRSDRDQHMDPSQSVKPSPNEDGEIKTLKLPGMGHRPSILHEHIGSS 2319 1191 PIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIKNAREGTRSPRTAHEISLKRSYESV 1250 -----ISLRRKF--L 1913 EGNIKQGMSMRESPVSAPLEGLI ---- C--RALPRGSPHS-----DLKERTVLSGSI 1296 1974 MECRPPVVEPDINSTVEHDDNRTIAHSPSSFIDASCKDSQSTAAILSPPSPDRPHSQTSG 2033 1336 KPYDGITTIKEMGRSIHEIPR----QDILTQES---RKTPEVVQSTRPIIEGSISQGTPI 1388 2084 L---SSGLRSIGSRRHSTSSLSPLRSKL-RIMSPVRTGSAYSRSSVSSVPSLGTATDPEA 2139 1426 NIKVVERGKYEDVKAG------ETVRSRHTS-VVSSGPSVLR--STLHEAPKAQ 1470 1471 LSPGIYDDT-SARRTPVSYQNTMSRG----SPMMNRTSDVTIPPNKSTNHERKSTLTPTQ 1525 1526 RESI------PAKS--PVPGVD------PVVSHSPFDPH-HRGST 1555 2377 CNNVSSEKIGDKVLPLSGVPKGQSTQVEGSSKELQ-----APRKCSVKVTPLKMEGENQ 2430 2541 IPFYSNSTGKKRGKRSAEGQVDGADDLSTSDEDDLYYYNFTRTVISSGGEE--RLASHNL 2598 | : : | : : | : : | 2599 FREEE---QCDLPKISQLDGVDDGTESDTSVTATSRKSSQI----PKRNGKENGTENLKID 2652 MQGTP-----RATTE-----SFEDGLKYPKQIKRE--SPPIRAFEGAITKG 1335 1556 AGEVYWSHLPTQLDPAMPFHRA---LDPAAAAYLFQRQLSP-----TPGYPSQYQLYA 1605 1606 MENTRQTILNDYI----- 1644 1712 ------AERERERERERERERERIAAASSDLY------LRPGSEQPGRPGSHGY 1753 1754 VRSPSPSVRTQETMLQQRPSVFQGT-NGTSVITPLDPTAQLRIMPLPAGGPSISQGLPAS 1812 1813 RYNTAADALAALVDAAA--SAPQMD----VSKTKESKHEA----ARLEENLRSRSAAVS 1861 1862 EQQQLEQKTLEVEK-----RSVQCLYTSSAFPSG-----KPQPHSSVVYSEAGKDKGP 1909 1910 PPKSRYEEELRTRGKTTITAANFIDVIITRQIASDKDARERGSQSSDSSSSLSSHRYETP 1969 2762 SPESS-SSELLTLGEGLGLDSNREKDIGLFEVFSQQLPATEPVDSSVSSSISAEEQFELP 2820 1389 KFDNNSGOSAI---KHNVKSLITGPSKLSRGMPPLEI------VPE-----VPE-2200 LVKGEKNRTSSSKSTDGSAHSTAYPGIPKLTPQVHNATPGELNISKIGSFAEPSTVPFSS 1645 -----2486 NLPEQDRNLMIPD----GPKPQEDGSFKRRYPRRSARARSNMFFGLTPLYGVRSYGEED 2653 RPEDAGEKEHVIKSAVGHKNEPKLDNCHSVSRVKAQCQDSLEAQLSSLESSRRVHTSTPS 1671 STPPMDRITYIPGTQITFPPRPYNSASMSPGHPTHLAAAAS--------VPENG-FEVFRNFVDFEG------1888 1251 셤 g οχ Q οχ Dp Ω g QΫ́ g ŏ g δ g δ Q ò Dp 셤 g g δ ò qq ò δy ద δ ò δý a ογ g ŏ ŏ

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2980 NMOPLYVLQTLPNGVTQKIQLTSPVSSTPSVMETNTSVLGPMGSGLTLTTGLNPSLPPSP 3039
                                                                                                                                                                                                                                                                                                                                                                                --AEQRNDARSPGSISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGGGDSDMAAAQ--- 2230
                                                                                                                                                                                                                                                                                                                                           SLFPPASKGLL -- SVPHHQHLHSFPAAAQSSFPPN -- - ISSPPSGLLIGVQPPPDPQLLG 3094
   -------EKLQTYQPEVVKANQAENDPTRQYEGPL 2014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --OGYLGTERPSSVSSVHSEGDYHRQTPGWAWEDRPSS--TGSTQFPYNPLTMRMLSSTP 2397
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01-0cT-1996 (Rel. 34, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
21NC FINGER PROTEIN 40 (TRANSCRIPTION FACTOR ALPHAA-CRYBP1) (ALPHA CRYSTALLIN-BINDING PROTEIN I) (ALPHA A-CRYBP1).
MUSP ION SIM40 ON CRYABP1.
Mus musculus (Mouse).
                                                                                                    3152 NFTPSQLSNHPSLLDLGSL-----NPSSHRTVPNIIKRSKSGIM--YFEQAPLLPPQ
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                                                                                                                                                                                     2920 RNSGTPGLQVPVSPTVPVQNQKYVPSSTDSPGPSQISNAAVQTTPPHLKPATEKLIVVNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         --PGTEIFNLPAVTTSGSVSSRGHSFADPASNLGLEDIIRKALMGSFDDKVEDHGVVMSQ
                                     2821 LELPSDLSVLTTRSPTVPSQNPSRLAVISDSGEKRVTITEKSVAS--SEGDPALLSPG--
                                                                                                                                                     RNQ-----VSSQTPQQ----PPTSTFQNSPS-----ALVSTPVRTKTSNR----
                                                                                                                                                                                                                            -------RPGSRVSP
                                                                                                                                                                                                                                                                                                     2122 ENLVDKSRGSRPGKSPERSHVSSEPYEPIS--PPQVPVVHEKQDSLLLLSQRGAEP----
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Mammalia; Eutheria; Rodentia; Sciurognathi, Muridae, Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brady J.P., Kantorow M., Sax C.M., Donovan D.M., Piatigorsky J.; "Murine transcription factor alpha A-crystallin binding protein Complete sequence, gene structure, expression, and functional inhibition via antisense RNA."; J. Biol. Chem. 270:1221-1229(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Lens epithelium;
MEDLINE-90287161; PubMed-1694016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 2024-2688 FROM N.A.
1970 SDA---IEVISPASSPAPPQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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Q03172;
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                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SE-DSPENATSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAET 792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEQMDVDQQEHSAEEGSVCDPPPATKADSVDVEVRVPENHASKVEGDNTK-----ERDL 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AE-----DPTRLSGLVS-PKKTSSPHQRSELRRWRSEGS----DPTRLSGLDGQRDS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              847 DRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDV---DGEPERQRMFPMDS 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----KPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTPVSGYAL 959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                               DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0048; ZINCFINGER.
PROSTIE: PSO0028: ZINC_FINGER_C2H2_1; 4.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
Transcription regulation; Zinc-finger; Metal-binding; DNA-binding;
                                                                SPECIFICALLY TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSSSSK-----ARTDNSECSSPCCSTTPPSYTSTAFDYLLKAMEPELSTLSQKGS
      complex class I gene and other genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 762;
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18.6%; Pred. No. 2.1e-05;
Ive 267; Mismatches 742; Indels 76
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ZINC FINGERS.
C2H2-TYPE.
C2H2-TYPE.
POLY-SER.
POLY-PRO.
C2HC-TYPE (POTENTIAL).
POLY-SER.
ZINC FINGERS.
major histocompatibility complex class I gene a Mol. Cell. Biol. 10:3700-3708(1990).
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C2H2-TYPE.
                                                                                                                                                   SUBCELLULAR LOCATION: NUCLEAR, DOMAIN: CONTAINS TWO SETS OF 2
                                                                                                                                                                                                                                                                 SIMILARITY: STRONG, TO HIVEP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L36825; AAA98810.1; JOINED.
EMBL; L36826; AAA98810.1; JOINED.
EMBL; L36827; AAA98810.1; JOINED.
EMBL; L36828; AAA98810.1; JOINED.
EMBL; K68946; CAA48762.1; JOINED.
HSSP; P15822; 42NF.
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                                                                                                                                                                                                                                      ZINC-FINGER IN-BETWEEN
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Οy	OY 960 YORHIKAMHESALLEEQRQRQEQIDLECRSS	066
QQ	266HVASTOKSEOVAA	SQQNQQLPGHLGFTGSL 312
οy	991	ITNLPEGVRLPTTRPTR 1031
QQ	Db 313 TNLHTLESTKLEPIYNTAVTSTVGLT-SPSTRTQVTPPHQQMDSVSPLSVSPASSTQS	MDSVSPLSVSPASSTQS 369
6 6	Qy 1032 PPPPLIPSSKTTVASEKPSFIMGGSISQGTPGTYLTSH-NQA	IYLTSH-NQA 1072   : :   :   :
ò	1073SYTOETPKPSV	
g 8		
δy	1099	PEGLLVRAQHEGVVR 1133
QQ	Db 483 ALSVHSDIEDSGESDEEGLADGRONNPCVKDLOPVQTWKTVSNPESLPKLIPSNSDHVVR	PESLPKLIPSNSDHVVR 542
אַ לַ	QY 1134 GTAGAIQEGSITRGIPTSKISVESIPSLRGSITQGTPALPQTEDTBALV Dh 543 GESCANDEGRSCAS PIPE I STANDARD CONTROL OF A STANDARD DE PROVINCIA DE CONTROL OF A STANDARD DE PROFESSION UNA	LPQTGIPTEALV 1183
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δλ	1243 LKRSYESVEGNIKOGMSMRESPVSAPLEGLICE	LKERTVLSGSIMQGTPR 1302
Q	Db 640 LQRQQATEDPQEQQGKLLLSPRSLGSTDSGYFSR	FSR 673
δy	Qy 1303 ATTESFEDGLKYPKQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHEIPRQDILTQ	EMGRSIHEIPRODILTQ 1362
g G	674SESADQAVSPPTPFARTFPTMDP-DPAKNGGAPG	PR 708
δλ	1363 ESRKTP	SLITGPSKLSRGMPPL- 1420
q	602	SVVTGQMRPPLA 735
οy	1421	
qq	Db 736 TKTLEERISKLISDNEALVDDKQLDSVKPRRTSLSRRGSIDSPKSY-	DSPKSY- 781
ōλ	-	HERKSTLTPTQRESIPA 1531
qq	782	JIPKSPFTPTEKSKQVF 819
δλ	QY 1532 KSPVPGVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAAYLFQRQL	HRALDPAAAAYLFQRQL 1591
qq	Db 820 LLSVPSLDCLPITRSNSMPTTGYSAIPANIIPPPPSLRG	LRG 858
δλ	QY 1592 SPTPGYPSQYQLYAMENTRQTILNDYITSQQMQVNLRPDVARGLSPREQPLGLPYPATR-	USPREQPIGLPYPATR- 1650
QQ	859SPDDKIGTLYDDVFVS	GPNPSMPPSGHHRPLVRQ 894
οy	Qy 1651 -GIIDLINMPPTILVPHPGGTSTPPMDRITYIPGTQITFPPRPYNSASMSPGHPTHLAAA	INSASMSPGHPTHLAAA 1709
qq	Db 895 AAVEDSTASESHVPGSGGSVDESCQGCPSSEAGPVQSKAA	GCPSSSEAGPVQSKAA 935
δλ	Qy 1710 ASAERERERERERERERERERIAAASSDLYLRPGSEQPGRPGSHG	JYLRPGSEQPGRPGSHG 1752
qq	DD 936 QTPHLEKKKSHQGRGTMFECETCRNRYRKLENFENHKKFYCSELH-GPKTKAAVREAEHG	H. GPKTKAAVREAEHG 994
δλ	QY 1753 YVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTA	ITPLDPTA 1791
qq	DD 995PAPGGAQPQVLHYRVAAPTAVWEGTPQIRKRRKMKSVGDEEDLQPHESGRSPESAD	SEDLQPHESGRSPESAD 1050
. ¥0		SKTKESKHEAARLEE 
qq		ER 1089
ò	1852 NLRSRSAAVSEOOOLEOKTLEVEKR	-SVOCLYTSSAFPSGKPOP-HSSVVYS- 1901

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1210 RLVRQHNIQVPEILVTEEPDRDLEAQSHDEE---KSEKFTWPQRS-ETLSKL----PTE 1260
                                          1902 -EAGK------DKGPPPKSRYEEEL---RTRGK-----TTITAANFI---- 1933
                                                                                                    -----DVIITRQIASDKDARERGSQSSDSSSSLSSHRYETPSDAIEVISPASSPAPPQE 1987
                                                                                                                                                                                        1261 KLPPKKKRLRLAEIEHSSTESSFESTLSRSLSRESSLSHASSFSASLDLEDISKVELAPK 1320
                                                                                                                                                                                                                                      1321 IDFPSKAEFLLIPLGSNTLSVPGSHREMRRA------ASEQISC-VPTLMEVSDF 1368
                                                                                                                                                                                                                                                                                                 2148 EPISPPQ-----VPVVHEKQDSLLLLSQRGAEP-AEQRNDARSPGSISYLPSF 2194
                                                                                                                                                                                                                                                                                                                                                                                                              2195 -----FTKLENTSPMVKSKKQEIFRKLNSSGGDSDMAAAQPGTEIFNLPAVTTSGSVS 2248
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P15146;
01-AFR-1990 (Rel. 14, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
MICROTUBULE-ASSOCIATED PROTEIN 2 (MAP2B) [CONTAINS: MAP2C].
RATLUS norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Ettheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                             1988 KLQTYQPEVVKANQAENDPTRQYEGPLHHYRPQQESPSPQQQLPPSSQAEGMGQ-----
                                                                                                                                                                                                                       2042 --------VPRTHRLITLADHICQIITQDFARNQVSSQTPQQPPTSTF
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[2]
STRAIN-WIGTAR; TISSUB-Brain;
MEDLINE-90251471; PubMed-2339070;
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1822 PTDSLSSRPSTFAVTD 1837
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Pred. No. 1.9e-05

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                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                      from
indler S., Schwanke B., Schulz B., Garner C.C.;
Complete cDNA sequence encoding rat high and low molecular weight.
                                                                                              2b and 2c
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MISSING (IN ISOFORM WITH 3 TAU/MAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alternative splicing; Calmodulin-binding.
                                                                                                                                                                    embryonic rat MAP2c.";
                                                                                                                                                                                                                      Papandrikopoulou A., Doll T., Tucker R.P., Garner C.C., Matus "Embryonic MAP2 lacks the cross-linking sidearm sequences and dendritic targeting signal of adult MAP2.";
Nature 340:650-652[1899].
                                                           STRAIN-WISTAR; TISSUE-Brain;
MEDLINE-91060576; PubMed-2174050;
Kindler S., Schulz B., Goedert M., Garner C.C.;
"Molecular structure of microtubule-associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42DCF116D21EF54E CRC64;
                                                                                                                                    SEQUENCE OF 1-151; 1515-1694 AND 1726-1861 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 3 OR 4 TAU/MAP REPEATS
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TAU/MAP MOTIF.
TAU/MAP MOTIF.
TAU/MAP MOTIF.
                                                   SEQUENCE OF 1-1694 AND 1726-1861 FROM N.A.
                                                                                                                                              MEDLINE-90221819; PubMed-2326166; ADIL T., Papandrikopoulou A., Matus A.; Nucleotide and amino acid sequences of Nucleic Acids Res. 18:361-361(1990).
                              Nucleic Acids Res. 18:2822-2822(1990)
                                                                                                               J. Biol. Chem. 265:19679-19684(1990).
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                                                                                                                                                                                                 DISCUSSION OF SEQUENCE.
MEDLINE-89365159; Pubmed-2770869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X51842; CAA36135.1; -. EMBL; X17682; CAA35667.1; -. EMBL; X71487; CAA50588.1; -. PIR; S07887; S07887.
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                                                                                                     rat brain.";
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                                                                                                         QPAPHQLITNLPEGVRLPTTRPTRPPPPLIPSSKTTVASEKPSFIMGGSISQGTPGTYLT 1067
                                                                                                                                                                                                                                             1068 SHNQASYTQETPKPSVGSISLGLPRQQESAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQ 1127
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                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            315 SPFHGGSFTLPLDIVKDERVTEGSQPFAPVFFQSDDKMSLQDISGSATSKESSKDEEPQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          521 TSEPEAVSEKREIQGLFEEDIADK-----SKLEGAGSATVAEV--EMPFYEDKSGMSKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          573 FETSALKEDVTRSTGLGSDYYELSDSRGN--AQESLDTVSPKNQ---QDEKELLAKASQP
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                                    Indels 603;
                                    Mismatches 588;
ilarity 20.0%; Pre
Conservative 237;
Best Local Similarity
Matches 357; Conserv
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  1420 EKEARRPSLEKHRKEKPFK----TGRGRISTPERREVAKKEPSTVSRDEVRKKAVYKKA 1475
                                                                                                                                                                                                                                                                                                                                            ------MVKSKKQEIFRKLNSSGGG-----DSDMAAAQPGT----EIFNLPAVTTSG 2245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2330 SNSRKSKSPIPGQGYLGTERPSSVSSV----HSEGDYHRQTPGWAWEDRPSSTGSTQFPY 2385
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 ---KETAP---ERAEKGLS 1023
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002952; 0099970; 000498; 000310;
01-FEB-1994 (Rel. 28, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
4-KINASE ANCHOR PROTEIN 12 (A-KINASE ANCHOR PROTEIN 250 KDA) (AKAP 250) (WTASTHENIA GRAVIS AUTOANTIGEN GRAVIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nauert J.B., Klauck T.M., Langeberg L.K., Scott J.D.;
Gravin, an autoantigen recognized by serum from myasthenia gravis
patients, is a kinase scaffold protein.";
Curr. Biol. 7:52-62(1997).
                       SQ-----
                                                                                                                                                                         1300 TVVQTTTDEGELGSHSVRFAAPVQPEEERRPYPHDEELEVLMAARAQAEPKDGSPDAPAT
                                            SVPEVAEVETTTKADQGLDVAAKKDDQSPLDIKVSDFGQMASGMSVDAGKTIELKFEVDQ
                                                                                                                ----PPSSQAEGMGQVPRT
                                                                                                                                                            HRLITLADHICQIITQDFAR--NQVSSQTPQQP--PTSTFQNSPSALVSTPVRTKTSNRY
                                                                                                                                                                                                                                                     ----KSPERSHVSSEPYE---PISPPQV--PVVHEKQDSLLLLSQRGAEPAEQRNDARSP
                                                                                                                                                                                                                                                                                                GSISYLP-----SFFTKLENTSP----
                                                                                                                                                                                                                                                                                                                                                                                         SVSS----RGHSFADPASNLGLEDII-------RKALMGSFD------D
                                                                 1958 SSSLSSHRYETPSDAIEVISPASS-----PAPPQEKLQTYQPEVVKANQAENDPTRQY
                                                                                        1084 OLTLSS---EAPQETDSFMGIESSHVKDGAKVSETEVKEKVAKPDLV--HQEAVDKEESY
                                                                                                                                     ESSGEHESLTMESLKPDEGKKETSPETSLIQDEVALKLSVEIPCPPPVSEAD-----
                                                                                                                                                                                                        SPESQAQSVHHQR-------PGSRVSPENLVDKSRGSRPG------
                                                                                                                                                                                                                                                                                                                                                                                                                                       KVEDHGVVMS-----QPMGVVPGTANTSVVTSGETRREEGDPSPHSGGVCKPKLISK
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.
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                     T----RGKTTITAANFIDVIITRQIASDKDAR--ERGSQSS-
                                                                                                                EGPLHHYRPQQES------PSPQQQL-----
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GDKVELFGLGVTYEQTSAKELITT-
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AKAC_HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INVOLVED IN BINDING PKC.
-1- DISEASE: ANTIBODIES TO THE C-TERMINAL OF GRAVIN CAN BE PRODUCED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: CYTOPLASMIC. MAY BE PART OF THE CORTICAL CYTOSKELETON.
-CYTOSKELETON.
-I- SUBCELLULAR LOCATION: CYTOPLASMIC. MAY BE PART OF THE CORTICAL CYTOSKELETON.
-I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; MAY BE PRODUCED BY ALTERNATIVE SPLICING.
-I- TISSUE SPECIFICITY: EXPRESSED IN ENDOTHELIAL CELLS, CULTURED FIBROBLASTS AND OSTEOSARCOMA, BUT NOT IN PLATELETS, LEUKOCYTES, MONOCYTIC CELL LINES OR PERIPHERICAL BLOOD CELLS.
-I- INDUCTION: ACTIVATED BY LYSOPHOSPHATIDYLCHOLINE (LYSOPC).
-I- DOMAIN: POLYBASIC REGIONS LOCATED BETWEEN RESIDUES 265 AND 556
                                              TISSUB-Umbilical vein endothelial cells;
MEDLINE-98269042; PubMed-9604001;
Sato N., Kokame K., Shimokado K., Kato H., Miyata T.;
Changes of gene expression by lysophosphatidylcholine in vascular endothelial cells: 12 up-regulated distinct genes including 5 cell growth-related, 3 thrombosis-ralated, and 4 others.";
J. Blochem. 123:1119-1126(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytoplasmic antigen recognized by myasthenia gravis sera.";
J. Clin. Invest. 90:92-999(1992).
-i- FUNCTION: ANCHORING PROTEIN THAT MEDIATES THE SUBCELLULAR COMPARTMENTATION OF PROTEIN KINASE (PKA) AND PROTEIN KINASE C
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AKAP 2.

AKAP 3.

POLX -GLU.

INVOLVED IN PKC-BINDING (PROBABLE).

RII-BINDING (PROBABLE).

MISSING IN ISOFORM 2).

EEEVIVTE -> MLGTITIT (IN ISOFORM 2).
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TISSUE-Umbilical vein endothelial cells;
MEDLINE-92395179; Pubmd=1522245;
Gordon T., Grove B., Loftus J.C., O'Toole T., McMillan R.,
Lindstrom J., Glabberg M.H.;
"Molecular cloning and preliminary characterization of a novel
                                                                                                                                                                                                                                                                                                                                                                      vein
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NRN -> TPEI (IN REF. 2 AND 3).
                                                                                                                                                                                                                                                                                                      TISSUE-Umbilical vein endothelial cells;
Bowditch R.D., Ginsberg M.H.;
"Sequence of gravin cDNA isolated from a human umbilical endothelial cell library.";
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
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G -> S (IN REF. 2
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[2]
SEQUENCE FROM N.A. (ISOFORM 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antigen; Alternative splicing.
                                                                                                                                                                                                                                                                               SEQUENCE OF 43-1781 FROM N.A.
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                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-0CT-1993 (Rel. 27, Created) 
01-NOV-1995 (Rel. 32, Last sequence update) 
01-CCT-2000 (Rel. 40, Last annotation update) 
ZINC FINGER PROTEIN HEX (ALL-1) (TRITHORAX-LIKE PROTEIN). 
MLL OR HRX OR ALLI OR TRX1 OR HTRX.
 3969 AA
 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93265134; PubMed=1303259;
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STANDARD;
                                                                                                                                                                                                                      Cell 71:691-700(1992).
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HRX_HUMAN
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Megonigal M.D., Cheung N. K.V., Rappaport E.F., Nowell P.C.,
Milson R.B., Jones D.H., Addya K., Leonard D.G.B., Kushner B.H.,
Milson R.B., Jones D.H., Addya K., Leonard D.G.B., Kushner B.H.,
Millans T.H., Lange B.J., Felix C.A.;
Millans T.H., Lange B.J., Felix C.A.;
The foct of leukemia associated MLL-GAS7 translocation early during chemotherapy with DNA topoisomerase II inhibitors.";
Proc. Natl. Acad. Sci. Us.A. 97.2814-2819(2000).
C. -- FUNCTION: POSSIBLY ACTS AS A TRANSCRIPTIONAL REGULATORY FACTOR.
C. -- SUBCELLULAR LOCATION: NUCLEAR.
C. -- TISSUE SPECIFICITY: HEART, LUNG BRAIN AND TAND B LYMPHOCYTES.
C. -- TISSUE SPECIFICITY: HEART, LUNG BRAIN AND MLLTI/FUL;
C. -- TISSUE SPECIFICITY: HEART, LUNG BRAIN AND MLLTI/FUL;
C. -- TISSUE SPECIFICITY: HEART, LUNG SPECIFICITY: HEART, LUNG MLL AND MLLTI/FUL;
C. -- TISSUE SPECIFICITY: HEART, LUNG-SPECIFICITY: HEART INVOLVES MLL AND MLLTI/FARI;
C. -- TISSUE SPECIFICITY: HEART, LUNG-SPECIFICITY: HAT INVOLVES MLL AND MLLTI/FARI;
C. -- THAT INVOLVES MLL AND MLLTI/FORD AND MLLTI/FARI;
C. T(1):11)(P12:Q23) THAT INVOLVES MLL AND MLLTI/FORD AND MLLTI/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE TRITHORAX FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: CONTAINS 1 BROMODOMAIN.
-!- SIMILARITY: CONTAINS 1 SET DOMAIN.
-!- SIMILARITY: CONTAINS 3 PHD ZINC-FINGER DOMAINS.
                                                                                CHROMOSOMAL TRANSLOCATION WITH GAS7. MEDLINE-20183971; Pubmed-10706619;
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EMBL; Z69744; CAA93625.1; -.
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VRIIPSSKRTDATIAKQLLORA -> VSSLILNWKSPRKSG
KTRKEHLHLOKKIRQLSDKALEGLSOLGLFLLOKGOMOPLL
                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002857; -. Pfam; PF00628; PHD; 3. Pfam; PF008569; PHD; 3. Pfam; PF008569; SET; 1. Pfam; PF008069; zf-CXXC; 1. PROSITE; PS50014; BROMODOMAIN_2; 1. PROSITE; PS50280; SET; 1. PROSITE; PS50280; SET; 1. Nuclear protein; Chromosomal translocation; DNA-binding; Bromodomain; Nuclear protein; Zinc-finger; Metal-binding; Transcription regulation; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BREAKPOINT FOR TRANSLOCATION TO FORM MLL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSAASQHSSQMSSDSSRSSSPSVDTSTDSQASELIQVLPEERSDTPEVHPPLPISQSPEN 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ING (IN ISOFORM 14P-18B).
ELTTQIPCSWRTKGHIHDKKTEPFRLLAWSWCLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       > SCTE (IN REF. 2 AND 7).

> C (IN REF. 6).

> H (IN REF. 4).

> S (IN REF. 4).

> G (IN REF. 2).

> D (IN REF. 2).

> G (IN REF. 2).

> G (IN REF. 2).
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A.T HOOK (BY SIMILARITY).
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A.T HOOK (BY SIMILARITY).
PHD-TYPE 1.
PHD-TYPE 2.
PHD-TYPE 3.
BROWODOMAIN (DIVERGENT).
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0 -> E (IN REF. 2).
R -> G (IN REF. 5).
S -> SGTE (IN REF. 2 A.
S -> C (IN REF. 6).
C -> H (IN REF. 4).
P -> S (IN REF. 4).
R -> G (IN REF. 2).
R -> A (IN REF. 2).
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InterPro; IPR001214; -. InterPro; IPR001487; -. InterPro; IPR001965; -.
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MIM; 159555; -.
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ογ	1005	EVLQPAPHQLITNLPEGVRLPTTRPT 1030
q	1566	GNFCPLCDKCYDDDDYESKAMQCGKCDRWVHSKCENLSDEMYEILSNLPESVAYTCVNCT 1625
δý	1031	RPPPPLIPSSKTTVASEKPSFIMGGSISQGTPGTYLISHNQASYTQETPKPSVGSISLGL 1090
g	1626	ERHP1673
οy	1091	PRQQESAKSATLP 1112
qq	1674	PETEESIPSRSSPEGPDPPVLTEVSKQDDQQPLDLEGVKRKMDQGNYTSVLEFSDDIVKI 1733
οý	1113	RSQNSQPEGLLVRAQHEGVVRGTAGAI 1139
qq	1734	IQAAINSDGGQPEIKKANSMVKSFFIRQMERVFPWFSVKKSRFWEPNKVSSNSGMLPNAV 1793
δy	1140	QEGSITRGTP-TSKISVESIPSLRGSITQGTPALPQTGIPTEALV 1183
g	1794	LPPSLDHNYAQWQEREENSHTEQPPLMKKIIPAPKPKGPGEPDSPTPLHPPTPPIL 1849
Qy	1184	KGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGH 1218
qq	1850	STDRSREDSPELNPPGIEDNRQCALCLIYGDDSANDAGRILYIGQNEWTHVNCALWSAE 1909
0 y	1219	
QQ	1910	VFEDDDGSLKNVHMAVIRGKQLRCEFCQKPGATVGCCLFSCTSNYHFWCSRAKNCVFLDD 1969
ογ	1230	
<del>Q</del>	1970	KKVYCQRHRDLIKGEVVPENGFEVFRRVFVDFEGISLRRKFLNGLEPENIHMMIGSMT 2027
δō	1267	
Q	2028	IDCLGILNDLSDCEDKLFPIGYQCSRVYWSTTDARKRCVYTCKIVECRPPVVEPDINSTV 2087
ζς Q	1306	ESFEDGLKYPKQIKRESPPIRAFEGAITKGKPYDCITTIKEMGRSI 1351 
0	1352	IEGSISOGTPIKEDNNSGOSAIKH
· 6	2140	TPSYSPIQRSPGCRPLPSAGSPT-PTTHEIVIVGDPLLSSGLRSIGSRRH
δy	1402	NVKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVKAGETV-RSRHTSVVSSGPSV-L 1459
g	2196	STSSLSPQRSKL-RIMSPM
oy g	1460	RSTLHEAPKAQLSPGIYDDTSARRIPVSYONTMSRGSPMMNRTSDVT 1506 
à	1507	
<del>Q</del>	2297	
Qy	1567	QLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENT 1609
qq	2351	FAEPSSVSFSSKEALSFPHLHLRGQRNDRDQHTDSTQSANSSPDEDTEVKTLKLSGMSN- 2409
δλ	1610	RQTILNDXITSQQM1632
Q	2410	RSSIINEHMGSSSRDRROKGKKSCKETFKEKHSSKSFLEPGQVTTGEEGNLKPEFMDEVL 2469
٥y	1633	
연	2470	TPEYMGQRPCNNVSSDKIGDKGLSMPGVPKAPPMQVEGSAKELQAPRKRTVKVTLTPLKM 2529
δλ	1653	1DLTNMPT1LVPHPGGTS 1671
g	2530	2530 ENESQSKNALKESSPASPLQIESTSPTEPISASENPGDGPVAQPSPNNTSCQDSQSNNYQ 2589

ΟŊ	1672	TOITFPPRPYNSASMSPGHPTHLAAAAS1	711
QQ	2590 1		644
οy	1712	PGRPGSHGY 1	753
qq	2645		702
QY	-	PSVRTQETMLQQRPSVFQGT-NGTSVITPLDPTAQLRIMPLPAGGPSISQGLPAS 1 : :         ::     ::	_
đ		FREEEQCDLPKISQLDGVDDGTESDTSVTATTRKSSQIPRRNGKENGTENLKID 27;	756
70 OX	13	RYNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAVS 18	861
αΩ	2757 1		2816
ΟŊ	1862	EQQOLEQKTLEVEKRSVQCLYISSAFPSGKPQPHSSVVXSEAGKDKGP 19	606
QQ	2817 I	KNLLDTYNTELLKSDSDNNNSDDCGNILPSDIMDFVLKNTPSMQALGE 2	865
QY	1910	PPKSRYEEELRIRGKTIITAANFIDVIITRQIASDKDARERGSQSSDSSSSLSSHR 19	965
ΟQ	2866 \$		2919
δ	1966	NQAENDPTR : :	2008
qq	2920	-LSVLTTRSPTVPSQNPSRLAVISDSGEKRVTITEKSVASSESDPAL 2	976
Οy	2009	QYEGPLHHYRPQGESPSPQQQLPPSSQAEGMGQVPRTHRLITLADHICQIITQDFA 20	064
đ	2977	LSPGVDPTPEGHMTPDHFIQGHMDADHISSPPGGSVEQGHG 30.	017
Qy	2065 F	RNQVSSQTPQQPPTSTFQNSPSALVSTPVRTKTSNRYSPESQAQSVHHQRPGS 21	2117
qq	3018	NNQDLTRNSSTPGLQVPVSPTVPIQN3(	051
δλ	<b>&amp;</b>		2177
QQ	3052	PHLKPATEK LIVVNONMOPLY	3089
δλ	2178 (	FRKLNSSGGGDSDMAAAQP 2	231
đ	3090	VLQTLPNGVTQKIQLTSSVSSTPSVMETNTSVLGPMGGGLTLTTGLNP 31.	137
δy	2232	SNLGLEDIIRKALMGSFDDKVED	2281
QQ	3138	SLPTSQSLFPSASKGLLPMSHHQHLHSFPAATQSSFPPNIS- 31	3178
Qy	2282	GVCKPKLISKSNSRKS 2	335
qq	3179	nppsglligvqppddpglLvsesqrtdlsttvatpssglkkrpisklqtrkn 3	231
Qy	2336 F	GWAWEDRPSSTGSTQFPYNPLTMRML 2	393
qq	3232 F	KKLAPSSTPSNIAPSDVVSNMTLINFTPSQLPNHP-SLLDL 33	271
δy	2394 8	SSTPPTPIACAPSAVNQAAPHQQNRIWEREPAPLL 2428	
qq	3272	GSLNTSSHRTVPNIIKRSKSSIMYFEPAPLL 3302	
RESU			
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2 E E	P3042, 01-APE	; OU888U; OU888I; el. 25, Created)	
6 6 6	01-0C1	40,	
OS OS	PLEC1.	norvegicus (Bat).	
88	Eukary	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria: Rodentia: Sciuroquathi: Muridae: Murinae: Rattus	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of variants with distinct first coding exons and tissue distribution of variants with distinct first coding exons and rodless isoforms."; Genomics Acils-125(1997).

C. I. FUNCTION: PLECTIN IS PROPOSED TO PLAY A ROLE IN CROSS-LINKING WITH MICROTUBULES AND TO ANGHOR INTERMEDIATE FILAMENTS TO MEMBRANES, TO INTER-LINK INTERMEDIATE FILAMENTS TO MEMBRANES. TO THE PLASMA MEMBRANE AND TO THE PLASMA MEMBRANE AS TO THE FORM WENGENES. THAT STABLILES THE CYTODLASM.

C. I. SUBUNIT: A TETRAMEBLE AND COVERLAP TO A GREAT EXTERT.

IN ONE MOLECULE ARE PARALLEL AND OVERLAP TO A GREAT EXTERT.

ARE ARRANGED ANTIPMEALLEL AND OVERLAP TO A GREAT EXTERT.

C. I. TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION IN SKELETAL MUSCLE AND LOWEST IN THYMUS.

C. I. TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION IN SKELETAL MUSCLE AND LOWEST IN THYMUS.

C. I. SIMILARITY: TO DESMOPLAKIN AND TO BULLOUS PEMPHIGOID ANTIGEN.
                                                                                                         Wiche G., Becker B., Luber K., Weitzer G., Castanon M.J.,
Hauptmann R., Stratowa C., Stewart M.;
"Cloning and sequencing of rat plectin indicates a 466-kD polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARTIAL SEQUENCE FROM N.A. (ISOFORMS 2; 3; 4), AND TISSUE SPECIFICITY
                                                                                                                                                                          chain with a three-domain structure based on a central alpha-helical coiled coil.";
                                                                                                                                                                                                                                                                                      TISSUE-Glial tumor;
MEDLINE-96210632: PubMed=8633055;
MILL C.-G., Maercker C., Castanon M.J., Hauptmann R., Wiche G.;
"Huna plectin: organization of the gene, sequence analysis, and chromosome localization (8q24).";
Proc. Natl. Acad. Sci. U.S.A. 93:4278-4283(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Glial tumor;
MEDLINE-97321050; PubMed-9177781;
Elliott C.E., Becker B., Oehler S., Castanon M.J., Hauptmann R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTIN'BINDING (BY SIMILARITY).
GLOBULAR.
CENTRAL FIBROUS ROD DOMAIN R.
RI COLLED COIL.
R2 COLLED COIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Repeat; Structural protein; Cytoskeleton; ng; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001101; -.
InterPro; IPR001715; -.
Pfam; PF00307; CH; 2.
Pfam; PF00681; Plectin_repeat; 21.
PROSITE; PS00019; ACTININ_1; FALSE_NEG.
PROSITE; PS50020; ACTININ_2; FALSE_NEG.
PROSITE; PS50221; CH; 2.
                                                                                    MEDLINE-91268156; PubMed-2050743;
                                          SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                      Cell Biol. 114:83-99(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X59601; CAA42169.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U96274; AAC53209.1; -. U96275; AAC53210.1; -. U96276; AAC53211.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A39638; A39638.
PIR; S21876; S21876.
HSSP; Q01082; 1AA2.
                                                                   tumor;
NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71247
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                                                                 TISSUE=Glial
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                                                                                                                                                                                                                                                                     REVISIONS
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2.5%; Score 317; DB 1; Length 4687;
18.3%; Pred. No. 0.0002;
1ve 398; Mismatches 1096; Indels 932; Gaps 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYAGMIMPLOOLRAIYEVLEREGYWVAKKDRRPRSLHPHVP
GVTNLQVWRA -> DVSNGSSGSPSPGDTLPWNLGKTQRSR
RSGGGSVGNGSVLDPAERAVIRIA (IN ISOFORM 4).
MISSING (IN ISOFORM 2 AND ISOFORM 3).
MISSING (IN ISOFORM 4).
WF. 9966CAF71B929751 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MVAGMIMPLDQLRAIYEVLFREGVMVAKKDRRPRSLH ->
MSQQRLRVPEPEGLGSKRTSSEDNLYLAVLRASEGKK (IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LREEAERRAQQQA------EAERAREEAERELERWQLKANEALRLRL------ 1786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1546 EAAVDAQQQK---RSIQEELQHLRQSSEAEIQAKAQQVEAAERSRMRIEEEIRVVRLQLE 1602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKRQAEAELAL-----RVKAEAERARE-----KQRAL------QALDELKLQA 1685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QAEEVAQQKSLAQADA----EKQKEEAEREARRRGKAEEQAVRQRELAEQ----ELEKQR 1838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 QQLRRRPSLLSEFHPGSDRPQE----RRTSYEPFHPGPSPVDHDSLESKRPRLEQVSDSH 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 FQRVSAAVLPLVHPLPEGLRASADAKKDPAFGGKHEAPSSPISGQPCGDDQNASPSKLSK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EELIQSMDRVDREIAKVEQQILKLKKKQQQLEEEAAKPPEPEKPVS-PPPVEQKHRSIVQ 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IIYDENRKKAEEAHKIFEGLGPKVELPLYNQPSDTKVYHENIKTNQVMRKKLILFFKRRN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 QGAFSTEQSRYPPHSVQYTFPNTRHQQEF-----AVPDYRSSHLEVSQASQLLQQQQQ 62
R2-A SUBDOMAIN (POTENTIAL).
R2-B SUBDOMAIN (POTENTIAL).
R2-C SUBDOMAIN (POTENTIAL).
R2-E SUBDOMAIN (POTENTIAL).
GLOBULAN.
COLLED COIL (POTENTIAL).
INTERCTION WITH VIMENTIN AND LAMIN B.
6 X TANDEM REPEATS OF MOTIF A. (APPROXIMATE).
MOTIF A (APPROXIMATE).
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1839 QLTEGTAQQRLAAEQELIRLRAETEQGEHQRQLLEEELARLQHEATAATQKRQELEAELA 1898

DOMAIN

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à	382	EIIDGLSEQENNEKQMRQLSVIPPMMFDAEQRRVKFINMNGLMEDPMKV 430	
Q	1899	KVRAEMEVLLASKARAEEESRSTSEKSKQRLEAEAGRFRELAEEAARLRALAEEARR- 1955	
ογ	431	YKDRQFMNVWTDHEKEIFKDKFIQHPKNFGLIASYLERKSVPDCVLYYYLTKKN 484	
QQ	1956	HELAEEDAARQRAEADG	
οy	485	ENYKALVRNYGKRRGRNQOIARPSQEEKVEEKEEDKAEKTEKK 528	
Ω	2004	ERLRRLAEDEAFORRRLEEQAAQHKADIEERLAQLRKASESELERQKGLVEDTLRQRRQV 2063	
9y Dp	529	EBEKKDEBEKDEK EDSKENTKEKDKIDGTAEET EEREQATPRGRKTANSGCRRK 582 	
ò	583	GRITRSMTNEAAAASAAAAAATEEPPPPLPPPEPISTEPVETSRWTEE-EMEVAK 637	
· A	2124		
οy	638	KGLVEHGRNWAAIAKMVGTKSEAQCKNFYFNYKRRHNLDNLLQQHK 684	
q	2175	: : :       : : :   : :	
oy Db	685	KTSRKPREERDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSEDSPENAT 742 : : :     : :     : :	
ò	743		
· 6	2288		
οy	787	SISAETAEQMDVDQQEHSAEEGSVCDPPPATKADSVDVEVRVPENHASKVEGDN 840	
g	2348	:      : :     ELQRENTEAENGREATORE   ::  :  :  :  ELQRENTEAENGRETORE   ::  :  :  :  :  :  :  :  :  :  :  :	
ογ	841	TKERDLDRASEKVEPRDEDLVVAQQINAORPEPQSD876	
qq.	2398		
δÿ	877	EPERQRMFP 900	
qq	2458	AVQEATRLKAEAELLQQQKELAQEQARRLQADKEQMAQQLVEETQGFQRTLEAERQRQLE 2517	
οy	901	MDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTPVSGYALY 960	
qq	2518	MSAEGEKLKLRMAEMSRAQARAEEDAQRFRKQAEEIGEKLH 2558	
δy	961	Ξ	
q	2559	RETELATQEKVILVQTLEIQRQQSDQDAERLREAIAELEREKEKLKQEAKLLQLKSEEMQT 2618	
٥y	1017	NLPEGVRLPTTRPTRPPPPLIPSSKTTVASEKPSFIMGGSISQGTPG 1063	
g G	2619	VQQEQILQETQALQKSFLSEKDSLLQRERFIEQEKAKLEQLFQDEVAKA 2667	
οy	1064	TYLTSHNQASYTQETPKPSVGSISLGLPRQQESAKSATLPYIKQEEFSPRSQNSQPEG 1121	
qa	2668	KQLQEEQQRQQQMEQEKQELVASMEEARRRQREAEEGVRRKQEELQRLEQQRQQQE 2724	
οy	1122	LLVRAQHEGVVRGTAGAIQEGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGIPTEA 1181	
g	2725	KLLAEENQRLRERLQRLEEEHRAALAHSEEIATSQAAATKALPNGRDA 2772	
٥y	1182	LVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIKNAREGTRSP 1235	
ფ	2773	LDGPSWEAEPEYTFEGLRQKVPAQQLQEAGILSWEELQRLTQGH 2816	
٥٧ م	1236	RTAHEISLKRSYESVEGNIKQCMSMRESPVSAPLEGL-ICRALPRGSPHSDLKERT	
g	2817	TTVAELTQREDVRHYLKGGSSIAGLLLKPTNEKLSVYTALQRQLLSPGTALILLEAQ 2873	

3202 AGTGHIIDPATSARLTVDEAVRAGLVG------PEWHEKLLSAEKAVTGYRDPYSGQ 3252 1622 OMOVNLRPDVARGLSPREQPLGL--PYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRIT 1679 3457 LLASKILSRTQFEQLKDGKTSVKDLSEVGSVRTLLQGSGCLAGIYLEDSKEKVTIYEAMR 3516 2072 -----TPQQPPTST-FONSPSALVSTPVRTKTSN 2099 3806 FREGIKSLREVLEMESAWRYLYGIGSVAGVYLPGSRQTLTIYQALKKGLLSAEVA---- 3860 2100 RYSPESQAQSVHHQRP--GSRVSPENLVDKSRGSRPG------KSPERSHVS-SEP 2146 1291 VLSGSIM---QGTPRATTESFEDGLKYPKQIKRESPPIRAFEGAITKGK-PYDGITTIKE 1346 2927 ---SLFQAMKKDLIVRDHGIRLLEAQIATGGIIDPVHSHRVPVDVAYQRGY--FDEEMNR 2981 2982 VLADPSDDTKGFFDPNTH---ENLTYLQ------LLERCVEDPETGLRLLPLTD 3026 |:| ::|| |||| | : || ||| | 3253 --SVSLFQALKKGLIPREQGLRLLDAQLSTGGIVD-------PSKSHRVPLD-VA 3297 1745 -- PGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMPLPAGG 1802 3414 FRICKVIVEKVIKILIIIVEEVETQRQERLS-FSGLRA--------PVPASE 3456 1803 PSISQGLPASRYNTAADALAALVD------AAASAPQMDVSKTKESKHEAAR 1848 3575 GYKDPYSGSTISLFQAMKKGLVLRDHAIRLLEAQIATGGIIDPVHSHRLPVDV-AYQRGY 3633 3027 KAAKGGEL---VYTDTEARDVFEKATVSAPFGKFQGKTVTIWEIINSEYFTAEQRRDLLR 3083 1499 MNRTSDVTIPP-----NKSTNHERKSTLT-PTQRESIPAKSPVPGVDPVVSHSPFDPHH 1551 1552 RG-----EVYWSHLPTQ 1567 3142 RGERSVREVAEADEVRQALRGTSVIAGVWLEEAGQKLSIYEALRRDLLQPEVAVALLEAQ 3201 1680 XIPGTQITFPPRPYNSASMSPGHPTH-------------LAAA 1709 3298 YARG----YLDKETNRALISPRDDARVYLDPSIREPVIYSQLQQRCRSDQLIGLSLLPLS 3353 -----SSDLYLRPGSEQ---- 1744 1849 LEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSG--KPQPHSSVVYSEAGKD 1906 1952 ------SQSSDSSSSL---SSHRYETPSDAIE--VISPASS----PAPPQEKLQTYQ 1993 1994 PEVVKANQ--AENDPTRQYE-----GPLHH----YRPQQESPSPQQQ---LPPSS 2034 MGRSIHEIPRQDILTQE-SRKTPEVVQSTRPIIEGSISQGTPIKFDNNSGQSAIKHNVKS 1406 LITGPSKLSRGM--PPLEIVPENIKVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRSTL 1464 HEAPKAQLSPGIYDDTSAR----RTPVS--------YQNTMSRGSPM || :|: |: |: |: |: |: || 3084 QFRTGRITVEKIIKIVITVVEEHERKGQLCFEGLRALVPAAELLD--SGVISHEVYQQLQ 1568 -----LDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITSQ 3354 EKAVRARQEEVYSELQARETLERAKVEVPVGGFKGRALIVWELISSEYFTEEQRQELLRQ 1907 KGPPPKS-----RYEEELRTRG-----KTTITAANFIDVIITRQIASDKDARERG-3634 FDEEMNRVLADPSDDTKGFFDPNTHENLTYLQLLERCVEDPETGLRLLPLRGAEK----2035 QAEGMGQVPRTHRLITLADHI--CQIITQ-----DFARNQVSSQ----1710 ASAEREREREKE-RERERIAAA-----셤 g δ q δŽ g δ qq g q QY Dp Qy Db q οy qq ŏ g ŏ g  $_{\rm Q}$ qq δy g g ò QΥ QY ŏ ŏ g ŏ δ

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LISSUES.";
J. BAOL. Chem. 270:3914-3918(1995).

J. BAOL. Chem. 270:3914-3918(1995).

-! FUNCTION: MAY PLAY A ROLE IN INTERCELLULAR SIGNALING AND IN CONNECTING CELLS WITH THE EXTRACELLULAR MATRIX. MAY TAKE PART IN THE REGULATION OF CELL MOTILITY, GROWTH AND DIFFERENTIATION. BINDS
                                                                                                                                                                                                                                                                                               4085
-----LLSAE-RAVTGYKDPYSG-----KLISLFQAM 4169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-95181355; PubMed-7876137; Zako M., Shinomura T., Ujita M., Ito K., Kimata K.; "Expression of PG-M(V3), an alternatively spliced form of PG-M without a chondroitin sulfate attachment in region in mouse and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: SECRETED; EXTRACELLULAR MATRIX.
ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS; V0 (SHOWN HERE), V1,
V2 AND V3; AEE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: V2 IS FOUND ONLY IN BRAIN.
DEVELOPMENTAL STAGE: DISAPPEARS AFTER THE CARTILAGE DEVELOPMENT.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 1 CTYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                         -----PMVKSKK---
                                                                                                                                                                                                                                                                                                                                                                      ----QRG----
                                                                                                                                                                                                   3971 KDTHDQLSEPSEVRSYVDPSTDERLSY----TQLLKRCRRDDNSGQMLLPLSDARKLTF
                                                                                                                                                                                                                                                                                          4026 RGLRKQITVEELVRSQVMDEATALQLQEGLTSIEEVTKNLQKFLEGTSCIAGVFVDATKE
                                                                                                                                                                                                                                                                                                                                                                                                                              2274 SFDDKVEDHGVVMSQPMGVVPGTANTSVVTSGETRREEGDPSPHSGGVCKPKLISKSNSR
                                                                                                                                                                                                                                                     ------QEIFRKINSSGGDSDMAAA-----
                                                                                                                                                                                                                                                                                                                                          ------QPGTEIFNLPAVTTSGSVSSRGHSFADPASNLGL--EDIIRKALMG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V_MOUSE STANDARD; PRT; 3358 AA.

QCCV_MOUSE STANDARD; PRT; 3358 AA.

QCS059; QCS058; CRel. 35, Created)

Q1-NOV-1997 (Rel. 35, Last sequence update)

Q1-OCT-2000 (Rel. 40, Last annotation update)

VERSICAN CORE PROPER PROPENSOR (LARGE FIBROBLAST PROTEOGLYCAN)

(CHONDROITIN SULFATE PROTEOGLYCAN CORE PROTEIN 2) (PG-M).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ito K., Shinomura T., Zako M., Ujita M., Kimata K.;
Multiple forms of mouse PG-M, a large chondroitin sulfate
proteoglycan generated by alternative splicing.";
J. Biol. Chem. 270:958-965(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-348 AND 3053-3358 FROM N.A. (VARIANT V3)
                                                               2147 Y--EPISPPQ-----VPVVHEKQDSLLLLS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (VARIANTS V0; V1 AND V2).
STRAIN-C57BL/6, AND SWISS WEBSTER; TISSUE-Brain;
MEDLINE-95122551; Pubmed-7822336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2334 KSKSPIPGQGYLGTERPSSVSSVHSEGDYHR 2364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKGLILKDHGIRLLEAQIATGGIIDPEESHR 4200
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
-!- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CALCIUM-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAG-ALPHA (GLUCOSAMINOGLYCAN ATTACHMENT
DOMAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi; Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain; Hyaluronic acid; Alternative splicing.
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EGF-LIKE 2, CAI
C-TYPE LECTIN.
SUSHI.
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PROSITE; PS000101; ASC.HUDROXXL; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01186; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS00615; C_TYPE_LECTIN_2; 1.
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                                                                                                                                                                       EMBL; D28599; -; NOT_ANNOTATED_CDS.
EMBL; D32040; BAA06802.1; -.
HSSP; P00740; 11XA.
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                                                                                                                                                                                                                                                             DR InterPro; IPR000561; -... cerpro; IPR000561; -... DR InterPro; IPR001304; -... DR InterPro; IPR001308; -... DR InterPro; IPR001481; -... DR Pfam; PF00009; EGF; 2... R Pfam; PF000193; X1ink; 2... Pfam; PF000047; ig; 1... Pfam; PF000084; sushi; 1... PRINTS; PR00100; Prome
                                                                                                                                                          EMBL; D16263; BAA03796.1; -.
                                                                                                                                                                                                                                        IPR000152; -.
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InterPro; IPR000152; -.
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YD 951 951 N-LINKED (GLCNAC) (POTENTIAL).  YD 1305 1305 N-LINKED (GLCNAC) (POTENTIAL).  YD 1372 1372 N-LINKED (GLCNAC) (POTENTIAL).  YD 1679 N-LINKED (GLCNAC) (POTENTIAL).  YD 2054 2054 N-LINKED (GLCNAC) (POTENTIAL).  YD 2344 2244 N-LINKED (GLCNAC) (POTENTIAL).  YD 2362 2362 N-LINKED (GLCNAC) (POTENTIAL).  YD 2627 2627 N-LINKED (GLCNAC) (POTENTIAL).  YD 3030 3030 N-LINKED (GLCNAC) (POTENTIAL).  YD 3342 3342 N-LINKED (GLCNAC) (POTENTIAL).  YD 3342 MISSING (IN ISOPORM V2).  CC 1309 3052 MISSING (IN ISOPORM V2).  CC 348 358 As; 366938 WW; 071B80026BC076cD CRC64;	tch al Similarity 19.6%; Ered. No. 0.00017; 457; Conservative 282; Mismatches 803; Indels 795; Gaps 119; KGRITRSMINEA-AAASAAAAATEEPPPPLEPPEPISTE-PVETSRWT 629	KQNISEATTIEMNILAETSSPSLSKEPHMVPDRATPVIPLATELPIFTTHFPPAGNIVNS 408  EEEMEVAKKGLVEHGRNWAAIAKMVGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRK 689    :	PREERDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSEDSP 738	ENATSRGNTEPAVELEPTTE-TAPSTSPSLAVPS 771	TVRSDQSTRVFSQIPEVITVSKTSED-TTYSQLGDLESISTSTITMLGTDRSLIDKEKEP 626	AEEGSVCDPPPATKADSVDVEVRVPENHASKVEGDNTKERDLDRASE 851	KVE-PRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDV 889 :	DGEPERQR	VSSPLKPNPLDLPQLQHRA-AVIPPMVSCTPCNIPIGTPVSG-YALYQRHI 964	KAMHESALLEEGROROEQIDLECRSSTSPCGTSKSPNREWEVLQPAPHQLITNL 1018	PEGVRLPTTRPTRPPPPLIPSSKTTVASEKPSFIMGGSISQGTPGTYL-TSHNQAS 1073	YTQETPKPSVGSISLGLPRQOESAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVR 1133    :   :   :   :   :     :     .	GTAGAIQEGSITRGTPTSKISVESIPSLRGSITQGTP 1170
CARBOHYD CAR	Query Match Best Local Matches 45	349 7 630 5 409	, 690 , 450	739	772 568	805	, 852 o 687	, 890 ) 743	916	965	7 1019	7 1074	, 1134
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Qy	8HI 124
QQ	:   1134 TLRPFQTHVTQLMEETTEEGKKASLDYTDLGSGLFEPRATELPKFPSTFSDISVFTAIDS 1193
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οy	1383 SQGTPIKFDNNSGQSAIKHNVKSLITGPS-KLSRGMPPLEIVPENIKVVE- 1431
qq	1346 LPELPDSFEIDIYHSEEDEGGEEDCVNATDVTTTPSVQYINGKQLVTTVPKDPEAAEA 1403
Οy	1432 - RGKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQN 1490
đ	QYESVAPSONFPD
δy	1491 TMSRGSPMMNRTSDVTIPPNKSTNHERKSTLTPTQRESIPAKSPVPGVDPVVSHSP 1546
q	1429 ILAETESSTTMOFKKSKEGTELLEITWKPETYPETPDHVSSGEPDVFPTLS 1479
δy	AGEVYWSHLPTQLE
Op	1480SHDGKTTRWSESITESSPNLENPVHKQPKPVPLFPEESSGE 1520
δλ	1604 YAMENTRQTILNDYITSQQMQVNLRPDVARGLSPREQ 1640
qq	1521 GAIEQASQETILSRATEVALGKETDQSPTLSTSSILSSSVSVNVVLEEEPLTLTGISQTDE 1580
Qγ	1641 PLGLPYPATRGIIDLTNMPPTILVPHPGGTSTP- 1673
පි	1581 SMSTIESWVEITPSQTVKFSESSSAPIIEGSGEVEENKNKIFNMVTDLPQRDPTDTLSPL 1640
δλ	ITF
οp	1641 DMSKIMITNHHIYIPATIAPLDSKLPSPDARPTTVWNSNSTSEWVSDKSFEGRKK 1695
ΟŊ	1722 KERERERIAAASSD-LYLRPGSEQPGRPGSHGYVRSPSPSVR 1762
qq	1696 KENEDEEGAVNAAHQGEVRAATERSDHLLLTPELESSNVDASSDLATWEGFILETTPT-E 1754
οy	
qq	1755 SEKEMANSTP-VFRETIGVANVEAQPFEHSSSSHPRVQEELTTLSGNPPSLFTDLGSGDA 1813
QY	1815 NTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAV 1860
qq	1814 SIGMELITASLFTLDLESETKVRKELPSTPSPSVEISSSFEPTGLTPSTVLDIEIA 1869
δŏ	1861 SEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKS 1913
qq	1870 GVMSQTSQKTLISEISGKPTSQSGVRDLXTGFPMGEDFSGDFSEYPTVSYPTMK- 1923
οy	1914 RYEEELRIRGKITIITAANFIDVIIITRQIASDKDARERGSQSSDSSSLSSHRYETPSDAI 1973
qq	1924EETVGMGGSD-DERVRDTQTSSSIPTTSDNIYPVPDSKG 1961
δλ	1974 EVISPASSPAPPQEKLQEV 1996
qa	1962 PDSTVASTTAFPWEEVMSSAEGSGEQLASVRSSVGPVLPLAVDIFSGTESPYFDEEFEEV 2021

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EPYEPISPPQVPVVHEKQDSLLLLSQRGAEPAEQRNDARSPGSISYLPSFFTKLENTSPM 2204
    ----RQYEGPLHHYRPQQESPSPQQQLPP-SSQAE 2037
                                                                                                                                                                                                                                                                                      -----PEAPGKSHSFSATALVTESGA-----AR----SVLMDSSTQEEESIKL 2208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-1175 FROM N.A. MEDILINE-98094255; Pubmed-9434167; Takeuchi T., Chen B.-K., Qiu Y., Sonobe H., Ohtsuki Y.; "Molecular cloning and expression of a novel human cDNA containing CAG
                                      2022 AAVTEANERPTVLPTAASGNTVDLTENGYIEVNSTMSLDFPQTMEPSKLWSKPEVNLDKQ 2081
                                                                                                                                                             2085 PSALVSTPVRTKTSNRYSPESQAQSVHHQRPGSRVSPENLVDKSRGSRPGKSPERSHVSS 2144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Moran E.;
"The human SWI-SNF complex protein p270 is an ARID family member with non-sequence-specific DNA binding activity.";
Mol. Cell. Biol. 20:3137-3146(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN SPLEEN, THYMUS, PROSTATE,
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN SPLEEN, THYMUS, PROSTATE,
LOVARY, MALL INTESTINE, COLON, AND PBL, AND AT A MUCH
LOWER LEVEL IN HEART, BRAIN, PLACENTA, LUNG, LIVER, SKELETAL
MUSCLE, KIDNEY, AND PANCREAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWF1_HUMAN STANDARD; PRT; 1902 AA.
014497; Q9UP21;
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last sequence update)
SWI/SNF-RELATED, MATRIX-ASSOCIATED, ACTIN-DEPENDENT REGULATOR OF CHROMATIN SUBFAMILY F MEMBER 1 (SWI-SNF COMPLEX PROTEIN P270) (B120).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2339 ---IPGQGYL-----GTERPSSVSSVHS-EGDYHRQTPGWAWEDRPSSTGSTQ 2382
                                                                                                          2310'EEG-----DPSPH---SGGVCKPK-----LISKSNSRKSK----SP
                                                                                2038 GMGQVPRTHRLITLADHICQIITQDFARNQV-----SSQTPQQPPTST-----FQNS
                                                                                                                                                                                                     2127 DYSMLTT-LKTYITNKEVEEEGMSIAHMSTPG-------PGIKDLESYTTH
                                                                                                                                                                                                                                                                                                                             ----VKSKKQEIFRKLNSSGGDSDMAAAQPGTEIFNLPAVTTSGSVSSRGHSFADPASN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Dallas_P.B., Pacchione S., Wilsker D., Bowrin V., Kobayashi R.,
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Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: BINDS DNA NON-SPECIFICALLY.
-! SUBGUNIT: PART OF THE SWI-SNF COMPLEX.
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or send an email to license@isb-sib.ch).
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Best Local Similarity 17.4%; Pred. No. 0.00011;
Matches 340; Conservative 260; Mismatches 678; Indels 672; Gaps
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1752 GYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPT-----AQLRIMPLPAG- 1801 1802 GPSISQGLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAVS 1861 1862 EQQQLEQXTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDK-GPPPKSRYEEELR 1920 1921 TRGKTTITAANFIDVIITRQIASDKDARERGSQ---SSDSSSSLSSHRYETPSDAIEVIS 1977 PSSQAEGMGQVPRTHRLITLADHICQIITQDFARNQVSSQTPQQPPTSTFQNSPSALVST 2091 PSN-----YQPPPSMQNHIPQVSSPA 1206 2092 PVRTKTSNRYSPESQAQSVHHQRPGSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEPIS 2151 2152 PPQVPVVHEKQDSLLLLSQRGAEPAEQRNDARSPGSISYLPSFFTKLENTSPMVKSKKQE 2211 2212 IFRKLNSSGGGDSDMAAAQPGTEIFNLPAVTTSGSVSSRGHSFADPASNLGLEDIIRKAL 2271 1309 ----NILLYDDNSIMTFNLSQLPGLLELLVEYFRRCLIEIFGILKEYEVGDPGQRT---- 1360 2323 KPKLISKSNSRKSKSPIPGQGYLGTER----PSSVSSVHSEGDYHRQTPGWAWEDRPSS 2377 924 P----DSYGNDFD--SGMXSPSRYPPQQQQQQQRH------DSYGNQFSTQ-GTPSG- 968 Borrow J., Stanton V.P. Jr., Andresen J.M., Becher R., Behm F.G., Chaganti R.S.K., Civin C.I., Disteche C., Dube I., Frischauf A.M., Horsman D., Mitelman F., Vollinia S., Watmore A.E., Housman D.E.; "The translocation t(8;16)(pl1;pl3) of acute myeloid leukaemia fuses a putative acetyltransferase to the CREB-binding protein."; -----S 1978 PASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEG--PLHHYRPQQESPS----PQQQLP 2272 MGSFDDKVEDHGVVMSQPMGVVPGTANTSV-----VTSGETRREEGDPSPHSGGVC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI\_TaxID=9606; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) MONOCYTIC LEUKEMIA ZINC FINGER PROTEIN (ZINC FINGER PROTEIN 220). ZNF220 OR MOZ. 2004 AA. | : :: | ::: | : 1416 ENSEEKLISKFDKLPVKIVQKNDPFVVDCS 1445 2378 TGSTQ---FPYNPLTMRMLSSTPPTPIACA 2404 PRT; SEQUENCE FROM N.A. MEDLINE-96376968; PubMed-8782817; STANDARD; Homo sapiens (Human). MOZ\_HUMAN Q92794; RESULT 30 MOZ\_HUMAN 1056 2032 1186 1092 1250 g δ g δ ద ŏ a ŏ qq δ g ò g ŏ qq δ οy g ŏ q ò g à g

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Genet. 14:33-41(1996).
FUNCTION: MAY REPRESENT A CHROMATIN-ASSOCIATED ACETYLTRANSFERASE
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                  SUBCELLULAR LOCATION: NUCLEAR.
DISEASE: PARTICIPATES IN A T(8;16)(P11;P13) CHROMOSOMAL
PRANSLOCATION THAT PRODUCES A MOZ-CAP CHIMAERA OBSERVED IN THE
M4/M5 SUBTYPE OF ACUTE MYELOID LEUKEMIA.
SIMILARITY: CONTAINS 2 PHD ZINC-FINGER DOMAINS.
SIMILARITY: BELONGS TO THE MYST (SAS/MOZ) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKLKKKQQQLEEEAAKPPEPEKPV------SPPPVE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BREAKPOINT FOR TRANSLOCATION TO FORM
                                                                                                                                                                                                                                                             Proto-oncogene; Chromosomal translocation; Zinc-finger; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 17.1%; Pred. No. 0.00013;
hes 358; Conservative 276; Mismatches 640; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9FFBBAC3792854BA CRC64;
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                                                                                                                                                                                                                                                                                                                              ASP/GLU-RICH (ACIDIC).
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GLN/PRO-RICH.
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POLY-PRO.
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---NOVMRKKLILFFKRRNHARKQREQKICQRYD----QLMEA 317
                                                                                                                                                                       LDHKTLYYDVEPFLFYVLTQNDVKGCHLVGYFSKEKHCQ------QKYNVSCIMILPQ 652
                                                                                                                                                                                                                                                                                                WEKK-----VDRIENNPRRKAKESKTREYYEKQFPEIRKQREQQERFQRVGQRGA---- 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----GLSATIARSEHEISEIIDGLSEQENNEKQMRQLSVIPPMMFDAEQRRVKFINMNGL 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                683 LSDLGRLSYMAYWKSVILECLYHQNDKQISIKKLSKLTGICPQDITSTLHHLRMLD---- 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDPMKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNFGLIASYLERKSV-PDCVLYYYLTK 482
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---SVVSEEEEEEAEEGENEEPQCQERELEISVG 814
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: :     : 05ELIELKEEEEIPHSED 1421	55 VESIPSLRGSITQGTPALPQTGIPTEALVKGSISRMPIEDSSPEKGREEAASKGHVIYEG 1214 	15 KSGHILSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPLEGLIC 1274 1	75 RALPRGSPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYPKQIKRESPPIRAFEGAI 1332 	33 TKGKPYDGITTIKEMGRSIHEIPRQDILTQESRKTPEVVQSTRPIIEGSISQGT 1386	87PIKFDNNSGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIK 1428 	29 VVERGKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPRAQLSPGIYDDTSARRTPVSY 1488 ::::	89 QNTMSRGSPMMNRTSDVTIPPNKSTNHERKSTLIPTQRESIPAKSPVPGVDPVVSH 1544 1 :	45 SPFDPHHRGSTAGEVYMSHLPTQLDP-A 1571 	72 MPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYIT 1619 	20 SQQMQVNLRPDVARGLSPREQPLGLPYPATRGIIDL 1655           :     : : : : : : : : : : : :	56 TUMPPTILVPHPG-GTSTPPMDRITYIPGTQITFPPRPYNSASMSPGHP 1703   :	04 THLAAAASAERERERERERERERIAAASSDLYLRPGSEQPGRPGSHGYVRSPSPS 1760   :	OUSE CBP_MOUSE STANDARD; PRT; 2441 AA. P45481; CBP_MOUSE STANDARD; PRT; 2441 AA. P45481; D1-NOV-1995 (Rel. 32, Created) O1-FEB-1996 (Rel. 36, Last annotation update) O1-FEB-1996 (Rel. 36, Last annotation update) O1-FEB-1998 (Rel. 36, Last annotation update) O1-FEB-1998 (Rel. 36, Last annotation update) CREBBP OR CBP. MUS musculus (Mouse). CREBBP OR CBP. Mus musculus (Mouse). Mus musculus (Mouse).  CREBBP OR CBP. Mus musculus (Mouse).  (A)  TASOURCE FROM N.A. TISSUE-Brain; MEDLINE-94019866; PubMed-8413673; Goodman R.H.; Goodman R.H.; Goodman R.H.; Phosphorylated CREB binds specifically to the nuclear protein CBP."; Nature 365:855-859(1993).
1405	1155	1215	1275	1333	1387	1429	1489	1545	1572 1769	1620	1656 1885	1704	RESULT 3. CBP_MOUSE 1. LD CBP_J AC CBP_ACOUSE 1. AC P4541 DT 01-N DT 01-N DT 15-J DT 1
qq.	Qy Db	Oy Dp	Qy Dp	Qy Dp	Oy Dp	oy Db	Qy Db	OY Dp	Qy Dp	Qy Dp	Qy Db	ΟΥ Dp	RESULT TO P P P P P P P P P P P P P P P P P P P

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps 122;
FUNCTION: MEDIATES CAMP-GENE REGULATION BY BINDING SPECIFICALLY TO PHOSPHORYLATED CREB PROTEIN. ACTING AS A COACTIVATOR, CBP AUGMENTS THE ACTIVITY OF PHOSPHORYLATED CREB TO ACTIVATE TRANSCRIPTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 FGQPFSQTGGQQMG-ATGVNPQLASKQSMVNSLPAFPTDIKNTS----VTTVPNMSQLQTS 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 PLNQGDSST------PNLPKQA-----ASTSGPTPPASQALNPQAQKQVG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 LRRRPSLLSEFHPGSDRPQERRTSYEPFHPG--PSPVDHDSLESKRPRLEQVSDSHF--- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 AAKPPEPEKPVSPPPVEQKHRSIVQ----IIYDENRKKAEEAHKIFEGLGPKVELPLYNQ 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269 PSDTKVYHENIKTNQVMRKKLILFFKRRNHARKQREQKICQ-----RYDQLMEAWEK--K 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424 HDCPVCLPLKNASD-------KRNQQTILGSPASGIQNTIGSVGAGQQNAT 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------HCRI---MKNVL-----NHMTHCQAPKACQVAHCASSRQIISHWKNCTR 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 VDRIENNPRRKAKESKTREYYEKQFPEIRKQREQQERF------QRVGQRGAGLSATI 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         374 ARSEHEISEIIDGLSEQE-----NNEKQMRQLSVIP---PMMFDAEQRRVKFINMN 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 PPNQGAFSTEQSRYPPHSVQYTFPNTRHQQEFAVPDYRSSHLEVSQASQLLQQQQQQQ-- 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription regulation; Nuclear protein; Activator; Bromodomain. DOMAIN 1104 1176 BROMODOMAIN.

DOMAIN 1062 1065 POLY-GLU.
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                                                                             SUBCELLULAR LOCATION: NUCLEAR. SIMILARITY: CONTAINS 1 BROMODOMAIN.
                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000197; -
InterPro; IPR000433; -
InterPro; IPR001487; -
Pfan; PF00569; 22; 1.
Pfam; PF00439; bromodomain; 1.
Pfam; PF00135; zf TAZ; 2.
PRINTS; PR00503; BROMODOMAIN.
PROSITE; PS50014; BROMODOMAIN.
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A: 265474 F
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TRANSFAC; T01318; -.
MGD; MGI:1098280; Crebbp.
                                                           CAMP-RESPONSIVE GENES.
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SLSNPNPIDPSSMQRAYAALGLPYMNQPQTQLQPQVPGQQPAQPPAHQQMRTLN	GLMEDPMKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNFGLIASYLERKSVPD	ALGNNPWSVPAGGITTDQQPPNLISESALPTSLGATNPLANDGSNSGNIGSLSTIP-	CVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEKVEEKEEDKAEKTEK	KEEEKKDEEEKDEKEDSKENTKEKDKIDGTAEETEEREQATPRGRKTANSGGR :	RKGRITRSMINEAAAAAAAAAATEEPPPPLPPPFFISTEPVETSRWIEEEMEV	ILGNQPALFASGAQFPVIPFAGSYRPPNGFLFLPVNRMQVSQGMNSFNPMSL AKKGLVEHGRNMAAIAKMVGTKSEAQCKNFYFNYKRRHNLDNILOOHKOK-TSRKPP	GNVQLPQAPMGPRAASPMNHSVQMNSMASVPGMAISPSRMPQPPNNMGTHANNIMAQAPT	EERDVSQCENASTVSAQEDEDIEASNEEENPEDSEVEAV : : :   :	KPSEDSPENATSRGNTEPAVELEPTTETAPSTSPSLAVPST	KDAEDROVETOVINGTOABROADVINGTOERABERGOVODSDDB#		KADSVDVEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQS	SQAAASIDNRVPTPSTVTSAETSSQQPGPDVPMLEMKTEVQTDDAEPEPTE	DNDSSATCSADEDVDGEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAA : : :       : : : : : :       : : : :	VIPPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEQRQRQBQIDLECRS-STSPC	GTSKSPNREWEVLQPAPHQLITNLPEGVRLPTTRPTRPPPPLIPSSKTTVASEKPSF	QPRKKIFKPEELRQALMPTLEALYRQDPESLPFRQPVDPQLLGIPDYFDIVKNPMDLS	IMGGSISQGTPGTYLTSHNQASYTQETPK	SLGLPROQESAKSATLPYIKOEEFSPRSQNSQPEGLLVRAQHEGVVRGTA-GALQEGSIT	GYCCGRKYEFSPQTLCCYGKQLCTIPRDAAYYSYQNRYHFCGKCFTEIQGENVT	RGTPTSKISVESIPSLRGSITQGTPALPQTGIPTEALVKGSISRMPIEDSSPEKGREEAA	LGDDPSQPQTTISKDQFEKKKNDTLDPEPFVDCKECG	SKGHVIYEGKSGHILSYDNIKNAREGTRSPRTAHEISLKRSYESVEGN	RKMHQICVLHYDIIWPSGFVCDNCLKKTGRPRKENKFSAKRLQTTRLGNHLEDR	IKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIMQGTPRATT ::::	THE DESIGNATIONS EVET TO VESSOR FEATURE FUNDE DESIGNATION VESTORIANCE TO SERVICE TO SERV	ALFBIDGV-DVCFFGMHVQDTALIAPHQBIDGV-DVCFFGMHVQDTALIAPHQ
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qq	1426	
Qy	1408	TGPSKLSRGMPPLEIVPENIKVVERGKYEDVKAGE 1442
Op	1470 AHIWACP	CPPSEGDDYIFHCHPPDQKIPKPKRLQEWYKKMLDKAFAERIINDYKDIFKQANE 1529
ογ	3 TVR	SGPSVLRSTLHEAPKAQLSPGIYDDFSARRTPVSYQNT 149
οgα	1530DR	DRLTSAKELPYFEGDFWPNVLEESIKELEQEEEERKKEESTAASETPEGSQGDSKNA 1586
οy	1492 MSRGSI	MSRGSPMMNRT-SDVTIPPNKSTNHERKSTLTPTQRESIPA 1531
qq	1587 KKKNN	KKKNNKKTNKNKSSISRANKKKPSMPNVSNDLSQKLYATMEKHKEVFFVIHLHAGPVIST 1646
δλ	1532 KSPVP	KSPVPGVDPVVSHSPFDPHHRGSTAGEVYWS1562
QQ	1647 QPPIVI	OPPIVDPDPLLSCDLMDGRDAFLTLARDKHWEFSSLRRSKWSTLCMLVELHTQGQDRFVY 1706
οy	1563	HLPTQDPAMPFHRALDPAAAYL 1586
Q	1707 TCNEC	TCNECKHHVETRWHCTVCEDYDLCINCYNTKSHTHKMVKWGLGLDDEGSSQGEPQSKSPQ 1766
Qy	1587 FORQLS	S
QQ	1767 ESRRE	ESRRLSIQRCIQSLVHACQCRNANCSLPSCQKMKRVVQHTKGCKRKTNGGCPVCKQLIAL 1826
Qy	1607	
Op	1827 CCYHA	CCYHAKHCQENKCPVPFCLNIKHNVRQQQIQHCLQQAQLMRRRMATMNTRNVPQQSLPSP 1886
οy	1638 REQPLO	REQPIGLEYPATRGIIDLTNMPPTILVPHPGGTSTP-PMDRI-TYIPGTQITEPP 1690
qq	1887 TSAPPGT	GTPTQQPSTPQTPQPPAQPQPSPVNMSPAGFPNVARTQPPTIVSA 1936
QY	1691 -RPYN	ΙŊ
qq	1937 GKPTN	GKPINQVPAPPPPAQPPPAAVEAARQIEREAQQQQHLXRANINNGMPPGRDGMGTPG 1993
Qγ	1750 SHGYV	SHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMPLPAGGPSISQGL 1809
QQ	1994 SQ	MTPVGLNVPRPNQVSGPVMSSMPPGQWQQAPIPQQQPMPGM 2036
Qy	1810 PASRY	ı,
QQ	2037 P	RPVMSMQAQAAVAGPRMPNVQPNRSISPSA-LQDLLRTLKSPSSPQQQQQ 2086
Qy	1870 TLEVE	TLEVEKRSVQCLYTSSAFSSV 1898
qq	2087 VLNIL	PGMHQQPSLQ
Οy	1899 VYSEA	VYSEAGKDK-GPPPKSRYEEELRTRGKTTITAANFIDVIITRQI- 1941
QQ	2144 NAMQAG	NAMQAGVPRPGVPPPQPPAMGGLNPQGQALNIMNPGHNPNMTNMNPQYREMVRQLL 2199
οχ	1942ASD	ASDKDARERGSQSSDSSSLSSHRYETPSDAIEVISPAS-SPAPPQEKLQTYQ 1993
qq	2200 04000	QHQQQQQQQQQQQQQQQNSASLAGGMAGHSQFQQPQGPGGYAPAMQQQRMQHL 2253
ογ	1994 P	EVVKANQAENDPTRQYEGPLHHYRPQQESPSPQQLPP 2032
QQ	2254 PIQGS	PIQGSSMGQMAAPMGQLGQMGQPGLGADSTPNIQQALQQRILQQQQMKQQIGSPGQPNPM 2313
Qγ	2033 SSQAE	THRLITLADHICQIITQDFARNQVSSQTPQQPPTSTFQNSPSALV
qq	2314 SPQQHI	SPQQHMLSGQPQASHLPGQQIATSLSNQVRSPAPVQSPRPQS 2355
δλ	2091 TPVRT	TPVRTKTSNRYSPESQAQSVHH 2136
qq	2356 QPPHS	QPPHSSPSPRIQPQPSPHHVSPQTGTPHPGLAVTMASSMDQGHLGNPEQSAMLPQLN 2412

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Matches 479;
                 InterPro;
                             InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATED CREB PROTEIN. ACTING AS A COACTIVATOR, CBP AGGRENTS THE ACTIVITY OF PHOSPHORYLATED CREB TO ACTIVATE TRANSCRIPTION OF CAMP-RESPONSIVE GENES.
SUBCELLULAR LOCATION: NUCLEAR.
DISEASE: INVOLVED IN ACUTE LEGKEMIAS BY CHROMOSOMAL TRANSLOCATIONS T(8;16)(P11;P13) INVOLVING CBP AND MOZ, AND T(11;16)(Q23;P13.3)
                                                                                                                                                                                                                                                                                               Zeleznik-Le N.J.;
"MLI. 1s fused to CBP, a histone acetyltransferase, in therapy-related acute myeloid leukemia with a t(11:16)(q23:p13.3).";
Proc. Natl. Acad. Sci. U.S.A. 94:8732-8737(1997).
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97321049; PubMed-9177780; Giles R.H., Petrij F., Dauwerse H.G., den Hollander A.I., Lushnikova T., van Ommen G.J.B., Goodman R.H., Deaven L.L., Doggett N.A., Peters D.J.M., Breuning M.H.; "Construction of a 1.2-Mb contig surrounding, and molecular analysis of, the human CREB-binding protein (CBP/CREBBP) gene on chromosome 16p13.3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INVOLVING CEPT AND MILE.

INVOLVING CEPT AND MILE.

DISCRASE: DEFECTS IN CEPT ARE THE CAUSE OF RUBINSTEIN-TAYBI
SYNDROME (RTS), A DISORDER CHARACTERIZED BY CRANIOFFACIAL
ABNORMALITIES, BROAD THUMBS, BROAD BIG TOES, MENTAL RETARDATION
AND A PROPENSITY FOR DEVELOPMENT OF MALIGNANCIES.
                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                           MEDLINE-97385172; PubMed-9238046;
Sobulo O.M., Borrow J., Tomek R., Reshimi S., Harden A.,
Schlegelberger B., Housman D., Doggett N.A., Rowley J.D.,
                                                                                       CBP_HUMAN STANDARD; PRT; 2442 AA. 029.793; 016376; 000147; 15-UL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) CREB-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 1 BROMODOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; '047741; AAC51770.1; -. EMBL; U85962; AAC51331.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U89354; AAC51339.1; -. U89355; AAC51340.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomics 42:96-144(1997).
                                                                                                                                                                                Homo sapiens (Human)
2137 -PERSHVSSE 2145
                         2413 TPNRSALSSE 2422
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                        NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 PVDHDSLES------KRPRLEQVSDSHFQRVSAAVLPLVHPLPEG-----LRAS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 QVMNGSLGAAGRGRGAGMPYPTPAMQGASSS----VLAETLTQVSPQMTGHAGLNTAQAG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 ADAK-----KDPAFGGKHEAPSSPISGQPCGDDQNASPSKLSKEELIQSMDRVDREIAKV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   318 S---VINVPNMSQMQTSVGIVPTQALATGPTADPEKRKLIQQQLVLLLHAHKCQRREQAN 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 GMAKMGITGNTSPFG----QPFSQAGGQPMG-ATGVNPQLASKQSMVNSLPTFPTDIKNT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         308 CQRYD-----QLMEAWEKK------VDRIEN------NPRKAKESK 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               482 QRAYAALGLPYM-NQPQTQLQPQVPGQQPA------------QPQTHQQM 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 KIFEGLGPKVELPLYNQPSDTKVYHENIKTNQVMRKKLILFFKRRNHARKQRE----QKI 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----GEVRACSLPHCRTMKNVLNHMTHCQAGKACQVA------HCASSRQIISHWKN 421
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                                                                                                                      PROSITE; PS00633; BROMODOMAIN_1; 1.
PROSITE; PS50014; BROMODOMAIN_2; 1.
Transcription regulation; Nuclear protein; Activator; Bromodomain;
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REF. 2).
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18.3%; Pred. No. 0.00021;
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ED -> VV (IN REF
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POLY-PRO.
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                  Pfam; PF00569; ZZ; 1.
Pfam; PF00439; bromodomain; 1.
Pfam; PF02135; Zf-TAZ; 2.
PRINTS; PR00503; BROMODOMAIN.
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DOMAIN 363 430
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:   LAEKI	000,100	I: II	CKNFY	VPGMA	VSAQEDED		2 ;	-AEEG	ddŏad.	DRASE	LLNPT		MHESA		LPTTR    :   LPFRO	OETPK	::   :	QNSQP	SYQNR	OGTPALPQTGIP  :    -DDPSOPOTTIS	KNAREG	VCDNC	RGSPH	- EVFVRVVASSDK	ESPP-	ОСРРР	ITTIK 	DDYIF	HNVKS	
: ЭЕҮҮНГ	מממשמי	IEEFFF IIPQAQ	-VGTKSEAQCKNFYFNY   :	INSMGS			ENAISKGNIEPAVELE ::	OOEHS	POPOT	rKERDI   : PGPDV	IDSKPS	: :	RHIKA		PEGVE     PES	OASYT	I I	S	NDAAYY	TOGTF	1	WPSGF	CRALP	·-EVFV	-KYPKQIKRESPP	'QEYGS	KPYDG	PPSEG	NNSGQSAIKHNVKSLIT :   : :  -HDYKDIFKQATEDRLT	
: ::	70000	A       SAQPPV	VG1	NHSVQ			PSLOH1	EOMDVE	AOAQVI	VEGDNT	DRMEPN	KEETDI	GYALYÇ		OLITNI      ALYROE	-TPGTYLTSHNQASYTQETPK	:   : WENN	EEFSPF	LCTIPF	SLRGS	LSYDNI	:         : VLHYDIIWPSGFVCDNCLKK	PLEGLI		KYF	FFGMHV	GAITKGKPYDGITTIKEMG	SHIWAC	FDNNSC:	
SHLVHKLVQAIFPTPDPAALKDRRMENLVAYAKKVEGDMYESANSRDEYYHLLAEKIYKI	A FETTERROATION OF THE PROPERTY OF THE SMILLER OF THE PROPERTY	NOTT NEGOTIANT NEEDEN PER	EEMEVAKKGLVEHGRNWAAIAKM-   :   :	LSL-PVNRMQVSQGMNSFNPMSLGNVQLPQAPMGPRAASPMNHSVQMNSMGSVPGMAISP	KRRHNLDNLLQQH-KQKTSRKPREERDVSQCESVASTVSAQEDED     ::   ::   :   :     SRMPOPPNAMCAHTNNAMAOAPAOSOFI-PONORPSSSGAMSVGMGOPPAOTGVSOGNYPG		AALDNPLNMLGPQASQLPC-PPVTQSPLHPTPPPASTAAGMPSLQHTTPPGMTPP	PITETAPST SPSLAVPSTKPAEDESVETOVNDSISAETAEOMDVDOOEHS-AEEGSVC		DPPPATKADSUDVEVRVPENHASKVEGDNTKERDLDRASEKVE 	PRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDVDGEPERQRMFPMDSKPSLLNPTGSI	:   :   :   :   :   -   -   -   -	LVSSPLKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLE      ::: : :		EQRQRQEQIDLECRSSTSPCGTSKSPNREWEVLQPAPHQLITNLPEGVRLPTTRPTR : : :	TPGT		PSVGSISLGLPRQQESAKSATLPYIKQEEFSPRS-	FCSKLAEVFEQEIDPVMQSLGYCCGRKYEFSPQTLCCYGKQLCTIPRDAAYYSYQNRYHF	- PGLLVRAQHEGVVRGTAGAIQEGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGIP 	TEALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNI		IKOGMSMRESPVSAPLEGLICRALPRGSPHSD	TGRPRKENKFSAKRLQTTRLGNHLEDRVNKFLRRQNHPEAG-	DGL	TVEVKPGMKSRFVDSGEMSESFPYRTKALFAFEEIDGVDVCFFGMHVQEYGSDCPPPNTR		RVYISYLDSIHFFRPRCLRTAVYHEILIGYLEYVKKLGYVTGHIWACPPSEGDDYIFHCH	RSIHEIPRQDILTQESRKTPEVVQSTRPIIEGSISQGTPIKFDNNSGQSALKHNVKSLIT	
II	SMTNEZ	ILGNOI	HGRNW?	APMGPF	KRRHNLDNLLQQH-KQKTSRKPREERDVSQCESVAST		TPPPAS	LSGNAC	i PTQSTF	EVRVPE     RVPTPS	ADEDVE	:     : MEEDIC	PCNIPI		REWEVI : 1 ELRQAI	! ! !	YQEPWC	AKSATI	SPOTLC	PTSKIS	HVIYEG	 HQIC	GMSMRE	FLRRON	1	AFEEIC		LEYVKK	BGSISC	
 ENLVA	GRITER	41110	KGLVE	VQLPQ	RDVSQ : :   OFT.PO	2	SPLHP	ESVET	PSA-T	DSVDV  :  ASTDN	SATCS	: PRSEM	MVSCT		SPN      FKPE	-9ÖSI	LDTGQ	ROOES	RKYEE	ITRGT	AASKG	CGRKM	IKO	DRVNK	-LKERTVLSGSIMQGTPRATTESFE-	TKALF	1	ILIGY	TRPIII     ERII-	
::: Kdrrm	CGRRK		MEVAK   :	MSTGN	KPREE   :	N D C E D	PPVTQ	KPAED	TPGSV	KA   	SDNDS	ESKGE	AVIPP 	'KV	GTSK- 1 QPRKK	IMGGS	: TIKRK	SLGLP	GYCCG	IQEGS	KGREE	: L 'VDCKE	ND	GNHLE	GTPRA	SFPYR		АVҮНЕ	EVVQS : : DKAFA	
 DPAAL	2KT ANS	RSRLHKQG	五二 正	INSFNF	COKTSE ::	FVEAT	SOLPC-	AVPST	1: 30TPF	-PPAT- 	RPEPC	:  repdpg	OLOHRA	-KSEPMEVDEKKPEVKV	SSTSPC       STSPS	SEKPSF	: VPMDLS	SVGSI	ISOMA	GTAGA    -	SDSSPE	- I - DPEPF	SYESVE	OTTRI	SGSIMO	GEMSE		RCLRT	SSRKTP : I TYKKML	
AIFPTI	ATPRGI		RWTE-	JV SQG	LOOH-F	- NDED	LGPOAS	SPSI	PVSSSC	ТРУНАС	OOINAC		PLDLP(	PMEVD	DLECRS: NGTAS(	KTTVAS	FDIVK	-	EQEID	HEGVVI     SENVTI	SRMPIE	: OTL:	ISLKR!	FSAKRI	ERTVLS	SRFVDS	IRAFE-	IHFFRE	OILTOE   : KRLQEV	
HKLVQ	REREO	II:	ISTEPVETSRWTE-	PVNRM	NLDNL:   : OPPNM	TEASUREE NDROSEWEAW DSEDSE	NPLNM)	TAPST	TOPST	3000P	DLVVA(	a	PLKPN 	KSE	RQEQIA : EESSSI	PPPPLIPSSKTTVASEKPSFIMGGSISQG	 GIPDY		LAEVF	-EGLLVRAQHEGVVRG' 	VKGSI	:   :         KDQFEKKNDTLDPEPFVDCKECGRKMHQIC-	TRSPRTAHEISLKRSYESVEGN-	RKENK	LK)	K PGMK		SYLDS	RSIHEIPRQDILIQESRKIPEVVQSTRPI 	
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602	5.58	662	618	708	670	717	827	755	882	812	855	1001	915	1042	975	1032	1117	1081	1177	1120	1179	1264	1232	1315	1286	1368	1325	1428	1349	
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QC C	1533 SAKELPYFEGDFWP	NVLEESIKELEQ-EEEERKKEESTAASETTEGSQGDS 1582
Qy	1463 LHEAPKAQLSPGIYDDŢSARRT	ARRIPVSYQNIMSRGSPMMNRISDVTIPPNKSTNHERKSTLT 1522
qq	1583 -KNAKKKN	
ď.	1523 PTQRESI	CVDPVVSHSPFDPHHRGS
qq	1625 MEKHKEVFFVIHLHAGPVINTLP	INTLPPIVDPDFLLSCDLMDGRDAFLTLARDKHWEFSSL 1681
Qy	1557 GEVYWS	
qa	1682	RRSKWSTLCMLVELHTQGQDRFVYTCNECKHHVETRWHCTVCEDYDLCINCYNTKSHAHK 1741
Qy	1577 ALDP	DPAAAAYLFQRQLS1592
qa	1742	: MYKWGLGLDDEGSSQGEPQSKSPQESRRVSIQRCIQSLVHACQCRNANCSLPSCQKMKRV 1801
δy	1593PTPGYPSQYQLYAM-	YQLYAMENENTRQTILNDYITS 1620
qq	1802	VQHTKGCKRKTNGGCPVCKQLIALCCYHAKHCQENKCPVPFCLNIKHKLRQQQIQHRLQQ 1861
Qy	1621 QQMQVNLRPDVAI	VNLRPDVARGL-SPREQPLGLPYPATRGIIDLINMPPTILVPHPGGTS 1671
qq	1862	ACLMRRRMATMNTRNVPQQSLPSPTSAPPGTPTQQPSTPQTPQPPAQPQPSPVSMS 1917
QY	1672TPPMDRIT	NSASMSPGHPTHL
qa	1918 PAGFPSVARTQPPTTVSTGKPTSQVPAPPPP-	: :
δλ	1722 KERERERIAAASSDLYLRI	PGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGT 1781
q	1968	QQQHLYRVNINNSMPPGRTGMGTPGSQMAPVSLNVPRPNQVSGP 2011
QY	1782 SVITPLDPTAQLRIMPLP	SVITPLDPTAQLRIMPLPAGGPSISQCLPASRYNTAADALAALVDAAASAPQMDVSKTKE 1841
qa	2012VMPSMPPGGWQQAPLPQQQPMPGLP	
Qy	1842 SKHEAARLEENLRSRSAA	SKHEAARLEENLKSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAF 1887
qa	2061	
QY	1888	H
qq	2115	MQPQPGLQSQPGMQPQPGMHQQPSLQNLNAMQAGVPRPGVPPQQQAMGGLNPQGQA 2170
δλ	1930 ANFID	VIITRQIASDKDARERGSQSSDSSSSLSSH-R 1965
qq	2171	LI III MIPGHIPIMASMIPQYREMLIRQLLQQQQQQQQQQQQQQQQQQQGGSAGMAGGMAGHGQ 2230
Qy	1966 YETPSDAIEVISPASSPAPPQEKLQTYQP-	EVVKANO
qq	2231 FQQPQ	-GPGGYPPAMQQQQRWQQHLPLQGSSMGQMAAQMGQLGQMGQPGLGADST 2284
, Oy	2006 PTRQYEGPLHHYRPQ(	THRLE
qq	2285	PNIQQALQQRILQQQQMKQQIGSPCQPNPMSPQQHMLSCQPQASHLPGQQIAT 2337
QY	2061 ODFARNOVSSOTPOOPPIS	SQA(
QQ	2338 SLSNQVRSPAPVQSPRPQ-	POSQPPHSSPSPRIQPQPSPHHVSPQTGSP 2383
οy	2114 RPGSRVSPENLVDKSRGSRPGKS	XPGKSPERSHVSSE 2145
qq	2384 HPGLAVTMASSIDQGHLG	HPGLAVTMASSIDQGHLGNPEQSAMLPQLNTPSRSALSSE 2423
RESUL PGCV_ ID AC	RESULT 33 PGCV_HUMAN ID PGCV_HUMAN STANDARD; AC P13611; P20754; Q13010; Q13189;	PRT; 3396 AA. Q13189; Q15123;
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MEDLINE-96213482; PubMed-8627343;
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CONNECTING CELLS WITH THE EXTRACELLULAR MATRIX. MAY TAKE PART IN
THE REGULATION OF CELL MOTILITY, GROWTH AND DIFFERENTIATION. BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIANE=95181355; PubMed=7876137; Zako M., Shinomura T., Ujita M., Ito K., Kimata K.; "Expression of PG-M(V3), an alternatively spliced form of PG-M without a chondroitin sulfate attachment in region in mouse and human
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01-OCT-2000 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krusius T., Gehlsen K.R., Ruoslahti E.;
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lectin-like and growth factor-like sequences.";
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                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID-9606;
                                                                                                                                                         Naso M.F., Zimmermann D.R., Iozzo R.V.;
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                                                                                                                                                                                                                                                                                                                                                   Dours-Zimmermann M.T., Zimmermann D.R.;
"A novel glycosaninoglycan attachment domain identified in two
alternative splice variants of human versican.";
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                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-1335 AND 3090-3396 FROM N.A. (VARIANT V2)
                                                                                                                                                                                                                       SEQUENCE OF 1-347 AND 1336-3396 FROM N.A. (VARIANT V1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 251-347 FROM N.A.
MEDLINE-93122792; PubMed=1478664;
IOZZO R.V., Naso M.F., Cannizzaro L.A., Wasmuth J.J.,
McPherson J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-347 AND 3090-3396 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 262:13120-13125(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissues.";
J. Biol. Chem. 270:3914-3918(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Lung fibroblast;
MEDLINE-88007514; PubMed=2820964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-89174663; PubMed-2466833;
                                                                                                                                              MEDLINE-95105188; PubMed-7528742;
                                                                                                                                                                                                                                                                                                                           TISSUE-Glial tumor;
MEDLINE-95105187; PubMed-7806529;
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 2711-3396 FROM N.A.
                                                                                                                                 SEQUENCE FROM N.A. (VARIANT VO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LISSUE SPECIFICITY OF ISOFORMS.
                                                                                                                                                                                                                                                                         "Multiple domains of the Lambo J. 8:2975-2981(1989).
                                       BINDING PROTEIN) (GHAP).
                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARTIAL SEQUENCE.
                                                                                                                                                                                                                                      FISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Brain;
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SUBCELLUIAR LOCATION: SECRETED; EXTRACELLULAR MATRIX.

ALTERNATURE PRODUCTS: AT LEAST 4 LOSTORNAS; VO (SHOWN HERE), VI, V2 AND V3; ARE PRODUCTED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: CEREBRAL WHITE MATTER. VO AND V1 IS EXPRESSED IN ONRAAL BRAIN, GLIOMAS, MEDULICOLASTONAS, SCHWANNOMAS, NEUROPPIBROMAS, AND MENILOGICALSTONAS, SCHWANNOMAS, NEUROPPIBROMAS, V3 IS FOUND IN ALL THESE TISSUES EXCEPT
                                                                                                                                                                                                             -!- DEVELOPMENTAL STAGE: DISAPPEARS AFTER THE CARTILAGE DEVELOPMENT.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
-!- SIMILARITY: CONTAINS 2 LITH DOMAINS.
-!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-!- SIMILARITY: CONTAINS 1 SUSHI (SCR) REPEAT.
-!- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAG-ALPHA (GLUCOSAMINOGLYCAN ATTACHMENT DOMAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CALCIUM-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi; Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain; Hyaluronic acid; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
VERSICAN CORE PROTEIN.
IG-LIKE V-TYPE DOMAIN.
LINK 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-TYPE LECTIN.
SUSHI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY
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FGF-LIKE 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAG-BETA
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C_TYPE_LECTIN_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, U16306; AAA65018.1; --
EMBL; X15998; CAA34128.1; --
EMBL; U2655; AAA67565.1; --
EMBL; D32039; BAA06801.1; --
EMBL; J02814; AAA36437.1; --
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Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000538; -.
InterPro; IPR0010561; -.
InterPro; IPR001304; -.
InterPro; IPR001438; -.
InterPro; IPR001881; -.
InterPro; IPR001081; -.
Pfam; PP00108; EGF; 2.
Pfam; PF00103; XIInk; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
3396
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3163
3292
3353
130
                                                                                                                                                                                       MEDULLOBLASTOMAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; SO6014; SO6014.
PIR; A29348; A29348.
PIR; A30358; A30358.
HSSP; PO1132; IEPH.
MIM; 118661;
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PROSITE; PS00615;
PROSITE; PS50041;
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Page 59

13.2   KARESKTREYTEK	VILLGNPWPUULLSIKESWVE-AIFRQVVELSGOSSIFIIEGSGEAEEUEUIMFINVIUL
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1058   SQ-GTPGTYLTSHNQASYTQETPKPSVGSISLGLPRQQESAKSATLPYIKQEEFSPR   1	DESCRIPTION OF THE PROPERTY OF	AFPWEETTSSAEGSGEQLVTVSSSVVP-VLPSAVQKFSGTASSIIDEGL GQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKV	1533SPV	1725 ERERIAAASSDLYLRPGSEQPGRDGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVI 17  2413 EPT
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2809 DTTLAVSTFAK--LSSQTPSSPLTIYSGSEASGHTEIPQPSALPGIDV---GSSVMSPQD 2863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2254 FADPASNIGLEDIIRKALMGSFD----DKVEDHGVVMSQPMGVVPGTANTSVVTSGETRR 2309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3080 VEGTAIYLPGPDRCKMNPCLNGGTCYP----TETSYVCTCVP--GYSGDQCELDFDECH 3132
EIELE-GATOWPHSTSASATYGVEAGVVPWLSPQTSERPTLSSSPEINPETQAALIRGOD 3023
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SEQUENCE FROM N.A.

GOTO H., Mishitahi H., Umene K.I., Nakabepu Y., Nishimoto T.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: UPON LYTIC INFECTION OF PERMISSIVE CELLS, THE HSV
TRANSACTIVATOR PROTEIN VP16 ASSOCIATES WITH HCF. BINDING TO HCF
ACTIVATES VP16 FOR ASSOCIATION WITH THE OCTAMER NOTIF-BINDING
PROTEIN OCT-1, TO FORM A MULTIPROTEIN-DNA COMPLEX RESPONSIBLE FOR
ACTIVATING TRANSCRIPTION OF THE HSV IMMEDIATE EARLY GENES (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBGNIT: COMPOSED PREDOMINANTLY OF SIX POLYPEPTIDES RANGING FROM 110 TO 150 KDA AND A MINOR 300 KDA POLYPEPTIDE. THE MAJORITY OF N AND CY-TERMINAL CLEAVAGE PRODUCTS REMAIN TIGHTLY, ALBEIT NONCOYALENTLY, ASSOCIATED (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR.
DOMAIN: THE HCF REPEAT IS A HIGHLY SPECIFIC PROTEOLYTIC CLEAVAGE SIGNAL (BY SIMILARITY).
PY SIMILARITY).
PTH: EXISTS AS A FAMILY OF POLYPEPTIDES THAT ARISE THROUGH
                                                             -----ANQAENDPT-RQYEGPLHHY
                                                                                                2692 SLPIPRKSATVIPEIEGIKAEAKALDDMFESSTLSDGQAIADQSEIIPTLGQFERTQEEY
                                                                                                                                                                                  2752 EDKKHAGPSFQPEF--SSGAE-EALVDHTPYLSIATTHLMDQSVTEVPDVMEGSNPPYYT
                                                                                                                                                                                                                          -----DFARNQVSSQTPQQPPT-----STFQNSPSALVSTPVRTKTSNRYSPES
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN) (HFC1) (VCAF)
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                                                                                                                                        2018 RPQQES-PSPQQQLPPSSQAEGMGQVPRTHRLITLADHIC-QIITQ----
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                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                     KELCH 5.

8 X 26 AA APPROXIMATE REPEATS.

HCF REPEAT 1.

HCF REPEAT 2.

HCF REPEAT 3.

HCF REPEAT 6.

HCF REPEAT 6.

HCF REPEAT 6.

HCF REPEAT 7.

HCF REPEAT 7.
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          AT'A DEFINED SITE, PPCE/THET, WITHIN 'SIMILARITY').
SIMILARITY: CONTAINS 5 KELCH REPEATS.
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Pfam; PF00041; fn3; 2.
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1654 LMYTGLTPEELAVTAAAEAAAQAAATEEAQALAIQAVLQAAQQAVMAGTGEPMDTSEAAA 1713
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-----ELASAVPST-VALLPSTAT 1807
                                                                                 1436 EDVKAGETVRSRHTSVV--SSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMS 1493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---STPPMDRITYIPG----TQITFPPRPYNSASMSPGHPT 1704
                                                                                                                                                                                                                                                                                                                                    -----TLSSQVINPTAITVSAAQTTLTAAGGLTTPTITMQPVSQPTQVTLITAPSGVE 970
SGT---GAPAKIITAVPKIATGHGQQGGVTQVVLKGAPGQPGAILRTVPMSGVRLVTPVTV 862
                                                                                                                                                                  SAVKPAVT-----TLVVKGTTGVTTLGTVTGTVSTSLAGAGAHSTSASLATPITTLGTIA
                                                                                                                                                                                                                                                       1494 RGSPMMNRTSDVTIPPNKSTNHERKSTLT--------PTQRESIPAKSPV-
                                                                                                                                                                                                                                                                                                                                                                                                                              --PG-VDPVVSHSPFDPHHRGSTAGEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               971 AQPVHDLPVSILASPTTEQPTATVTIADSGQGDVQPGTVTLVCSNPPCETHETGTT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1560 YWSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1620 SQQMQVNLRPDVARGLS--PRE-QPLGLPYPATRGIIDLTNM-----PPTILVPHPGGT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAVGQON--GNVVRVCSNPPCETHETGTTNTATTATSNMAGQHGCSNPP--CETHETGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLAAAASAERERERERERERERERIAAASSDLYLRPGSEQPGRPGSHGYVRSPSVRTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETMLQQRPSVFQGTNGTS------VITPLDPTAQLRIMPLPAGGPSISQGLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1494 TTVTQSTPVPGPSVPNISSLTETPGALTSEVPIPATITVTIANTETSDMPFSAVDILQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1554 EELQVSPGPRQQLPPRQLLQSASTPLMGESSEVLSASQTPELQAAVDL------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----NTATTTVVANLGGHP-QPTQVQFVC---DRQEAAASLVT
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2289
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MEDLINE-20105772; PubMed-10637508;
Huntsman D.G., Chin S.-F., Muleris M., Batley S.J., Collins V.P.,
Wiedemann L.M., Aparicio S., Caldas C.;
While, the second human homolog of the Drosophila trithorax gene, maps
to 19913.1 and is amplified in solid tumor cell lines.";
                              1808 ESLAPSNIFVAPQPVVVASPAKMQAAATLIFVDNGIESLGVKPDLPPPPSKAPVKKENOW 1867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

TATERNATURE PRODUCTS: 2 ISOPORMS; A LONG FORM (SHOWN HERE) AND A TRUNCATED FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST LEVELS IN TESTIS.
ALOS POUND IN BRAIN, BONE MARROW, HEART, MUSCLE, KIDNEY, PANCREAS, SPLEEN, THYMUS, PROSTATE, OVARY, INTESTINE, COLON, PERIPHERAL BLOOD LYMPHOCYTES, AND PLACENTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lamerdin J.E., McCready P.M., Adamson A.W., Burkhart-Schultz K., Garcia E., Kyle A., Ramirez M., Stilwagen S., Garnes J., Danganan L., Bruce R., Quan G., Montgomery M., Ow D., Kobayashi A., Olsen A.O., Carrano A.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can
                                                                                                                                                                                                                                            TRX2_HUMAN STANDARD; PRT; 2715 AA.
09UMNG; 09UX25; 095836; 09Y668; 015022;
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 2 (MILED LINEAGE LEUKEMIA GENE HOMOLOG 2 PROTEIN).
                                                                                     2290 -- MGVVPGTANTSVVTSGETRREEGDPSPHSGGVCKPKLISKSNSRKSKSPIPGQGY 2344
                                                                                                               TISSUE-Placenta, and Bone marrow;
MEDLINE=9933983; PubMed=10409430;
FitzGerald K.T., Diaz M.O.;
"MLL2: A new mammalian member of the trx/MLL family of genes.";
Genomics 59:187-192(1999).
-i- FUNCTION: POSSIBLY ACTS AS A TRANSCRIPTIONAL REGULATORY FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (LONG ISOFORM).
Angrand P.O., Valvatne H., Jeanmougin F., Adamson A.,
van der Hoever F., Olsen L., Tekotte H., Huang N., Pooh O.,
Lamerdin J., Chambon P., Losson R., Stewart A., Aasland R.;
"Mammalian trithorax- and ASHL-like proteins: puttative chromatin
regulators which contain PHD fingers and SET domains.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PARTIAL SEQUENCE FROM N.A. (LONG AND TRUNCATED ISOFORMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence analysis of a 1 Mb region in human 19q13.1."; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
2244 SGSVSSRGHSFADPASNLGLEDIIRKALMGSFDDKVEDHGVVMSQP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 816-2715 FROM N.A. (LONG ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 111-2715 FROM N.A. (LONG ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            code for large proteins in vitro.";
DNA Res. 4:141-150(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (LONG ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97349984; PubMed=9205841;
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rissue-Brain;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VPQEPAPVPS -> PLSQSLLLPMTLQLSLSLGQWAAPTTS ACLDSPLWSPLLLRPRCPLTGLQL (IN ISOFORM TRUNCATED).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSARSSRVIKTPRRFMDEDPPKPPKVEVSPVLRPPITTSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                protein; Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 943; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   485 ENYKALVRRNYGKRRGRNQOIARPSQEEKVEEKEEDKAEKTEKKEEEKKDEEEKDEKEDS 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |::: : : | | :| : | | :| | 334 ESWQDVPQRRVGSGQGGSP--CWKKQEQKLDD-------EEEEKKEEEEEKDKEGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           545 KENTKEKDKIDGTAEETEEREQATPRGRKTANSQGRRKGRITRSMTNEAAAAAAAAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    605 EEPPPPL-PPPPEPISTEPVET--SRWTEEEMEVAKKGLVEHGRNWAAIAKMVGTKSEAQ
DISEASE: OFTEN AMPLIFIED IN PANCREATIC CARCINOMAS.
SIMILARITY: BELONGS TO THE TRITHORAX FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 2715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MISSING (IN ISOFORM TRUNCATED).
K -> E (IN REF. 5).
E -> Q (IN REF. 5).
E -> Q (IN REF. 5).
H -> Y (IN REF. 5).
D -> N (IN REF. 5).
D -> N (IN REF. 5).
D -> H (IN REF. 5).
WW; CO615B981BBEB7BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Alternative splicing.
A.T HOOK (BY SIMILARITY).
A.T HOOK (BY SIMILARITY).
A.T HOOK (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BROMODOMAIN (DIVERGENT)
                                         -!- SIMILARITY: CONTAINS 1 BROMODOMAIN.
-!- SIMILARITY: CONTAINS 1 SET DOMAIN.
-!- SIMILARITY: CONTAINS 3 PHD ZINC-FINGER DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASP/GLU-RICH (ACIDIC).
PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative 238; Mismatches 769;
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PHD-TYPE 2.
PHD-TYPE 3.
                                                                                                                                                                                                                                   EMBL; AD000671; -; NOT_ANNOTATED_CDS.
EMBL; AB002302; BAA20763.2; -
EMBL; AF186605; AAD56420.1; -
EMBL; AF104918; AAD17932.1; -
EMBL; AF105279; AAD26113.1; -
EMBL; AF105280; AAD26112.1; -
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                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002857; -.
Pfam; PF00628; PHD; 3.
Pfam; PF00856; SET; 1.
PF02008; zf-CXXC; 1.
PROSITE; PS50280; SET; 1.
DNA-binding; Bromodomain; Nuclear
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365
1252
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1471
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1362
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DNA_BIND
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464	699 504	735	795	855	906	966	1023	1079	1120	1180 883	1240 911	1300	1344	1402	1462	1512 1120	1534	1550
	CKNFYFNYKRRHNLDNLLQQHKQKTSRKPREBRDVSQC	GPPEDSPTVAPKSTTFLKNIRQFIMPOVSARSSRVIKTPRRFMDEDPRPPKPVVE-VSPVL	DSPENATSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQ	MDVDQQEHSAEEGSVCDPPPATKADSVDVEVRVPENHASKVEGDNTKERDLDRASEKVEP 	RDEDLVVAQQINAQRPEPQSDNDSSATCSADEDVDGEPERQRMFPMDSKPS	LLNPTGSILVSSPLKPNPLDLPQLQHRAAVIPPWVSCTPCNIPIGTPVSGYALYQRHIKA :	MHESALLEEQRQRQEQIDLECRSSISPCGTSKSPNREWEVLQPAPHQLITNLPEGVR ::	LPTTRPTRPPPPLIPSSKTTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQETP	KPSVGSISLG	GLLVRAQHEGVVRGTAGAIQEGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGIPTE	ALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIKNAREGTRSPRTAHE  :  :  :  :  :	ISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIMQGT	PRATTESFEDGLKYPKQIKRESPPIRAFEGAITKGKP-YDGITTI    :	KEMGRSIHEIPRQDILTQESRKTPEVVQSTRPIIEGSISQGTPIKFDNNSGQSAIKHN  :	VKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRST	LHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTSDVTIPPNKS   :   :     :     :     ARRCVKQRPSYDIFEDSDDSEPGGPPAPRRRTPRENELPLPEPEE	INHERKSTLTPTQR	HAD&dSH
422	662 465	700	736	796	856 655	907	967	1024 753	1080	1121 831	1181	1241	1301 949	1345 997	1403 1039	1463 1076	1513	1535
• qa	Oy Dp	Oy Dp	Qy Dp	oy D	Oy Dp	Qy Dp	Qy Db	Qy Db	Qy	Oy Dp	cy Op	Qy Dp	Qy	Oy Dp	S G	Oy Dp	Qy Db	δλ

1667 ARASYCIFQDDKKVFCQKHTDLLDGKEIVNPDGFDVLRRVYVDFEGINFKRKFLTGLEPD 1726 1727 AINVLIGSIRIDSLGTLSDLSDCEGRLFPIGYQCSRLYWSTVDARRCWYRCRILEYRPW 1786 PDFPAPPRRSRRPSPLAPRPP-----PSRWASPPLKTSPQLRVPPPTSVTALTPTSG 1956 1181 LENVWLMGGLSVLTSVPGGPPMVCLLCASKGLHELVFCQVCCDPFHPFCLEEAERPLPQH 1240 ---RGSTAGEVYWSHL-------1578 DPAAAAYLFQRQLSPTPG-----YPSQYQLYAMEN----TRQTILNDYITS 1620 HWICSACVRCKSCGATPGKNWDVEWSGDYSLCPRCTQLYEKGNYCPICTRCYEDNDY-ES 1352 HPTHLAAAASAERERE--------REREKERERERERIAAASSOLYLRPGSE 1743 QPG-----RPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITP-LDPT-AQLRIM 1796 1493 MKGLLLKLLESAFGWFDAHDPKYWRRSTRLP-----NGVLPNAVLPPSLDHVYAQWRQQ 1546 P-----LPAGGPSIS-OGLPASRYNTAAD----ALAALVDAAAS--APQMDVSKTKES 1842 1547 EPETPESGQPPGDPSAAFQGKDPAAFSHLEDPRQCALCLKYGDADSKEAGRLLXIGQNEW 1606 --YETPS--DAIE-----VISPASSPAPPQEKLQTYQPEVVKANQAE-NDPTRQYEGPLH 2015 HYRPQQES---PSPQQ-----QLP---PSSQAEG---MGQVPRTHRLITLADHICQIIT 2060 2061 QDF----ARNQVSSQTPQQPPTSTFQNSPSALVSTPVRTKTSNRYSPESQAQSVHHQRPG 2116 SRVSPENLYDKSRGSRPGKSPERSHVSSEPYEPISP--PQVPVVH--EKQDSLLLLSQRG 2172 AEPAEQRNDARSPGSISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGGGDSDMAAAQPG 2232 -----GIIDLINMPPTILVPHPGGTSTPPMDRITYIPGTQITFPPRPYNSASMSPG 1701 1443 HPGPCGLQAVSQRFEDGHYKSVHSFMEDMVGILMRHSEGGETPDR------RAGGQ 1492 ----SAFPSGKP---QPHSSV-----VYSEAGKD-----KGPPPKSRYEEELRTR 1922 -ELAP------PGPAP----SPPPEDLGPDFEDMEVVSGLSAADLDFAASLLG 1999 TEIFNLPAVTTSGSVSSRGHSFADPASNLGLEDIIRKALMGSFDDKVEDHGVVMSQPMGV 2292 SRYIHFPVTV----VSAPGLA---PSATPGAPRIEQ---LDGVDDGTDSEAEAVQQPRGQ 2081 2293 VPGTANTSVVTSG-----ETRREEGDPS------PHSGGVCKPKLISKSNSR 2333 2082 GTPPSGPGVVRAGVLGAAGDRARPPEDLPSEIVDFVLKNLGGPGDGG------AGPR 2132 KSKSPIPGOGYLGTERPSSVSSVHSEGDYHRQTPGWAWED-----RPSSTGSTQFPYNPL 2388 2133 EESLP-PAPPLANGSQPSQ-GLTASPAD---PTRTFAWLPGAPGVRVLSLGPAPEPPKPA 2187 QQMQ-----YNLRPDVARGLSPREQPL--GLP------YPATR-----KH-----EAARLEEN---LRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTS-----GKTTITAANFIDVIITRQIASDKDAR--ERGSQSSDSS-SSLSSHR----1579 1294 1353 1702 1744 1797 1843 1966 1787 2016 1846 1904 2117 1957 2173 2000 2233 1621 1651 1885 1923 2032 1551 g qq Qy Db qq QY Db qq a à g οy g ŏ ò ΩD δy Qγ QΩ ΟŸ δý QQ οy Ω οy g ŏ g δy δŽ QΥ g QΥ g ò

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashi K., Yamada S., Kanda K., Kimizuka F., Kato I., Sobue K.; "15 KDa fragment of h-caldesmon conserves two consensus sequences of the tropomyosin-binding domain in troponin T."; Biochem. Biophys. Res. Commun. 161:38-45(1989).
          ---SSTPPTPIACAPSAVNQAAPHQQNRIWEREPAPLL 2428
                               2188 TSKIILVNKLGQVFVKMAGEGEPVPPPVKQPPLPPTISPTAPTS----WTLPPGPLL 2240
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Yano H., Hayashi K., Haruna M., Sobue K.;
"Identification of two distinct promoters in the chicken caldesmon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (GIZZARD H-CAD; BRAIN L-CAD AND GIZZARD L-CAD).
MEDLINE-94071934; Pubmed-8250919;
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (GIZZARD H-CAD ISOFORM) TISSUE-Gizzard, and Oviduct; MEDLINE-89340480; PubMed-2760048;
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (GIZZARD H-CAD ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (BRAIN L-CAD ISOFORM)
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complementary DNA.";
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"Structural and functional relationships between h- and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 451-756 FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. Biophys. Res. Commun. 164:503-511(1989).
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                                                                                     P12957, Q90756; Q90761; Q92018; Q99230; Q03698; Q1-JAN-1990 (Rel. 13, Created) O1-OCT-2000 (Rel. 35, Last sequence update) O1-OCT-2000 (Rel. 40, Last annotation update) CALDESMN (CDM).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (GIZZARD L-CAD ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92042686; PubMed=1939602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-89273666; PubMed-2730665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              saldesmons.";
Biol. Chem. 266:355-361(1991).
                                                                                                                                                                  CALD1 OR CAD. Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              caldesmon genes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bryan J., Lee R.;
                                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                  rissue-Gizzard;
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        2389 TMRML----
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CHICK
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The phosphorylation sites.";

1. Biol. Chem. 266:19971-19975(1991).

2. FUNCTION: ACTIN. AND MYOSIN-BINDING PROTEIN IMPLICATED IN THE FEGULATION OF ACTOMYOSIN INTERACTIONS IN SWOOTH MUSCLE AND NONMUSCLE CELLS (COULD ACT AS A BRIDGE BETWEEN MYOSIN AND ACTIN FILAMENTS). STIMULATES ACTIN BINDING OF TROPOMYOSIN WHICH INCREASES THE STABILIZATION OF ACTIN FILAMENT STRUCTURE. IN MUSCLE TISSUES, INHIBITS AT REPOWNOSIN ATTRACED BY TROPOMYOSIN, TWO WOLECULES OF TROPOMYOSIN, INTERACTS WITH ACTIN, MYOSIN, TWO MOLECULES OF TROPOMYOSIN, INTERACTS WITH ACTIN, MYOSIN, TWO MOLECULES OF TROPOMYOSIN, INTERACTS WITH ACTIN, MYOSIN, TWO MOLECULES OF TROPOMYOSIN, INTERACTS AND RECEPTOR CAPPING.

2. SUBCELLULAR LOCATION: ON THIN FILAMENTS IN SMOOTH MUSCLE AND ON STREES FIBERS IN FIBROBLASTS (NONMUSCLE) (BY SIMILARITY).

2. STRESS FIBERS IN FIBROBLASTS (NONMUSCLE) (BY SIMILARITY).

3. STRESS FIBERS IN FIBROBLASTS (NONMUSCLE) (BY SIMILARITY).

5. STRESS FIBERS IN FIBROBLASTS (NONMUSCLE) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIRECT. THE N-TERMINAL PART SEEMS TO BE A MYOSIN/CALMODULIN-BINDING DOWAIN, AND THE C-TERMINAL A TROPOMYOSIN/ACTIN/CALMODULIN-BINDING DOMAIN. THESE TWO DOMAINS ARE SEPARATED BY A CENTRAL HELICAL REGION IN THE MUSCLE FORMS.

PTH: IN NON-WUSCLE CELLS, PHOSPHORYLATION BY CDC2 DURING MITOSIS CAUSES CALDESMON TO DISSOCIATE FROM MICROFILAMENTS.

PHOSPHORYLATION REDUCES CALDESMON BINDING TO ACTIN, MYOSIN, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: HIGH-MOLECULAR-WEIGHT CALDESMON (H-CALDESMON)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CALMODULIN AS WELL AS ITS INHIBITION OF ACTOMYOSIN ATPASE
ACTIVITY. PHOSPHORYLATION ALSO OCCURS IN BOTH QUIESCENT AND
DIVIDING SMOOTH MUSCLE CELLS WITH SIMILAR EFFECTS ON THE
INTERACTION WITH ACTIN ACCINDULIN AND ON MICROFILAMENTS
REDGANIZATION (BY SIMILARITY).
SIMILARITY: TO A TROPOMYOSIN BINDING SITE DOMAIN OF TROPONIN I.
                                                           MEDLINE-88293484; PubMed-3401222;
Mornet D., Audemard E., Derancourt J.;
Identification of a 15 kilodalton actin binding region on gizzard
caldesmon probed by chemical cross-linking.";
Biochem. Biophys. Res. Commun. 154:564-571(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IS PREDOMINANTLY EXPRESSED IN SMOOTH MUSCLES, WHEREAS LOW-MOLECULAR-WEIGHT CALDESMON (L-CALDESMON) IS WIDELY DISTRIBUTED NON-MUSCLE TISSUES AND CELLS, NOT EXPRESSED IN SKELETAL MUSCLE
                                                                                                                                                                                                                                                                                                                                          Mak A.S., Carpenter M., Smillie L.B., Wang J.H.; "Phosphorylation of caldesmon by p34cdc2 kinase. Identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                       PHOSPHORYLATION SITES, MEDLINE-92041815; PubMed=1939059;
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[8]
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BEQUENCE FROM N.A.
BESPOLINAGE P., Gimeno R.E., Holzmacher E., Teung P., Kaiser C.A.;
Reast SEC16 gene encodes a multidomain vesicle coat protein that
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SECIG OR YPL085W.
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                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 VAGELHNNNEHTQKIAVS---------AVEEDSFNEEEGENHDSIIISSLND 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDLFTQSSGDLGEVLPWESTDKNADVTSKSQEKHEDLFAASGNDEKLPWEV-SDGEVSSG 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WIDHEKEIFKDKFIQHPKNF-----K-GLIASYLERKSVPDCVLYYYLT-----K 482
                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                               STINSSFNDDSVNRTESDIASKSD--VPPV-SSSTNISPANETQLEIPDTQELHHK--LL 93
                                                                                                                                                                                                                  Golgi stack; Endoplasmic reticulum.
L->S: IN SEC16-4; TS ACCUMULATION OF
MEMBRANES.
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                                                                                                                                                                                                                                                   L->P: IN SEC16-3; TS ACCUMULATION OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 V-----SDSHFQRVSAAVLPLVHPLPEGLRASADAKKDPAF----GGKHEA-----
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                                                                                                                                                                                                                                                                                              W->R: IN SEC16-1; TS ACCUMULATION
                                                                                                                                                                                                                                                                                                                                               Query Match 2.4%; Score 298; DB 1; Length 2194;
Best Local Similarity 18.7%; Pred. No. 0.00043;
Matches 474; Conservative 324; Mismatches 897; Indels 842;
                                                                                                                                                                                                                                                                                                                 BB1E02D2AD4683E3 CRC64;
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L->P: IN SEC16-2;
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LAFLQTGNHDEALRLALSKRDYAIALLVGS---LMGKDRWSEVIQKYLYEGFTAGPNDQK 1192 PID-----QIIKPNDMLKSFP-----GPLGSAKLKKDLTKWMETTIKSISENESS 1075 ---TYLTSHNQASYTQETPKPSVGSISLGLPRQQESAKSAT 1101 LPYIKQE---EFSPRSQNSQPEGLLVRAQHEGVVRGTAGAIQEGSITRGTPTSKISVESI 1158 PSLRGSITQGTPALPQTGIPTEALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGH 1218 ILSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGM-----SMRESPV 1265 IFSYDP-KFKGFSSILPQKIYHASLLQ------EQGLNSLGTKYTDYLSSSVRKLPK 1369 SAPLEGLICRALPRGSPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYPRQIKRESPPI 1325 RAFEGAITKGKPYDGITTIKEMGRSIHEIPRQDILTQESRKTPEVVQSTRPIIEGSISQG 1385 NDSSATCSADEDVDGEPERQRMFP------MDSKPSLLNPTGSILVSS---PLKPN 923 607 ASNEEENPEDSEVEAVKPSEDSPEN--ATSRGNTEPAVELEP----TTETAPSTSPSLA 768 921 TDMI IWQLLEMKLNDKVNWKNI SKLLYNSDELLMYLSQPFPNGDMI PNAYRLDINCQMRV --NQQIARPSOEEKVEE 670 IPQSRKGSNNSNRPPVIPLGTQEPRSSR--TNSAISQSPVNYAFPNPYKIQQLQQAPIQS EAQCKNFYFNYKRRHNLDN---LLQQHKQKTSRKPREERDVSQCESVASTVSAQEDEDIE TKADSVDVEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSD PPPLP----PPP----EPISTEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAKMVGTKS VPSTKP-----AEDESVETQVNDSISAETAEQMDVDQQEHSAEEGSVCDPP-----PA PLDLPQLQHRAAVIPP--MVSCTPCNIPIGTPVSGYALYQRHIKAMHESAL--LEEQRQR QEQ-----IDLECRSSTSPCGTSKSPNREWEVL---QPAPH-QLITNL------ELAHFLLLIFQVFVGNSKMAIKSFYTNNETSQWASENWKSIVAAVLINIPENNED--PLL KEEDKAEKTEKKEEEKKDE------EEKDEKEDSKENTKEKDKIDGTAEETEEREQA IPPVVLEFLIEF-----GIFL-----TKKGLTAAASTLFIIGNVPLS---------PEGVRLPTTRPTRPPPPLIPSSKTTVASEKPSFIMGGSISQG-TPG-TPRGRKTANSQ-----GRRKGRITRSMTNEAAAAAAAA-------NEPVMADSDVIFE----SIGNMNTFES----GMPLPNTNIPPPALKVETTVSAPPIR---KNENYKALVRRNYGKRRGR-

Eukaryota; Metazoa;

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1717 EREREKERERERI-----AAASSDLYLRPGSEQPGRPGSHGYVRSPSPSV--RTQE 1765
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   ---STVDLTQTFTPF----QAQV 1461
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                             TPIKFDNNSGQSAIKHNVKS---LITGPSKLSRGMPPLEIVPENIKVVERGKYEDVKAGE
                                                     1462 TSQSYVDTTALLHNAHNYPSHSVLHSKPSNVSKG----LVEANLPYTHR--IGDSLQGS
                                                                                                                                                                                                                                                     1515 PORIHNTOFAAAEPOMASLRRVRTDOHTNEKALKSQOILEKKSTAYTPQFGON---HSVP
                                                                                                                                                                                                                                                                                                                         HISHDNSNAD---QNTLKDSADVTDETMDIEGPGFNDVKNLLPMEPNHQPTSTVNPIQTI
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                                                                                                1443 TVRSRHTSVVSSGPSV----LRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSP
                                                                                                                                                                  ----TIPPN--KSTNHERKSTLTPTQRESIPAKSPVPGVDPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKNVN--MKKETKPSNKDIDDKSNGWFGWLKKDTG--DKKVYKAKL--GHKNTL----YY
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(Rel. 17, Last sequence update)
(Rel. 35, Last annotation update)
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1422 DALNKKNDKKKVFDGFTP----GSSANS--
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                                                                                                                                                                 MMNRTSDV----
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MAP2_MOUSE
ID MAP2_MC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1122 LLVRAQHEGVVRGTAGAIQEGSITRGTPTSKISVESIPSLRGS------ITQGTPAL 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              952 TPVSGYALYQRHIKAMHESALLEEQRQRQEQIDLECRSSTSPCGTSKSPNREWEVLQPAP 1011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 HRSQGTYSDTKENGING-----ELTSADRETAEEVSARIVQ------VVTAEAVAVLKG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -------WGLAAPISPGPLT--PMREKDVLEDIPRWEGKQFDSPMPSPFHGGSFTL 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                832 HASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDVDG 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                       -!- FUNCTION: THE EXACT FUNCTION OF MAP2 IS UNKNOWN BUT MAPS MAY STABILIZE THE MICROFUBLIES AGAINST DEPOLYMERIZATION. THEY ALSO SEEM TO HAVE A SITEENING EFFECT ON MICROTUBULES.
-!- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.
                                                                                                                                                             [2]
SECUENCE: FROM N.A.
SECUENCE -89043973; PubMed=3142041;
Lewis S.A., Wang D., Cowan N.J.;
Lewis S.A., wang D., Cowan N.J.;
"Microtubule-associated protein MAP2 shares a microtubule binding
"Microtubule-associated Map Protein MAP2 Shares a microtubule binding
Chordata; Craniata; Vertebrata; Euteleostomi;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        892 EPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIG
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TAU/MAP MOTIF.
TAU/MAP MOTIF.
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1828 AA; 198980 MW; 200BC59E360538CA CRC64,
                                                                                                        Wang D., Lewis S.A., Cowan N.J.;
"Complete sequence of a cDNA encoding mouse MAP2.";
Nucleic Acids Res. 16:11369-11370(1988).
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Similarity 19.2%; Pred. No. 0.00039;
1; Conservative 226; Mismatches 669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGL: DEROLIGE : .
InterPro; IPRO1084; -
Ffam; PF00418; tubulin-binding; 3.
PROSTIE; PS00229; TAU_MAP_1; 2.
PROSTIE; Repeat; Calmodulin-binding.
                                                                      SEQUENCE FROM N.A.
MEDLINE-89083571; Pubmed-3205744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M21041; AAA39490.1; -
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PIR; A40115; A40115.
MGD; MGI:97175; Mtap2.
                   Eutheria;
                                    NCBI_TaxID=10090;
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1662
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Matches 371;
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1504 -LSCVKRKTTAASGDLAQAPGAFKQAKDYD-GISKSPEKRSSLPRPSSILPPRRG--- 1558
                                                                                                                                                                                                                                                                                                                                                     1245 IEAGGEYD------KLLFRSDTL-----QISDLLVSESREEFVETCPGELK 1284
                               ---TPVRTKT-----SNRYSPESQAQSVHHQRPGS-----RVSPEN 2123
                                                   1285 GVVESVVIIEDDFITVVQTTTDEGESGSHSVRFAAPAQPEEERRPRPHDEELEIEMAAEA 1344
                                                                                                          1405 LTEQLETIPKEERAEKDARRPSLEKHRKEKPFKTGRGRISTPERKVAKKEPSTVSRDEVR 1464
                                                                                                                                                                                                                                         1465 RKKAVYKKAELAKK-----SEVQAHSPSRKLILKPAI------KYTRPTH-- 1503
                                                                                                                                                                                                                                                                                                                                                                                              2358 SEGDYHRQTPGWAWEDRPSSTGSTQFPYNPLTMR------MLSSTPPTFIACAPS 2406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLIKE-87246694; PubMed-3036526;
Levy E., Liem R.K.H., D'Eustachio P., Cowan N.J.;
"Structure and evolutionary origin of the gene encoding mouse NF-M,
the middle-molecular-mass neurofilament protein.";
                                                                                       2124 LVDKSRGSRPG-KSPERSHVSSEPYEP-----ISPPQVPVVHEKQDSLL
                                                                                                                                                    LLSQRGAEPAEQR - NDARSP - - - - - - - GSIS - - - - - YLPSFFTKLENT
                                                                                                                                                                                                             2202 SPMVKSKKQEIFRKLNSSGGGDSDMAAAQPGTEIFNLPAVTTSGSVSSRGHSFADPASNL
                                                                                                                                                                                                                                                                        2262 GLEDIIRKALMGSFD------DKVEDHGVVMS-----QPMGVVPGTANTSV
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SEQUENCE OF 312858158637; PubMed-3103856;
Julien J.-P., Meyer D., Flavell D., Hurst J., Grosveld F.;
"Cloning and developmental expression of the murine neurofilament
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NFM_MOUSE STANDARD; PRT; 848 AA.
P08553; Q61961;
01-A07-1988 (Rel. 08, Created)
01-N07-1990 (Rel. 16, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
NEUROFILAMENT TRIPLET M PROTEIN (160 KDA NEUROFILAMENT PROTEIN)
(NEUROFILAMENT MEDIUM POLYPEPTIDE) (NF-M).
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Wilson A.C., Lamarco K., Peterson M.G., Herr W.;
"The VP16 accessory protein HCF is a family of polypeptides processed
from a large precursor protein.";
Cell 74:115-126(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                           819 ADSVDVEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDL-VVAQQINAQRPEPQSDN 877
                    RKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEK--VEEKEED-KAEK
                                                 ETKVED -----EKSEMEETLT -----AIAEELAASAKEEKEEAEEKEEEPEAEK
                                                                                 525 TEKKEEEEKKDEEEKDEKEDSKENTKEKDKIDGTAEETEEREQATPRGRKTANSQGRRKGR
                                                                                                   SPVKSPEAKEEEEEGEKEEEEEGQEEEEEED | : :| | : :| SPVKSPEAKEEEEEGEEKEGSSEKDEGE
                                                                                                                                               585 ITRSMTNEAAAAAAAAATEEPPPPLPPPEPISTEPVETSRWTEEEMEVAKK--GLVE
                                                                                                                                                                                                                643 HGRNWAAIAKMYGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRKPREERDVSQC---
                                                                                                                                                                                                                                           ----IKVEKPEKAKSPMPKSPVEEVKPK
                                                                                                                                                                                                                                                                              700 -ESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSEDSPENATSRGNTEPAVELEPTTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The HCF repeat is an unusual proteolytic cleavage signal.";
Genes Dev. 9:2445-2458(1995).
-I-FUNCTION: UPPO LYTIC INPECTION OF PERMISSIVE CELLS, THE HSV
TRANSACTIVATOR PROTEIN VP16 ASSOCIATES WITH HCF. BINDING TO HC
ACTIVATES VP16 FOR ASSOCIATION WITH THE OCTAMER MOTIF-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN) (HFC1) (VCAF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95130107; PubMed-7829097; Frattini A., Faranda S., Redolfi E., Zucchi I., Villa A., Patrosso M.C., Strina D., Susani L., Vezzoni P.; "Genomic organization of the human VP16 accessory protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 housekeeping gene (HCFC1) mapping to Xq28.";
Genomics 23:30-35(1994).
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MEDLINE-93327419; PubMed-8392914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96033796; PubMed=7590226; Wilson A.C., Peterson M.G., Herr W.;
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                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Baloinformatics and the EMBL Outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                            Intermediate filament; Heptad repeat pattern; Coiled coil; Neurone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202 LKKKQQQLEEEAAKPPEPEKPVSPPPVEQKHRSIVQIIYDENRKKA------EEAH
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SIMILARITY)
                SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY
COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION
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456 PTTTTIQVLPTVP-----GSSISVPTA-----ARTQGVPAVLKVTGPQAT TKADSVDVEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQ-----INAQRP

542 OMSGMAALAAAAAATOKI------PPSSRPTVLSVPAGTTIVKTMAVTPGTTTLPA 591

930 LQHRAAVIPPMVSCTPCN-----IPIGTPVSGYA-LYQRHIKAMHESALLEEQRQRQE 

TGTPLVTMR---PASQAGKAPVTVTS------LPAGVRMVVPTQSAQGTVIGSSP EPOSDNDSSATCSADEDVDGEPERORMFPMDSKPSLLN-PTGSILVSS-PLKPNPLDLPQ

496

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                                                                                 NONCOVALENTLY, ASSOCIATED.
SUBCELLUIALER LOCATION: NUCLEAR.
ALTERNATIVE PRODUCTS: A SHORT FORM MAY ARISE BY ALTERNATIVE
SPLICING. IN THIS VARIANT THE N- AND THE C-TERMINAL FRAGMENTS FAIL.
               ACTIVATING TRANSCRIPTION OF THE HSV IMMEDIATE EARLY GENES. SUBDIAT: COMPOSED PREDOMINATLY OF SIX POLYEPPTIDES RANGING FROM 110 TO 150 KDA AND A MINOR 300 KDA POLYEPPTIDE. THE MAJORITY OF NAND C-TERMINAL CLEAVAGE PRODUCTS REMAIN TIGHTLY, ALBEIT
                                                                                                                                                                                                               SIGNAL.

PTM: EXISTS AS A FAMILY OF POLYPEPTIDES THAT ARISE THROUGH
CLEAVAGE AT ONE OR MORE CENTRALLY LOCATED SITES. CLEAVAGE OCCURS
AT A DEFINED SITE, PPCE/THET, WITHIN THE HCF REPEAT.

PTM: GLYCOSYLATED; CONTAINS O-LINKED N-ACETYLGLUCOSAMINE RESIDUES.
SIMILARITY: CONTAINS 5 KELCH REPEATS.
 PROTEIN OCT-1, TO FORM A MULTIPROTEIN-DNA COMPLEX RESPONSIBLE FOR
                                                                                                                                                 TO ASSOCIATE.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FETAL TISSUES AND THE ADULT KIDNEY. PRESENT IN ALL TISSUES TESTED.
DOMAIN: THE HCF REPEAT IS A HIGHLY SPECIFIC PROTEOLYTIC CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nuclear protein; Repeat; Alternative splicing; Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 X 26 AA APPROXIMATE REPEATS
HCF REPEAT 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HCF REPEAT 3.
HCF REPEAT 4 (DEGENERATE).
HCF REPEAT 5.
HCF REPEAT 6.
HCF REPEAT 7 (DEGENERATE).
HCF REPEAT 7 (DEGENERATE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISSING (IN SHORT ISOFORM).
R -> A (IN REF. 1).
S -> SVS (IN CAA55790).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -> S (IN REF. 1).
-> G (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L20010; -; NOT_ANNOTATED_CDS.
EMBL; X79198; CAA55790.1; ALT_INIT.
MIM; 300019; -.
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Pfam; PF00041; fn3; 1.
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-----TRPPPPLIPSSK-TTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQETPK 1080

1030

982 QIDLECRSSTSPCGTSKSPNREWEVLQPAPHQLITNLPEGVRLPTTRP------

1081 PSVGSISLGLPRQ----QESAKSAT-LPYIKQEEFSP------RSQNSQPEGLL---

1169 TPALPQTGIPTEALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIKNA 1228

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877 T----TGVTTLGTVTGTVS-----TSLAGAGGHSTSASLATPITTLGTIATL

--VRAQH-----EGVVRGTAGAIQEGSITRGTP-----TSKISVESI-PSLRGSITQG 819 PKIATGHGQQGVTQVVLKGAPG--QPGTILRTVPMGGVRLVTPVTVSAVKPAVTTLVVKG

PGTTTIIKTIPMSAIITQAGATGVTSSPGIK ----SPITIITTKVMTSGTGAPAKIITAV

763

1124

1229 REGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRG---SPHSD 1285

920 SSQVINP-TAITVSAAQTTLTAAGGLTT-PTITMQPVSQPTQVTLITA-PSGVEAQPVHD

-----VPENIKV

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| :| |:| | | |
PCETHETGTTHTATTATSNGGTGQPEGGQQPPAGRPCETHQTTSTGTTMSVSVGALLPDA 1380
  1286 LKERTVLSGSIMQGTPRATTESFEDGLKYPKQIKR--ESPPIRAFEGAITKGKPYDGITT 1343
                                                   LPVSILASPITEQPTATVTIADSGQGDVQPGTVTLVCSNPPCETHETGTTNTAT ---TTV 1033
                                                                                                          1344 IKEMGRSIHEIPRQ-DILTQESRKTPEVVQSTRPIIEGSISQ--GTPIKFDNNSGQSAIK 1400
                                                                                                                                          : :| | | : : | : :| 1034 NALIGG--HPQPTQVQFYCDRQEAAASLVTSTVGQQNGSVVRVCSNPPCETHETGTTNTA 1091
                                                                                                                                                                                                                                                                  1092 TTATSNWAGQHGCSN--PPCETHETGTTNTATTAMSSVGANHQRDARRACAAGTPAVIRI 1149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RITRSMTNEAAAAAAAAAATEEPPPPLPPPPEPISTEPVETSRWTEEEMEVAKKGLVEH
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19.6%; Pred. No. 0.00049;
tive 226; Mismatches 780;
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Local Simhes 394;

Best Loca Matches 540 287 584 347

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MIM; 194540;
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    01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-OT-2000 (Rel. 40, Last annotation update)
ZINC FINGER PROTEIN 40 (HUMAN IMMUNOBELICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 1) (HIV-EP1) (MAJOR HISTOCOMPATIBILITY COMPLEX BINDING PROTEIN 1) (MBP-1) (POSITIVE REGULATORY DOMAIN II BINDING FACTOR 1)
1381 TSSHRTVESGLEVAAAPSVTPQAGTALLAPFPTQRVCSNPPCETHETGTTHTATTVTSNM 1440
                                                                                                                                                       1778 INGTSVITPLDPTAQLRIMPLPAGGPSISQGLPASRYNTAADALAALVDAAASA----P 1832
                                                                                                                                                                                                                                                                                                                                                                                                1833 QMDVSKT-----KESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSA 1886
                                                                                                                                                                                                                                                                                                                                                                                                                         1887 FPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVIITRQIASDKD 1946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1947 ARERGSQSSDSSSSLSSHRYETPSDAIEVISPASSPAPPQ-----EKLQTYQPEVVKA 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1924 SVYLAIQSSQAGGE-----LKSSTPAQLAFMRVYCGPSPSCLVQSSSLSNAHIDYTTKPA 1978
                                              --- LPYPATRGIIDLTNMPPTIL 1663
                                                                                                                              1664 VPHPGGTSTPPMDRITYIPGTQITFPPRPYNSASMSPGHPTHLAAAASAEREREREKE 1723
                                                                                                                                                                                                                                                             SQTPELPAAVDLSSTGEPSSGQESAGSAVVATVVVQPPPPTQSEVDQLSLPQELMAEAQA 1597
                                                                                                                                                                                                                                                                                                                                                    GTTTLMVTGLTPEE----LAVTAAAEAAAQA--AATEEAQALAIQAVLQAAQQAVMGTGE 1651
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MEDLINE-90169514; PubMed-2106471;
MEDLINE-90169514; PubMed-2106471;
Fan C.M., Maniatis T.;
"A DNA-binding protein containing two widely separated zinc finger motifs that recognize the same DNA sequence.";
                                                                                                                                                                                                                     RERERIAAA---SSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQETML---QQRPSVFQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2161 KQDSLLLLSQRGAEPAEQRNDARSPGSISYL-----PSFF---TKLENTSPMVKSKKQ
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                  1441 SSNQD-----PPPAASDQGEVESTQGDSVNITSSSAITTTVSSTLTRAVTTVTQSTP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1786 NGIESLGVKPDLPP----PPSKAPMKKENQWFDVGVIKGTNVMVTHYFLPPDD-----
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                                         1618 ITSQQMQVNLRPDVARGLSPREQPLG-
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P15822;
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ZEP1_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                           "High-resolution solution structure of the double Cys2His2 zinc finger from the human enhancer binding protein MBP-1.";
Biochemistry 31:3907-3917(1992).
-!- FUNCTION: THIS PROTEIN SPECIFICALLY BINDS TO THE DNA SEQUENCE 5.-GGGACTTTCC-3' WHICH IS FOUND IN THE ENHANCER ELEMENTS OF NUMEROUS VIRAL PROMOTERS SUCH AS THOSE OF SV40, CMV, OR HIV1. IN ADDITION, RELAFED SEQUENCES ARE FOUND IN THE ENHANCER ELEMENTS OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS I MC. INTERLEURIN-2 RECEPTOR, AND INTERFERON-BETA GENES. IT MAY ACT IN T-CELL ACTIVATION.
                                                                                                                                                                                              structure of a single zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- INDUCTION: BY MITOGEN AND PHORBOL ESTER.
-!- DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0048; ZINCFINGER.
PROSITE; PSO1028; ZINC_FINGER_C2H2_1; 4.
PROSITE; PSO1057; ZINC_FINGER_C2H2_2; 4.
Transcription regulation; Zinc-finger; Metal-binding; DNA-binding;
Nuclear protein; Repeat; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92232684; PubMed-1567844;
Omichinski J.G., Clore G.M., Robien M., Sakaguchi K., Appella E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D45D3CA951FEA561 CRC64;
                                                                                           MEDLINE-91064333; PubMed-2248949;
Omichinski J.G., Clore G.M., Appella E., Sakaguchi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-SER.
C2HC-TYPE (POTENTIAL).
ZINC FINGERS.
C2H2-TYPE.
                                                                                                                                                                                          "High-resolution three-dimensional structure of a strom a human enhancer binding protein in solution." Biochemistry 29:9324-9334(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZINC FINGERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C2H2-TYPE.
                                                      STRUCTURE BY NMR OF 2113-2142.
MEDLINE-91064333; PubMed=2248949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZINC-FINGER IN-BETWEEN.
SIMILARITY: STRONG, TO HIVEP2.
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                                                                                                                                                                                                                                                                                                                               STRUCTURE BY NMR OF 2087-2142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X51435; CAA35798.1; -.
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Dev. 4:29-42(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDB; 1BBO; 31-OCT-93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3ZNF; 15-JAN-92.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T00497; -.
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2087
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Length 2717;

DB 1;

2.3%; Score 295;

Q	Db 895 LVRQAAIEDSSANESHVLGTGQSLDESHQGCHAAGEAMSVRSKALAQGPHIEKKK	SHQGR 954
δy	1519 STLTPTQRESIPAKSPVI	'SHS 1545
Dp	Db 955 GTMFECETCRNRYRKLENFENHKKFYCSELHGPKTKVAMREPEHSPVPGGLQPQILH-	LH- 1011
οy	1546 PFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAAYL	-FQRQLS 1592
QQ	Db 1012YRVAGSSGIWEQTP-QIRKRRKKKKSVGDDEELQQNESGTSPKSSEGLQFQNALG	ALG 1064
ΟŽ	1593 PIPGYPSQYQLYAMENTRQFILNDYITSQQMQVNLRPD	163
Q	1065 CNPSLPKHSVTIRSDQQHKNIQLQNSHIHL	111
Oy	1640 OPLGLPYPATRGIIDLTNMPPTI	PPR 1691
Óβ	Db. 1113 QQISSAAQDKIELQRHGTGISVIQHTNSLSRPNSFDKPEPFERASPVSFQELN-	R 1166
δλ	1692 PYNSASMSPGHP	LYL 1738
Op	Db 1167 TGNSGSLKVIGISQEESHPSRDGSHPHQLALSDALRGELQESSRKSPSERHVLGQPSRLI	RLI 1226
Qy	1739 RPG	TTP 1786
qq	1227 RQHNIQVPEILVTEEPDRDLEAQCHDQEKSEKFSWPQRSETLSKLP	:   TEKLPP 1278
Qy	1787 LD	1842
qq	Db 1279KKKRLRLAEIEHSSTESSFDSTLSRSLSRESSLSHTSSFSASLDIEDVSKTEASPKID	KID 1336
Qy	1843	PSG 1890
QQ	Db 1337 FINKAEFIMIPAGINTLNVPGCHREMRRTASEQINCTQTSMEVSDLRSKSFDC	DCG 1390
οy	1891 KPQPHSSVVYSEAGKDKGPPPKSRYEEELRTR	RER 1950
qq	1391 SITPPQTTPLTELQPPSSPSRVGVTGHVPLL	- ERRR 1425
δλ	1951 GSQSSDSSSSLSSHRYET	NDP 2006
QD	1426 GPLVRQISLGI	SAN 1479
Qy	2007	LIT 2050
QQ	Db 1480 TLHSQTQVKDLQAETSNSSSTNVFPVQQLCDINLLNQIHAPPSHQSTQLSL	1530
οy	2051 LADHICQIITQDFARN	2106
QQ	Db 1531QVSTQGSKPDKNSVLSGSSKSEDCFAPKYQLHCQ	нсо 1564
οy	2107	IVSS 2144
ф	Db 1565 VFTSGPSCSSNPVHSLPNQVISDPVGTDHCVTSATLPTKLIDSMSNSHPLLPPELRPLGS	LGS 1624
Qy	2145 EPYEPISPPQVPUVHEKQDSLLLLSQRGAEP-	AEQRND 2181
qq	1625 QVQKVPSSFMLPIRLQSSVPAYCFATLTSLPQILVTQDLPNQPICQTNHSVVPI	QNS 1684
οy	QY 2182 ARSPGSISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGGGDSDMAAAQPGTEIFNLPAV	PAV 2241
ΩD	Db 1685VPTLQKGHQNALPNPEKEFLCENVFSEMSQNSSLSESLPITQKISVGRL	GRL 1733
δλ	2242 T	TSV 2301
qq	Db 1734 SPQQESSASSKRMLSPANSLDIAMEKH	1760
οy	OY 2302 VTSGETRREEGDPSPHSGGVCKPKLISKSN-SRKSKSPIPGGGYLGTERPS	SV- 2353
qq	1761QKRAKDENGAVCATDVI	GVM 1811
οy	2354SSVHSEGDYHRQTPGWAWEDRPSSTGSTQF	PYNPL 2388
qq	Dh 1812 LEKDVEGOBETGNEAVNI-MULDADNGCGETGVTEDTGELOFFENTKGGTG	TSL 1866

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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROC. Natl. Acad. Sci. U.S.A. 85:1998-2002(1988).

-!- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M, AND WHITCH ARE INVOLVED IN THE MAINTENANCE OF BURGNAL CALIBER.

-!- FUM. THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NEW IS PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS THOUGHT THAT PHOSPHORYLATION OF RESULTS IN THE FORMATION OF INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE OF AXONAL CALIBER.

-!- PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.
                                                  2389 TMRMLSSTPP----TPIACAPSAVNQAAPHQONR----IWEREPAPLLSAQYETLSD 2437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identification of the major multiphosphorylation site in mammalian neurofilaments.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myers M.W., Lazzarini R.A., Lee V.M.-Y., Schlaepfer W.W., Nelson "The human mid-size neurofilament subunit: a repeated protein sequence and the relationship of its gene to the intermediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-88158120; PubMed-2450354;
Lee V.M.-Y., Otvos L. Jr., Carden M.J., Hollosi M., Dietzschold
Lazzarini R.A.;
                                                                                                                                                                                                                                                                                                                                                      01-AUG-1988 (Rel. 08, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
NEUROFILAMENT TRIPLET M PROTEIN (160 KDA NEUROFILAMENT PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                  (NEUROFILAMENT MEDIUM POLYPEPTIDE) (NF-M) (NEUROFILAMENT 3)
                                                                                                                                                                                                                                                                                       915 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF ONE OF THE 13 RESIDUE REPEATS.
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                                                                                                                                                                                                                                                                                                                                     Created)
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INIT_MET 0 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 filament gene family.";
EMBO J. 6:1617-1626(1987).
                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001664; -.
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A30157; A30157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens (Human)
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Homo sapiens (Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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P07197;
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LINKED (GLCNAC) (BY SIMILARITY).
5F5D3DF34C9D9E50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   363; Indels 252;
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21.8%; Pred. No. 0.00022;
ive 133; Mismatches 363; Indels 2
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COIL 2B.
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A MEDLINE-88274407; PubMed-2455776;

KOSİK K.S., Orecchio L.D., Bakallıs S., Duffy L., Neve R.L.;

KOSİK K.S., Orecchio L.D., Bakallıs S., Duffy L., Neve R.L.;

Talzheimer neurofibrillary tangles.";

J. Neurochem. 51:587-598(1988).

T. FUNCTION: THE EXACT FUNCTION OF MAP2 IS UNKNOWN BUT MAPS MAY

STABILLIZE THE MICROTUBULES AGAINST DEPOLYMERIZATION. THEY ALSO

SEEM TO HAVE A STIFFENING EFFECT ON MICROTUBULES.

-I-ALTENNATIVE PRODUCTS: VARIOUS FORMS OF MAP2 ARE PRODUCED BY

ALTERNATIVE SPLICING OF THE SAME GENE. MAP2C, THE LOW MOLECULAR FORM OF MAP2, LACKS THE CENTRAL DOMAIN OF MAP2A/B.
                        751 VELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDVDQQEHSAEEGSV 810
                                                              737 VKEEAVAEVVTITK-SVKVHLEKETKEEGKPLQ-----QEKEKEKAGGEGGSEEEGSD 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-94124038; PubMed-8294038;
Albala J.S., Kalcheva N., Shafit-Zagardo B.;
"Characterization of the transcripts encoding two isoforms of human
microtubule-associated protein-2 (MAP-2).";
Gene 136:377-378(1993).
                                                                                                                                            811 CDPPPATKAD-SVDVEVRVPENHASKVEGDNTKERDLDRASEK------VEPRDE 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alternative splicing; Calmodulin-binding,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CALMODULIN-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                               P11137; Q99976; Q99975; 01-JUL-1989 (Rel. 11, Created) 01-JUN-1989 (Rel. 29, Last sequence update) 01-CT-2000 (Rel. 40, Last annotation update) MICROTUBULE-ASSOCIATED PROTEIN 2 (MAP2B) [CONTAINS: MAP2C].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISSING (IN ISOFORM MAP2C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                 PRT; 1827 AA
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                                                                                                                                                                                                                                                                                 STANDARD;
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MIM; 157130; -.
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/ Match 2.3%; Score 291; DB 1; Length 1827;
Local Similarity 19.0%; Pred. No. 0.00063;
les 414; Conservative 258; Mismatches 797; Indels 706; Gaps 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQGTYSNTKENGINGELTSADRETAEEV---SARIVQVVTAEAVAVLKAEQEKEAQHKDQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KTSRK-----PREERDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSE- 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KTEPSLVVPGIDLPKE------PPTPKEQKDWFIEMPTEAKKDEWGLVAPISPGPL 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 TPMREKDVFDDIPKWEGKQFDSPMPSPFQGGSFTLPLDVWKNEIVTETSPFAFLQPDD 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | : | : | : | : | | : | | 350 KKSLQQTSGPATAKDSFKIE------EPHEAKPDKMAEAPPSEAMTLPKDAHIPVVF 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    831 NHASKVEGDNTKERDLDRASEKVEPRD------EDLVVAQQINAQRPEPQSDNDSSATC 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               884 S-----ADEDV---TGSILVSSP 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      458 KESKPPKPADEEIGIIQTSTEHTFSEQKDQEPTTD-MLKQDSFPVSLEQAVTDSAMTSKT 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        683 LSRSLGL--GGRSAIEQRSMSINLPMSCLDSIALGFNFGRGHDLSPLASDILTNTSGSMD 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEKEEDKA------EKTEKKEEEKKDEEEKDE------KEDSKENTKEKDK 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401 EH---VMGKVLEEEKEAINQETVQQRDTFTPSGQEPILTEKETELKLEEKTTISDKEAVP 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---IPPMVSCTPC--NIPIGTPVSGYALYQRHI 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 TAALPLAAEETANLPPSPPPSPASEQTVTVEEDLLTASKMEFHDQQELTPSTAEPSDQKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----AKKGLVEHGRNWAAIAKMVGTKSEAQCKNFYFNYKRR-----HNLDNLLQQHKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    772 TKPAEDESVETQVNDSISAETAEQMDVDQQEHSAEEGSVCDPPPATKAD-SVDVEVRVPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEKAMTEPSALIEKSSIQELFEMRVDDKDKIEGVGAATSAELDMPFYEDKSGMSKY ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----DLPEEPSSPQERMFTIDPKVYGEKRDLHSKNKDD---LT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TGKESQPSPPAQEAGYSTLAQSYPS------
A -> G (IN REF. 2).
R -> A (IN REF. 2).
A -> G (IN REF. 2).
MISSING (IN REF. 2).
S -> K (IN REF. 2).
A -> GL (IN REF. 2).
V -> A (IN REF. 2).
WW; BAC3GD0030F5F455 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        554 IDGTAEETEE---REQATPRGRKTANSQGRRKGRITRSMTNEAAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAAAAAATEEP - - - PPPLPPPPEPISTEPVETSRWTEEEMEV -
                                                                                                                                                                                                                 Ψ¥.
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                                                                                                                                                                                                                 AA; 199610
      9
37
108
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187
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152
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1736
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1280 835	1340 861	1397 893	1456 946	1498 1002	1558 1025	1618 1053	1674 1098	1734 1144	1781 1203	1829 1262	1874	1925 1365	1964 1425	2023 1480	2081 1540	2131 1596	2179
YDNIKNAREGT-RSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRG	SPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYPKQIKRESPPIRAFEGAITKGKPYDG 	ITTIKEMGRSIHEIPRQDILTQESRKTPEVVQSTRPIIEGSISQGTPIKFDNNSGQS : :::  : :         :	AIKHNVKSLITGPSKLSRGM-PPLEIVPENIKVVERGKYEDVKAGETVRSRHTSVVSSGP :	SVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSPM	MNRTSDVTIPPNKSTHHERKSTLTPTQRESIPAKSPVPGVDPVVSHSPFDPHHRGSTAGE	VYWSHLPTQLDPAMPEHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYI ::: :	TSQQMQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPP	MDRITYIPGTQITFPPRPYNSASMSPGHPTHLAAAASABRERERERERERERIAAASS	DLYLRPGSEQPGRPGSHGYVRSP-SPSVRTQETMLQQRPSVFQGTNGT	SVITPLDPTAQLRIMPLPAGGPSISQGLPA-SRYNTAADALAALVDAAA 	SAPQMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVE	KRSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRGKT 	TITAANFIDVIITRQIASDKDARERGSQSSDSSSSLSSH	RYETPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGPL-HHYRPQQES 	PSPQQQLPPSSQAEGMGQVPRTHRLITLADHICQIITQDFARNQVSSQTPQQPPTSTF    :	ONSPSALVSTPVRTKTSNRYSPESQAQSVHHQRPGSRVSPENLVDKSRGS	RPGKSPERSHVSSEPYEPISPPQVPVVHEKQDSLLLLSQRGAEPAEQR
1222 Yi 1223 XI	1281 SE 836	1341 II 862 -8	1398 AI 894 GI	1457 S-       947 SK	1499 MNI 1003	1559 VY 1026	1619 TS 1054	1675 ME     1099 MR	1735 DI 1145 -I	1782 S-      1204 SK	1830 SA      1263 SG	1875 KRS' :  1321 RR-	1926 TI   1366 TE	1965 RY   1426 RK	2024 PS     1481 PS	2082 ON 1541 LP	2132
Qy Dp	0y Dp	oy Og	oy Dp	දු පු	Oy Dp	o d	oy Dp	Oy Db	Oy Db	oy Db	Oy Db	0y Db	oy Ob	Qy Db	Qy Db	Qy Db	ογ

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                                                                                                          |: :| ||: ||: || ||: |
TKKIDLSHVTSKCGSLKNIRH--RPGGGRVKIESVKLDFKEKVQAKVGSLDN--AHH--- 1748
                                                                                                                                                                                                   ------VPGGGNVKIDSQKLNFREHAKARVDHGA-----EIITQSPGRSS------ 1787
2180 NDARSPGSISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGGGDSDMAAAQPG----- 2232
                                      1649 TPPKSPAT --- PKOLRLINQPLPDLKNVKSKI -----GSTDNIKYOPKGGQVQIV 1695
                                                                                 2233 TEIFNLPAVITS-GSVSSRGHSFADPASNLGLEDIIR-----KALMGSFDDKVEDHGVV 2285
                                                                                                                                                                     2286 MSQPMGVVPGTANTSVVTSGETRREEGDPSPHSGGVCKPKLISKSNSRKSKSPIPGQGYL 2345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF115379; AAD09131.1; -. Pfan; PF00746; Gram_Dos_anchor; 1. PROSTIE; PS00343; GRAW_POS_ANCHORING; FALSE_NEG. Cell wall; Transmembrane; Antibiotic resistance; Glycoprotein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 X 2 AA TANDEM REPEATS OF D-[SAG].
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.3%; Score 289; DB 1; Length 1637;
Best Local Similarity 19.2%; Pred. No. 0.00066;
Matches 263; Conservative 170; Mismatches 460; Indels 476; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          503 QQIARPSQEEKVEEKEEDKAEKTEKKEEEKK----DEEEKDEKEDSKE--NTKEKDKIDG 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
METHICILLIN-RESISTANT SURFACE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | [1]
| SEQUENCE FROM N.A.
| STAIN=ISOLATE 1061;
| STAIN=ISOLATE 1061;
| Savolainen K., Kuusela P., Paulin L., Korhonen T.K.;
| Savolainen K., Kuusela P., Paulin L., Korhonen T.K.;
| Pls, a large repeat-rich surface protein of methicillin resistant
| Pls, a large repeat-rich surface protein of methicillin resistant
| Pls, a large repeat-rich surface protein of methicillin resistant
| Pls, a large repeat-rich surface protein of methicillin resistant
| Pls, a large repeat-rich surface protein of methicillin resistant
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MDDLINE-962707043; PubMed-8665912;
Hilden P., Savolainen K., Tyynelae J., Vuento M., Kuusela P.;
"Purification and characterisation of a plasmin-sensitive surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEINS.
IW; 75BE9ADB469BD309 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacieria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus. NCBL_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel. 33, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
METHICILLIN-RESISTANT SURFACE PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1637 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein of Staphylococcus aureus.";
Eur. J. Biochem, 236:904-910(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ::
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                                                                                                                                                                                                                                                            2346 GTERPSSVSSVHSEG 2360
                                                                                                                                                                                                                                                                                       | :|:| |
1788 -VASPRRLSNVSSSG 1801
                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..<u>..</u>
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01-FEB-1996 (Rel. 33,
01-OCT-2000 (Rel. 40,
01-OCT-2000 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1301
                                                                                                                                                                                                                                                                                                                                                                                                                 MRSP_STAAU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                    RESULT 44
MRSP_STAAU
                                                                                                                            1696
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QQ	74	EQSSANSNESDIPEQVDVTKDTTEQASTEEKANTTEQASTEEKADTTEQATTEEAPKAEG	133
Qy	557	TAE-ETEEREQATPRGRKTANSOGRRKGRITRSMINEAAAAAAAAATEEPPPPLPPPP	615
qq	134	VETEEAPKAEETDKATIEEAPKAEETDKATEEAP	170
δλ	616	EPISTEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAKMYGTKSEAQCKNFYFNYKRRHNL	675
op.	171	DKATTEEAPAA	186
δ	929	DNLLQQHKQKTSRKPREERDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSE	735
Q	187	EETSKAATEEAPKAEETSKAATEEAPKAEETEKTATEEAPKTEETDKVETEE	238
ΟŊ	736	DSPENATSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAED	777
g O	239	APKAEETSKAATEKAPKAEETNKVETEEAPAAEETNKAATEETPAVEDTNAKSNSNAQPS	298
y g	778	ESVETOVNDSISAETARQMDVDQOEHSAEBGSV	810
3 8	, ,	TI DATA WATER VALUE OF THE CONTROL O	0 1
g 8	359	COPPERATION OF VERY FEATURE OF VERY SERVICE OF	856 418
δλ	857	DSSATCSADEDVDGEP	893
QΩ	419	:	470
οy	894	γ	936
qq	471	GWGFMFTQGNGQDFLN-QGGILRDKGMANASGFKIDTAYNNVNGKVDKLDADKTNNLS	527
Οy	937		972
QQ	528	QIGAAKVGYGTFVKNGADGVTNQVGQNALNTKDKPVNKIIYADNTTHH	575
οy	973		1013
qq	576	LDGGFHGQRLNDVVLNYDAATSTITATYAGKTWKATTDDLGIDKSQKYNFLITSSHWQ (	633
δ	1014		1040
QQ	634	NRYSNGIMRINL-EGVIITIPQADLIDDVEVIKQPIPHKTIREFDPTLEPGSPDVIVQKG	269
Qy	1041	KTIVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQETPK	1080
qq	693		752
οy	1081		1117
QQ	753	DGTEEVPGKPGIKNPETGEVVTPPVDDVTKHGPKAGEPEVTKEEIPFEKKREFNPDLKPG 8	812
δο i	1118	QPEGLLVRAQHEGVVRGTAGAIQEGSITRGTPTSKISVESIPSLRG-SITQCTPALPQTG	1176
o o	813		852
δ f	1177	IPTEALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIKN 1	1227
3 ,			717
oy.	1228	CRA	1276
QQ	912	GPKAGEPEVTKEEIPFEKKREFNPDLKPGEEKVTQEGQTGEKTTTTPTTINPLTGEK 9	896
Oy Dp	1277	LPRGSPHSDGLKERTVLSG-SIMQGTPRATTESFEDGLKYPKQIKR ]	1320 1028
٥y	1321	KEMGRSIHEIPRQDILTQESRK-TPEVVQSTRPIIE	1379
qq	1029		1074

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InterPro; IPRO101356; -.
Pfam; PF00046; homeobox; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS00071; HOMEOBOX_2; 1.
HOMEODOX; DAY-binding; Developmental protein; Nuclear protein; Repressor; Coiled coil; Alternative splicing.
DOMAIN 7 363 COILED COIL (POTENTIAL).
551 610 'CUT'-REPEAT.
----GSISQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVERGKY 1435
                                                                                                                                                                                 1075 EGQTGEKTITIPITINPLIGE------KVGEGEPTTEVIKEPVDEITQFGG 1119
                                                                                                                                       EDVKAGET-------VRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGI 1475
                                                                                                                                                                                                                                                                          1476 YDDISARRIPVSYQNTMSRGSPMMNRTSDVTIPPNKSTNHERKSTLTPTQRESIPAKSPV 1535
                                                                                                                                                                                                                                                                                                                     A
BY
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MEDLINE-9350973; PubMed-1301999;
Neufeld E.J., Skalnik D.G., Lievens P.M.-J., Orkin S.H.;
Neufeld E.J., Skalnik D.G., Lievens P.M.-J., Orkin S.H.;
Human CCAAT displacement protein is homologous to the Drosophila homeoprotein, cut.";
Nat. Genet. 1:50-55(1992).
I. FUNCTION: PROBABLY HAS A BROAD ROLE IN MAMMALIAN DEVELOPMENT AS REPRESSOR OF DEVELOPMENTALLY REGULATED GENE EXPRESSION. MAY ACT PREVENTING BINDING OF POSITIVELY-ACTIVING CCAAT FACTORS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- ALTERNATIVE PRODUCTS: A NUMBER OF TRANSCRIPTS ARE PRODUCED BY
ALTERNATIVE SPLICING.
-!- DOMAIN: ASN AT POSITION 47 OF THE HOMEOBOX MAY PARTICIPATE IN
REGULATING DNA-BINDING ACTIVITY BY PROMOTING HOMO- AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HETERODIMERIZATION.
SIMILARITY: CONTAINS THREE CUT-REPEATS AND A HOMEOBOX DOMAIN
SIMILAR TO THOSE OF DROSOPHILA CUT PROTEIN. CDP MAY BE THE
MAMMALIAN COUNTERPART OF CUT.
                                                                                                                                                                                                                                                                                                                                                                                                              1536 PG------VDPVVSHSP-FDPHHRGSTAGEVYWSHLPTQLDPAMP 1573
                                                                                                                                                                                                                                                                                                                                                                                                                                                         | :| :| :| | | | | 1228 EGEPTTEVTKEPIDEIVNYAPEIIPH---GTREEI------DPNLP 1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-RAY-2000 (Rel. 39, Last annotation update)
CCAAT DISPLACEMENT PROTEIN (CDP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M74099; -; NOT_ANNOTATED_CDS.
HSSP; P10037; 1AU7.
TRANSFAC; T00100; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROMOTERS
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P39880;
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IAL). SOFORM) 1 CRC64	Lengt	MRQLS : DLRKQ	FMNVW :: LHDIE	YGKRR	KDKID   : : KTRTE	AATE-  :: LASQI	AQCKN	EENPE   : YEEVK	VETOV :: AALRI	NTKER    -	PMDSK	ALYQRHI-KAMHESAL       : ::  : -LLQRQLMQSFYSKAM	PAPHQ  : : PSOSE	HNQAS :    LSQGS	EGVVR : 1   QGRQR	GSISR   -  -SILE	RSYES
POTENTIAL) HORT ISOFO 8D4DE11 CR	DB 1; 0088; 690;	NNEKO   :	-YKDRQFMNVWTDHEKEIFKDKF   :: ::  ::: QLKVQRLHDIETENQKLRETL	LVRRN	ENTKE	SAAAA : : NHSLO	GTKSE	EASNE : : KGQAD	AEDES :  : !LQSEN	KVEGD : :QASNT	RORME	VSGYA	WEVLO	TYLTS  : HYVLG	SLLVRAQHEGVVRGTAGAI 	PTEALVKGSISRMPIEDSSPEKGR :: :     -SDEAIK-SILEQAKRELQVQKTA	EISLK
→ · · · · · · · · · · · · · · · · · · ·	284.5; DB No. 0.00088 matches 69	-IIDGLSEQENNEKQMRQLSVIPPMM : :	רפססור	NENYK? I: NQ	-EEKDEKEDSKENTKEKDKIDGTAEETEEREGA 	NEAAAA : ::! EQLSSA	AIAKM:: 1: SLTKL-	DEDEDJ   :  :   LEEKI	PSLAVPSTKPAEDESVETQVNDSISAETAEGM   : :   : :   : :   : : -VLLLEKNRSLQSENAALRISNSDLSGSARRK	VRVPENHASKVEGDN ::    -QLPRNPGEQASNTN	VDGEPE	PIGTE	-KSPNREWEVLQPAPHQLITNLPEGVRLP 	SQGTPC    -  SQRIFC	PEGLI :	н ,	SPRTAE
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Σ	Sco Pre 73;	SE     SEQSR	-FINM-NGLMEDPMKV  : :     AFLNVYKRLIDVPDPV	CVLYY :   :KIREY	DE	RKGRI I 'VAQRE	LVEH-	CESVA	TAPST	ADSVD	EPQSDNDSSATCS     :   -LSQDFFSSSLAS	PPMVS	S	KPSFI	EEFSP ::  IKQFLS	SITOG :   NITTR	NIKNA
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669 943 1126 1244 632 1505	ch 1 Similarity 18. 376; Conservative	RELDA	VK    SKEAE	FGLIA   : FAEVK	EKVEEKEEDKAEKTEKKEEEKKDE    :: :          :  : EKEQKLQNDFAEKERKLQETGMSTTS	TEMIM	ETSRW   EV-EL	NLLQQHKQKTSRK : :   : :     SQISQLEQQLSAK	SPENATSRGNTEPAVELE :	HSAEE    -  -SRRP	AQQIN	PNPLD	EQRQRQEQIDLECRSSTSPCGTS	Tdddd	PRQQESAKSATLPYIKQEEFSPRSQN   ::    :     PWNKLTVRGKE-PFHKMKQFLSDEQN	RGTPTSKISVESIPSLR   ::      RLEQEVPKRRNG	GHVIY
NCE CO	cch 11 Sim 376;	RGAGL-       RGARLK	DAEQRRVK    :    DALSKRSK	COHPKN ::   SEYNKE	SKVEEK    :: SKEQKL	TPRG   : TAKADE	STEPV	ALLOOH SQISQL	SPENAT :   APSEGA	DVDQQE     GKDQPE	DEDLW	VSSPLK ::  LNS	EORQRO	TTRPTR   TAE	ISLGLP	RGTPTS   R	EAASK
DOMAIN REPEAT REPEAT DNA_BIND VARSPLIC SEQUENCE	Ouery Match Best Local Matches 37	365 F	409	453 1 123 E	512 E	223 1	618 1 283 I	677 h	367	797 1	857 I	916 v 480 i	975 F	1026 T	1086 1	1146 F 640 F	1202 E
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δy	1557 GEVYWSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTR 1610	0
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QY	ISQGLPASRYNT 181	9
q	QPCPPIEASKDSKPPEPSDPASDSQPTTPLPLSGHS 111	7
ΟŻ	1817 AADALAALVDAAASAPOMDV-SKTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEK 1875	S
q	1113ALSIQELVAMSPELDTYGITKRVKEVLTDNNLGQRLFGETILGLTQ 1158	æ
Qy	1876 RSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDV 1935	Ŋ
q	1159 GSVSDLLARPKPWHKLSLKGREPFVRMQLWLNDPNNVEXL 1198	æ
Qy	1936 IITRQIASDKDARERGSQSSDSSSLSSHRYETPSDAIEVISPASSPAPPQEKLQTYQPE 1995	Ŋ
q	DMKRMEKKAYMKRRHSSVSDSQPCEPPSVGTEYSQGASPQPQHQLKKPR 124	æ
δλ	GPLHHYRPQQESPSPQQQLPPSSQAEGMGQVPRTHRLITLADHI 205	2
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Qy	FONSPSALVSTPVRT	7
q	RSGRAAPSSEGDSCDGVEA 134	3
Qy	2112 HQRPGSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVHEKQDSLLLLSQR 2171	П
qq	137	6
ΟŊ	2172 GAEPAEQRNDARSPGSISYLPSFTKLENTSPMVKSKKQEIFRKLNSSGGODSDMAA 2228	œ
qq	1380 TPGPDDARDDHEGGPVEGPGPLPSPASATATAAPAAPEDAATSAA 1425	2
οy	2229 AQPGTEIFNLPAVTTSGSVSSRGHSFADPASNLGLEDI 2266	

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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September 8, 2001, 14:36:58; Search time 28.24 Seconds (without alignments) 6581.654 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-522-753-11 12643 1 MSSSGYPPNQGAFSTEQSRY ......EREPAPLLSAQYETLSDSDD 2440

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:\* pir2:\* pir3:\* PIR\_68:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	nuclear receptor c	hypothetical prote		microtubule-associ	microtubule-associ	microtubule-associ	01	elastic titin - hu	hypothetical prote	adenomatous polypo	hypothetical prote	cell proliferation	ankyrin 2, neurona	hypothetical prote	nascent polypeptid	hypothetical prote	Bassoon protein -	cell proliferation	NF-180 - sea lampr	DNA-binding protei	hypothetical prote		hypothetical prote	Bassoon protein -	hypothetical prote		Ø	hypothetical prote	adenomatous polypo
SUMMARIES	QI	\$60254	T46489	S60255	T13564	A56577	A43359	QRMSP1	I38346	T15348	149505	T51023	B48666	S37431	T25752	T30826	T20532	T42730	A48666	151116	T42717	S15053	A41819	T16871	T42761	37	T02345	A47171	T20531	RBHUAP
	DB				~																						•	•	•	
	Query Match Length	2453	1047	1495	5327	2364	2774	2464	7962	5170	2845	2649	2897	3924	2361	2187	2722	3942	3256	1110	2282	1226	5762	2215	3938	2447	1791	3562	2526	2843
dР	Query	91	42.7	4	4.6	3.9	3.7	3.5	3.5	3.5	-:	•	3.3	•	•	٠		3.5		•	3.1				٠			•	5.9	
	Score	11536.5	5395	1879	584.5	487.5	465.5	447	444	440	437	429	415	411.5	409.5	408	405	405	404	402.5	391.5	390	389	381.5	380.5	376.5	376	374.5	372	365
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hypothetical prote	hypothetical prote	ankyrin 3, long sp	hypothetical prote	MHC class III hist	hypothetical Myb f	C14B9.6 protein -	hypothetical prote	All-1 protein +GTE	tpr protein - huma	MHC class III hist	microtubule-associ	alpha-A-crystallin	mucin MUC5B, trach	ALR protein - huma	TCOFI protein - mo
T26216	T26215	A55575	T34434	B35098	T38176	S44758	T34513	A48205	S33124	S36152	S13507	I49477	T45025	T03454	JC5630
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2.9	361 2.9	359 2.8	357 2.8	353 2.8	350 2.8	•		343 2.7	342 2.7	340 2.7	338 2.7	336 2.7	336 2.7	335 2.6	334.5 2.6

## ALIGNMENTS

B.; Kurokawa, R.; Ry ceptor mediated by a

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KEEEKKDEEEKDE 540                 KEEEKKDDEEKDD 540	SMTNEAAAASAAA 600    :     :    SMTSEAAAAN-AA 599	AAIAKMVGTKSEA 660               AAIAKMVGTKSEA 659	AQEDEDIEASNEE 720               AQEDEDIEASNEE 719	SLEPTTETAPSTS 764	DPPPATKADSVDV 824               PPAPTKADSVDP 839	EPQSDNDSSATCS 884      :   :        EPQSDDDSSATCS 896	HRAVIPPMVSCT 944                 RAAVIPPMVSCT 956	SPCGTSKSPNREW 1004                SPCSTSKSPNREW 1016	IMGGSISQGTPGT 1064               IMGGSISQGTPGT 1076	PRSQNSQPECLLV 1124               PRSQNSQPECLLV 1135	LPQTGIPTEALVK 1184               LPQAGIPTEALVK 1195	rsprtaheislk 1244 	.SGSIMQGTPRAT 1304                 SGSIMQGTPRAT 1315	IEIPRODILTOES 1364                   EIPRODILTOES 1375	SKLSRGMPPLEIVP 1424                SKLPRGMLEIVP 1433	PGIYDDTSART 1484   :   :       SPGLYDDSSART 1493	(SPVPGVDPVVSH 1544
KNENYKALVRRNYGKRRGRNQQIARPSQEEKVEEKEEDKAEKTEKI 	SKENTKEKDKIDGTAEETEEREQATPRGRKTANSGGRRKGRITR             :	TEEPPPPLPPPPEPISTEPVETSRWTEEEMEVAKKGLVEHGRNWAAI 	KNPYFNYKRRHNLDNLLQQHKQKTSRKPREERDVSQCESVASTVS 	PEDSEVEAVKPSEDSPENATSRGNTEPAVEI 	LAVPSTKPAEDESVETQVNDSISAETAEQMDVDQQEHSAEEGSVCDI    :	'ENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRP 	EDVDGEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHF 	NIPIGTPVSGYALYQRHIKAMHESALLEEQRQRQBQIDLECRSST: 	VLQPAPHQLITNLPEGVRLPTTRPTRPPPFLIPSSKTTVASEKPSF 	SHNOASYTOETPKPSVGSISLGLPRQDESAKSATLPYIKQEEFS 	HEGVVRGTAGAIQEGSITRGTPTSKISVESIPSLRGSITQGTPA 	SRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIKNAREGTF 	ESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLS  :   :	FEDGLKYPKQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHI 	PEVVQSTRPIIEGSISQGTPIKFDNNSGQSAIKHNVKSLITGP 	KVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSI 	YONTMSRGSPMMNRTSDVTIPPNKSTNHERKSTLTPTQRESIPAK
481 TKI     481 TKI	541 KED         541 KED	601 AAA?         600 AAA?	661 QCI 	721 ENI 1  720 ENI	765 PSI 	825 EVRVE  ::   840 EMQVE	885 ADI 	945 PCI   1   957 PCI	1005 EV     1017 EV	1065 YLT:   : 1077 YLS:	1125 RAQI 	1185 GSI   :   1196 GPV	1245 RSY      1256 RSY	1305 TES     1316 AES	1365 RKTI           1376 RKTI	1425 ENI     1434 ENI	1485 PVS
Qy Dp	OY Db	oy ob	Oy DD	Qy Db	Qy	Q <sub>Y</sub>	Oy Db	Q Q	Qy Dp	Oy Dp	Oy Dp	QY Db	Oy Op	Qy Dp	Oy Dp	OY DD	ΟY

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RESULT 2
T46489
hypothetical protein DKFZp434M075.1 - human (fragment)
c;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000
C;Accession: T46489
R;Duesterhoeft, A.: Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, January 2000
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                                                                                                                                              FQGTNGTSVITPLDPTAQLRIMPLPAGGPSISQGLPASRYNTAADALAALVDAAASAPQM 1834
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SPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLY 1604
          AMENTRQTILNDY ITSQQMQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPPTILV
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                                                                                              Length 1047;
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      A.Accession: T46489
A.Status: preliminary
A.Molecule type: mRAA
A.Residues: 1-1047 <AAA>
A.Crossreferences: EMBL:AL137641
A.Experimental source: adult testis; clone DKFzp434M075
C.Genetics:
A.Note: DKF2p434M075.1
                                                                                               Score 5395; DB 2;
Pred. No. 3.3e-202;
                                                                                                                 0; Mismatches
                                                                                               42.7%;
99.6%;
                                                                                                      Best Local Similarity 99.6
Matches 1043; Conservative
Reference number: 223035
                                                                                             Query Match
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C; Accession: $60255
R; Chen, J.D.; Evans, R.M.
Nature 377, 454-457, 1995
A; Title: A transcriptional co-repressor that interacts with nuclear hormone receptors A; Accession: $60255; MUID:96008552
A; Accession: $60255
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C.Species: Homo sapiens (man)
C.Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 05-Nov-1999
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A;Residues: 1-1495 <C
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A;Introns: 24/2; 52/3; 104/3; 179/1; 232/1; 1669/3; 2566/1; 4798/3; 5;
A;Note: EG:49E4.1
C;Superfamily: Drosophila 576K microtubule-associated protein homolog
                                                                                                                                                                                                                  Rispanos, L.; Papagiannakis, G.; Siden-Kiamos, I.; Louis, C. submitted to the EMBL Data Library, April 1999
A; Description: Sequencing the distal X chromosome of Drosophila B; Reference number: 217689
A; Accession: T13564
A; Accession: T13564
A; Molecule type: DMB
A; Residues: 1-5327 <SPA>
microtubule-associated protein homolog - fruit fly (Drosophila m N;Alternate names: hypothetical protein EG:49E4.1
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change
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4.6%; Score 584.5; DB 2;
Best Local Similarity 19.5%; Pred. No. 1.1e-14;
Matches 558; Conservative 412; Mismatches 1059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 PRLEQ--VSDSHFQRVSAAVLPLVHPLPEGLRAS--ADAKK---
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C;Genetics:
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677	721	773 1533	831 1584	888 1638	948 1673	1006	1066	1101	1158	1212 1938	1258 1998	1317	1372 2088	1431 2142	1470	1519	1561
22 -PVETSRWTEEEMEVAKKGLVEHGRNWAAIAKMVGTKSEAQCKNFYFNYKRRHNLDN   :	78 LLQQHKQKTSRKPREERDVSQCESVASTVSAQEDEDIEASNEEE :   .   .   .   .   .   .   .   .   .	22 NPEDSEVEAVKPSEDSPENATSRGNTEPAVELEPTTETAPSTSPSLAVPSTK : :	74PAEDESVETQVNDSISAETAEQMDVDQQEHSAEGGSVCDPPPATKADSVDVEVRVPEN	OI NO	<b>თ</b> თ	19 PIGTPVSGYALYQRHIKAMHESALLEEQRQRQEQIDLECRSSTSPCGTSKSPNREWEV	07 LQPAPHQLITNLPEGVRLPTTRPTRPPPPLIPSSKTTVASEKPSFIMGGSISQGTPGTYL	57 TSHNQASYTQETPRPSVGSISLGLPRQQESAKSAT		59PSLRGSITQGTPALPQTGIPTEALVKGSISRMPIEDSSPEKGREEAASKGHVIY	3 EGKSGHILSYDNIKNAREGTRSPRTAHEISLKRSY-ESVEGNIKQGM	59 SMRESPV-SAPLEGLICRALPRGSPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYPKQ	18 IKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHEIPRQDILTQESRKTPEVVQ	3 STRPIIEGSISQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSRG-MPPLEIVPENIKVVE	12 RGKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQ-   STATE   STATESVAGSVTADSARDDQSPLESKGASRPESVVDSVKDEAEKQES   SVKDDPVKSKEPSRRESVAGSVTADSARDDQSPLESKGASRPESVVDSVKDEAEKQES	11LSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTSDVTIPPNKSTNHERKS	
622	678	722	153	83	163	949	1007	1067	1102	115	121	125	131	1373	1432	1471	1520
Oy Dp	oy og	Qy Dp	Oy Dp	6 G	ري و	Š 8	ç G	g ç	\$ G	Qy Db	\$ A	oy Op	ç P	Oy Dp	Oy Op	Oy Dp	Oy Db

δλ	562 -	SHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQ	Ģ.
g	2305 R	ESLEDKSAVTSEKSVSRPLSVASDHEAAVAIEDDAKSSISPKDKSRPGFVA	364
δλ	09	YQLYAMENTRQTI	.653
QQ	2365 E	EATMEFSKIEVVEKSSLALSLØGGSGGKLØTDSSPVDVAEGDFSHAVA 2	412
οy	654	PGTQITFPPRPYNSASMSPGHPTHLAAA   :   :     ::	1709
q	2413 S	A	456
δ	1710 A	ASAERERERERERERERIAAASSDLYLRPGSEQPGRPGSHGYVRSPS 1	1758
qq	2457 D	EISRP	516
δλ	1759 P	OGTNGTSVITPLDPTAQLR	.817
QQ	2517 S	SAGETASSPIEEAPKDFAEFEQAEKAVLPLTIELKGNLPTLSSPVDVAHASVQ 2	569
Qy	1818 A	RLEENLRSRSAAVS 1	.861
QQ	2570 P	PAELSKVDIEKTASSPIDEAPKSLIGSPAEERPESPAESAKDAAESVEKSKDASRPPSVV 2	629
Qy	1862 E	OPHSSV 1	868
qq	2630 E	SASITGDSTKDVSRPASV 2	989
δλ	1899 V	SELRTRGKTTITAANFIDVIITRQIASDKDARERGSQSSDSS 1	958
Op	2687 V	ESVKDEHDKAESRRESIAKVESVIDEAGKSDSKSSSQDSQ-KDEK	2731
Qy	1959 S	PASSPAPPQEKLQTYQPEVVK 1	966
Q	2732 S	SGEPVPRESKSPLDSKDTSRPGSVVE	2791
οy	1999 AI	YEGPLHHYRPQQESPSPQQQLPPSSQAEGMGQVPRTHRLITLADHICQI	2058
QQ	2792 S	SVTAEDEKSEQASRRSSVDEL 2	835
οy	2059 I	VSSQTPQQPPTSTF-QNSPSALVSTPVRTKTSNRYSPESQAQSVHHQR- 2	1114
QQ	2836 LI	GSHKAMSTMGDESPMDKADKSKEPSRPESVAESIKHENT 2	890
δy	2115 -	GSRVS-PENLVDKSRGSRPG	2134
QQ	2891 KI	: :	2950
Qy	2135 K		174
qq	2951 VI	m	010
QY	2175 P	AEQRNDARSPGSISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGGGDSD	2225
qq	3011 PI	ESVTESVKDGKSPVASKEASRPASVAENAKDSA	3064
οy	2226 M	FNLPAVTTSGSVSSRGHSFADPASNLGLEDIIRKALMGSFDDKVEDHGVV 2	285
qq	3065 DE	SKEQRPESLPQSKAGSIKDEKSPLASKDEREKREESRRESVAEQFPL 3	114
Qy	2286 M	SQPMGVVPGTANTSVVTSGETRREEGDPSPHSGGVCKPKLISKSNSRK 2	334
qq	3115 V		3173
δλ	2335 -	SYLGTERPSSVS-SVHSEGDYHRQTPGWAWEDRPSSTGSTQFPYNPLTMRM 2	392
QQ	3174 AI	ESVKDEADKSKEESRRESGAEKSPL 3	216
δy	2393 L	SSTPPTPIACAPSAVN	
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RESULT 5 A56577 microtubule-associated protein MAP 1B - rat (fragment) C;Species: Rattus norvegicus (Norway rat) C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 16-Feb-1997 C;Accession: A56577 R;Zauner, W.; Kratz, J.; Staunton, J.; Feick, P.; Wiche, G. Eur. J. Cell Biol. 57, 66-74, 1992 A;Title: Identification of two distinct microtubule binding domains on recc A;Reference number: A56577; MUID:92347374 A;Accession: A56577 A;Ac	Db 689 Oy 703 Db 724 Oy 758 Oy 789 Db 847 Oy 789 Db 847	
Query Match 3.9%; Score 487.5; DB 2; Length 2364; Best Local Similarity 19.1%; Pred. No. 2.3e-11; Matches 494; Conservative 360; Mismatches 946; Indels 793; Gaps Qy 71 LLSEFHPGSDRPQERRTSYEPFHPGPSPVDHDSLESKRPRLEQVSDSHFQRVSAAVL 127	907 946 964	VIPPMVSCTPCNIPIGTPVSGYALYQRH 96
RHNLQDFINIKLNSA PCGDD 	1024 LPTTRPTRPPPPLIPS 1023 EISSEPTPMDEMSTPRDVMTD 1077 ETPRPSVGSISLGLP 1071 EYSKPVVASFN-GLSGSKTD	GSISQGTPGTVLTSHNQASYTQ :  :   :   :   :   :   :   :   :   :
SILLTHIGDDNLPGINSMLQ)LKLKKKQQQ) - - -     NPEPNIKMKRSTEEACFTLQ; PPPVEQKHRSIVQIIYDENRI	1125	RAOHEGVVRGTAGALOEGSITRGTPTSKISVESIPSLRGSITGGTPAL 1172
VKSSKEMQYFMQQWTGTN  VMR  ::   IIRVLFPGNSTQYNILEG  EAWEKKVDRIENNPRRKA	1228 1243 1287 1287	
419 LATOKDLTGOVSTPPVKOVKLKORADSRESLKPATKPLSSKSVRKESKEE 346 FPEIRKOREQOERFORVGORGAGLSATIARSEHEISEIIDGLSEQENNEKOMROLSVIPP	1341 1341 1389 1401	
DD   5.20 VKAEVAEKAA	Qy 1449 TSVVSSGPSVLRSTLHEAPKAQLSPGIY	TSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSR 1494
534 RITRSMINEAAAAAAAATEEPPPPLPPPPEPISTEPVETSRWIEE-EMEVAKKGLVE 11:::	Oy 1555 TAGEVYWSHLPTQLDPAMPFHR-1	TAGEVYWSHLPTQLDPAMPFHR-ALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQ 1611

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A;Status: preliminary
A;Molecule type: mRNAS, 370, OKN',374, 'PSPKGL',381-751, 'RSMMSQWNAQRR',764,'D',766,
A;Residuse: 73.364,'NRLRS',370,'OKN',374,'PSPKGL',381-751,'RSMMSQWNAQRR',764,'D',766,
WLKRNNCPOPROSP',851,'VY',883,'NSL',855,'LPHRWLRTN',865,'W',867,'HSQLPDGGD',877,'Q',87
A;Cross-references: EMBL:X66840
A;Experimental source: strain Sprague Dawley
C;Superfamily: microtubule-associated protein MAPIB
C;Reywords: microtubule binding; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----PPE----PEKPVSPPPVEQKHRSIVQIIYDENRKKAE 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKLAKREEVLEE---GAKEARSELAKELAKTEKKAKEPSEKPP-----EKPSKSERVRG 382
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                                                                                                                                                                                                                                                                                                                                         96 PSPVDHDSLESKRPRLEQVSDSHFQRVSAAVLPLVHPLPEGLRASADAKKDPAFGGKHEA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                 156 PSSPISGQPCGDDQNASPSKLSKEELIQSMDRVDRE-IAKVEQQILK-----LKKKQQQL 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FKRR---NHARKQ------REQKICQRYDQLMEA---W-----EKKVDRI---ENNPRR 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KAKE--SKTREYYEKQFP----------EIRKQREQQERFQRGQRGSGS 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LMEDPMKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNFGLIASYLERKSVPDCVLYYYLTK 482
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                                                                                                                                                                                                                                                                                               Indels 1053;
                                                                                                                                                                                                                                                     Length 2774;
                                                                                                                                                                                                                                                 Query Match 3.7%; Score 465.5; DB 2; Best Local Similarity 19.1%; Pred. No. 2e-10; Matches 570; Conservative 350; Mismatches 1012;
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microtubule-associated protein MAPIA - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 13-Aug-1999
C;Accession: A43359; S22108
R;LangKopf, A.; Hammarback, J.A.; Muller, R.; Vallee, R.B.; Garner, C.C.
A;Title: Microtubule-associated proteins 1A and LC2. Two proteins encoded in one A;Reference number: A43359; MUID:92355629
  EV--DYSPSDIQDSSL----SHKIPPTEEP---SYTQDNDLSELISVSQVEASPSTSSAH 1632
                                                                                                                                                                              -----LIPRESSP----TYSPGFSDSTSGAKESTAAYQ----TSSSPPIDAAA 1722
                                                                                                                                                                                                                                                                      ----AEPYGFRS-----SMLFDTMQHHLALSRDLTTSSVEKDNGGKTPGDFNYAYQKP 1771
                                                                                                                                                                                                                                                                                                               1837 SKTKES-----KHEAA------RLEENLRSRSAAVSEQQQLEQKTLEVEK 1875
                                                                                                                                                                                                                                                                                                                                                                                                     1876 RSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDV 1935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1936 IITRQIASDKDARERGSQSSDSSSSLSSHRYET-----PSDAIEVISPASSPAPPQE 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1988 KLQTYQ--PEVVKANQAENDPTRQYEGPLHHYRPQQESPS---------PQ 2027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1934 SAYCYETMEKITKTPQAS---TYSYETSDRCYTPERKSPSEARQDVDLCLVSSCEFKHPK 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2240 AVTISGSVSSRGHSFADPASNLGLEDIIR-----KALMGSFDDKVEDHGVVMSQPMGV 2292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; MOLECULE type: MRNA
A; Residues: 1-2774 <LAN>
A; Residues: 1-2774 <LAN>
A; Cross-references: GB:M33196; NID:g205537; PIDN:AAB48069.1; PID:g205538
A; Note: sequence extracted from NCBI backbone (NCBIN:111039; NCBIP:111040)
R; Cravchik, A.
                                                                     1633 TP------SQIASPLQEDILSDVVPPRDMSLYASLASEKVQSLEGEKLSPKSDISP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1732 ASSDLYLRPGSEQPGRPGSHGYVRSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTA
                                                                                                                                                                                                                                                                                                                                                | | | ::| ::|::| | ESTTESPDEEDYDYESHEKTIQAHDVGGYYEKTERTIKSPCDSGYSYETIEKTTKTPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----TEESERPLTQSGGAPPPSGGKQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2079 ESETIPTDKTVTYKHMDPPPAPMQDRSPSPRHPDVSMVDPEALAIEQNLGKALKKDLKEK
                                            TPPMDRITYIPGTQITFPPRPYNSASMSPGHPTHLAAAASAERERERERERERERIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                   2069 SSQTPQQPPTSTFQNSPSALVSTPVRTKTSNRYSPESQAQSVHHQRPGSRVSPENL--VD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2127 KSRGSRPGKSPERSHVS--SEPYEPISP-PQVPVVHEKQDSLLLLSQRGA----EPAEQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2139 AKTKKPG-----TKTKSSSPVKK------GDGKSKPSAASP----KPG
                                                                                                                                                                                                                          1792 QLRIMPLPAGGPSISQGLPASRYNTAADALAALVDAAASAPQMD------
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A; Reference number: S22108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1991 TELSPSFINPNPLEWFAGEEP
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Q	731	SYIQDETIPGYSETEQTISDEEIHDEPDERPAPPRFPTSTYDLSGPEGPGPFEASQ 786	
Δī	818	KADSVDVEVRVPENHASKVEGDNTKERDLDRASEKVEP 855	
۾	787		
<u>~</u>	856	RDEDLVVAQQINAQRPEPQSDNDSSATCSADED 888	
۵	843	VAEDQSVASLTAAPQTEETGKSSLLLDTVTSIPSSRTEATQGLDYVPSAGTISPTSSLEED 902	
<b>&gt;</b> -	883	VDGEPERQRWFPMDSKPSLLNPTGSILVSSP 919	
ā	903	KGFKSPPCEDFSVTGESEKKGETVGRGLSGEKAVGKEEKTVVTSEKLSGQYAAVFGAP 960	
<u>≻</u> ₁	920	LKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTPVSGYALYQRHIKAM 967	
۵	961	GHTLPPGEPALGEVEERCLSPDDSTVKMASPPPSGPPSAAHTPF 1004	
<u>بخ</u>	968	HESALLEBQRQRQEQIDLECRSSTSPCGTSKSPNREWEVLQPAPHQLITNLPEGVRLPTT  :	
۵	1005		
<u>ب</u> و	1028	RPTRPPPPLIPSSKTTVASERPSFIMGGSISOGT-PGTYLTSHNQAS 1073	
۶,	1074		
۾	1119		
>-	1124	VRAQHEGVVRGTAGAIQEGSITRGTPTSK 1152	
۾	1178	SPEDTQSLSFSEESPSKETSLDISSKQLSPESLGTLQFGELNLGKEERGPVMKAEDDSCH 1237	
<u>≻</u>	1153		
۾	1238	::	
<u></u>	1189		
۾	1298	LTKSPESLSSPAMEDLAVEWEGKAPGKEKEPELKSETRQQKGQILPEKVAVVEQDLII 1355	
<b>&gt;</b> 1	1227		
۵	1356	HQKDGALDEENKPGRQODKTPEQKGRDLDEKDTAAELDKGPEPKEKDLDREDQG 1409	
<b>≱</b> -	1278		
۵	1410	QRAGPPAEKDKASEQRDTDLQQTQATEPRDRAQERRDSEEKDKSLELRDRTP 1461	
٨	1333	TKGKPYDGITTIKEMGRSIHEIPRQDILTQESRKTPEVVQSTRPIIEGSISQGTPI 1388	
۾	1462	EEKDRILVQEDRAPEHSIPEPTQTDRAPDRKGTDD 1496	
۸.	1389	KPDNNSGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVRAGETVR	
Ω	1497	K-EQKEEASEEKEQVLEQKDWALGKEGETLDQEARTAEQ-KDETLKEDKT-Q	
<u>,</u>	1446	SRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRT 1502 ::    : :   :   :   :	
۾	1546	GQKSSFVEDKTTTSKETVLDQKSAEKADSVEQQDGAALEKTRALGLEESPAEGS 1599	
<u>~</u>	1503	SDVTIPPNKSTNHERKSTLTPTQRESIPAK-SPVPG-VDPVVSHSPFDPHHRG 1553	
٩	1600	KAREQEKKYWKEQDVVQGWRETSPTRGEPVGGQKEPVPAWEGKSPEQEVRYW 1651	
<u>ب</u> بخ	1554	STAGEVYWSHLPTQLDPAMPFHRALDPAMAAYLFQRQLSPTPGYPSQYQLYAM	
Ω	7691	KDKDITLDQQDAXWKELSCDKKVWFPHELDGQGARPKYCEEKESIFLDDEGPDEQEITPL	
ب م	,1607	ENT-RQTILNOYITSQQMQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMP 1659 ::	

ΟŊ	1660		1701
QQ	1768	:   WVPKDRPLPPAPLSPAP	1827
Οy	1702		1729
QΩ	1828	APPTPAPEPHTPVPFSWGLAEYDSVVAAVQEGAAELEGGPYSPLGKDYRKAEGEREGEG	1887
δy	1730		1789
qq	1888	AGAPDSSSFSPKVPEAGESLATRDTEQTEPEQREPTPYPDERSFQYADIYEQMMLTGLGP	1947
δy	1790		1846
qq	1948		1987
Qy	1847	ARLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYS-	1901
Dp	1988	VPPRQEPDPGPNVEPSI	2025
Qy	1902	IITRQI	1941
q	2026	TPPAVPPRAPISLSKDLSPPLNGSTVSCSPDRRIPSPKETGRGHWDDGTNDSDL	2079
Qy	1942		1973
qq	2080	EKGAREQPEKETRSPSPHHPMPMGHSSLWPETEAYSSLSSDSHLGSVRPSLDFPASAF:	2137
Qy	1974	ENDPTRQYEGPLHHY	2017
qq	2138	GFSSLQPAPPQLPSPAEPRSAPCGSLAFSGDRALALVPGTPTRTRHDEY	2186
Qy	2018	RPQQESPSPQQQLPPSSQAEGMGQVPRTHRLITLADHICQIITQDFARNQVSSQT	2072
QQ	2187		2218
Qy	2073	PQQPPTSTFQNSPSALVSTPVRTKTSNRYSP	2116
qq	2219		2275
Qy	2117		2144
qq	2276	SPAPSASLDLAPAPAPAPAPAPGLPGDLGDGTLPCRFECTGELTKRPSPFLSPSGDHEAN	2335
Qy	2145	SISYLPSFFTKLENT	2201
qq	2336	GPGETSLNPPGFVTATAEKEEAEAPHAWERGSWPEGAERSSRPDTLLSSE	2385
Οy	2202	QEIFRKLNSSGGGDSDMAAAQPGTEIFNLPAVTTSGSVSSRGHSFA-DPASN	2260
qQ	2386		2419
Oy	2261	DEKVEDHGVVMSQPMGVVPGTANTSVVTSGETRREEGD	2313
qq	2420	LAGKGGRRRVGR	2459
QY	2314		2348
Ωp	2460	PGA-TGGPCPMADETPPTSASDSGSSQSDSDVPPETEECPSITAEAALDSDEDGDFLPVD	2518
Qy	2349		2403
qa	2519	PPRPDVCMADPE	2558
οy	2404		
qq	2559	GLSSESGRVERLREKGRPGRRAPGRAKPASPARRLDIRGKRSPTP 2603	

RESULT 7 QRMSP1 microtubule-associated protein MAP1B - mouse

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2299
DT---SARRTPVSYQNTMSRGSPMMNRTSDVTIPPNKSTNHERKSTLTPTQRESIPAKSP 1534
                                                                                        1535 VPGVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHR-ALDPAAAAYLFQRQLSP 1593
                                                                                                                                   1629 TPVQD-----FSRQ----SSMSIEFGQESPEHSFAMD-----FSRQ--- 1661
                                                                                                                                                                                  1594 TPGYPS -- OYQLYAMENTRQTILNDYITSQQMQVNLRPDVARGLSPREQPLGLPYPATRG 1651
                                                                                                                                                                                                                                1662 SPDHPTLGASVLHITENGPTEV--DYSPCDIQDSSL----SHKIPPTEEP---SYTQDND 1712
                                                                                                                                                                                                                                                                             IIDLTNMPPTILVPHPGGTSTPPMDRITYIPGTQITFPPRPYNSASMSPGHPTHLAAAAS 1711
                                                                                                                                                                                                                                                                                                                        1713 LSELISVSQVEASPSTSSAHTP-----SQIASPLQEDTLSDVVPPREMSLYASLA 1762
                                                                                                                                                                                                                                                                                                                                                                       AERERERERERERERERIA----AASSDLYLRPG-----SEQPGRPGSHGYVRSPSPSVR 1762
                                                                                                                                                                                                                                                                                                                                                                                                                1763 SEKVQSLEGEKLSPKSDISPLTPRESSPLY-SPGFSDSTSAAKETAAAHQASSSPPIDAA 1821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMPLPAGGPSISQGLPASRY-----NT 1816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1822 TAE-----PYGFRS-----SMLFDTMQHHL-----ALNRDLTTSSVEKDSGGKT 1860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1817 AAD---ALAALVDAAASAPQMDVSKTKESK----HEAAR----LEENLRSRSAAVSEQQ 1864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1861 PGDFNYAYQKPENAAGSPDEEDYDYESQEKTIRTHDVVRYYYEKTERTIKSPCDSGYSYE 1920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1865 QLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRGK 1924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1921 TIEKTTKTPEDGGYTCEITEKTTRPEEGGYS---YEISEKTTRTPEVSGYTYEKTERSR 1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1925 TIITAANFIDVIITRQIASDKDARERGSQSSDSSSSLSSHRYET-----PSDAIEVI 1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1978 RLLD------DISNGYDDTEDGGHTLGD----CSYSYETTEKITSFPESESYSYE 2022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2023 TSTKTTRSPDTSAYCYETMEKITKTPQAS---TYSYETSDRCYTTEKKSPSEARQDVDLC 2079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------PQQQLPPS----SQAEGM-GQVPRTHRLITLADHICQIITQD-----FAR 2065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2080 LVSSCEFKHPKTELSPSFINPNPLEWFAGEEP-----TEESEKPLTQSGGAPPPSGG 2131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2132 KQQGRQCDETPPTSVSESAPSQTDSDVPPETEECPSITADANIDSEDESETIPTDKTVTY 2191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2123 NLVDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVHEKQDSLLL---LSQRGAEPAEQR 2179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2180 NDARSPGSISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGGGDSDMAAAQPGTEIFNLP 2239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2240 AVTISGSVSSRCHSFADPASNLGLEDIIRKALMGSFDDKVEDHGVVMSQPMGVVPGTANT 2299
                            2066 NQVSSQTPQQPPTSTFQNSPSALVS-TPVRTKTSNRYSPESQAQSVHHQR--PGSRVSPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2192 KHMDPPPAPMQDRSPSPRH------PDVSMV--DPDALAVDQNLGKAVKKDLKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2272 ALKESSDKVSR---VASPKK----KESVEKA------------TKTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1977 SPASSPAPPQEKLQTYQ--PEVVKANQAENDPTRQYEGPLHHYRPQQESPS-
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1478
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111; ---PVPEEKKPVPVPKKEP 6003 6357 V-TEFRKRVVKEEKVSIEAPKREPQPIKEVTIMEEKERAYTLEEEAVSVO-REEEYEEYE 6414 191 --EIAKVEQQILKLKKKQQQLEEEAAKPPE----PEKPV------SPPP-VE 229 KKVDRIENNPRRKAKESKTREYYEKQFPEIRKQREQQERFQRVGQRGAGLSATIARSEHE 379 380 ISEIIDGLSEQENNEKQMRQLSVIPPMMFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNV 439 WTDHEKEIF-----KDKFIQHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYKAL 490 TKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRKPREERDVSQCESVASTVSAQEDEDIE 715 716 ASNEEENPEDSEVEAVKPSEDSPENATSRGNTEPA--VELEP----TTETAP----STSP 765 Gaps 596 ASAAAAATEEPPPPLPPPPEPISTEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAKMVG 655 34 HQQEFAVPD---YRSSHL--EVSQASQLLQQQQQQLRRRPSLLSEFHPGSDRPQ-ERRT 88 SYEPFHPGPSPVDHDSLESKRPRLEQVSDSHFQRVSAAVLPLVHPLPEGLRASADAKKDP 230 QKHRSIVQIIYDENRKKAEEAHKIFEGLGPKVELPLYNQPSDTK------VYH VRRNYGKRRGRNQQIA--RPSQEEK-----VEEKE-----EDKAEKTEKKEEEKKDEE EKDEKE-DSKENTKEKDKIDGTAEETEEREQATPRGRKTANSQGRRKGRITRSMTNEAAA 148 AFGGK-HEAPSSPISGQ----PCGDDQNASPSKLSK-----EELIQSMDRVDR-------VMRKKLILFFKRRNHARKQREQKICQRYDQLMEAWE EHEEYITEPEKPIPVKPVPEEPVPTKP-----KAPPAKVLKKAVPEE-KVPVPIPKKL-Indels 804; Length 7962; Ouery Match 3.5%; Score 444; DB 2; L Best Local Similarity 18.3%; Pred. No. 5.2e-09; Matches 463; Conservative 332; Mismatches 934; GDB:127867; OMIM:188840 5961 APEEVAPVPIP --- KKVEPPAPKVPEVPKK --6232 KIPAKIEEPPPAKVPEAPKKIVPEKKVP----A,Gene: GDB:TTN A,Cross-references: GDB:1. A,Map position: 2q31-2q31 ENIKTNO----320 440 491 6529 ð 셤 à g ò g ŏ g ò q ò g δ Ω à q δy g ò g δ g οy g à d ò g us-09-522-753-11.rpr

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3	77.	FULVENAF LAR	*C*/
yo g	1842	SKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYS : D  ::    ::    ;       : DEVUDDARVDE	1901
ð	1902	EAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVIITRQIASDKDARERGSQSSSSL	1961
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qq	7512	PVAEEEEPEVPPP	566
ΟŸ	2018	RPQQESPSPQQQLPPSSQAEGMGQVPRTHRLITL	2051
qq	7567	RPPPPPAPPKEDVKEKIFQLKAIPKKKVPENPQVPEKVELTPLKVPGGEKKVRKLLPER	7626
ΟŸ	2052	FQNSPSALVSTPVRT	2095
qq	7627	KPEPKEEVVLKSVLRKRPEEEEPKVEPKKLEKVKKPAVPEPPPPKPVEEVEVPTVT	7682
δy	2096	KTSNRXSPESQAQSVHHQRPGSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEPI	2150
ΩQ	7683	KRERKIPBEPTKVPEIKPAIPLPAPEPKPKPEAEVKTIKPPFVEPEPTPIA	7732
δλ	2151	SLLLLSQRGAEPAEQRNDARSP-GSISYLPSFFTKLENTSPMVKSKK	2209
q	7733	APVTVPVVGKKKTPSPIEAER- APAKAPKEEAAKPKGPIKGVPKKTPSPIEAER-	7775
δ	2210	QEIFRKLNSSGGGDSDMAAAQPGTEIFNLPAVTTSGSVSSRGHSFADPASNLGLEDIIRK	2269
q	7776	RPGSGGEKPPDEA-PFTYQLKAVPL	7802
δλ	2270	ALMGSFDDKVEDHGVVMSQPMGVVPGTANTSVVTSGETRREEGDPSPHSGGV	2321
QQ	7803	KFVKEIKDIILTESEFVGSSAIFECLVSPSTAITTWWKDGSNIRESP	7849
δλ	2322	CKPKLISKSNSKK 2334	
QQ	7850	-KHRFIADGKDRK 7861	
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R;G subi	attung, mitted	. S. to the EMBL Data Library, February 1996	
A; D(	escript	tion: The sequence of C. elegans cosmid B0350,	
A; A	ccessic	on: T15348	
A; S	tatus: olecule	preliminary; translated from GB/EMBL/DDBJ : type: DNA	
A; R.	A; Residues	Residues: 1-5170 <gat> Cross-reference: FMB: 050071: NID: 01208871: DID: 01208877: DIDN: NANGA47</gat>	47 1. CESD.BO
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A; G A; I1	;Gene: CE; ;Introns:	CESP:B0350.1 is: 48/1; 5039/3; 5116/3	
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TVSAQEDEDIEA	SI		0 78
VTREYFDEHEPLVSQEI SPENAT-SRGNTEPAVE             EQEPTTVSREVYETAEG TYPAEDESVE TTTMTSREYDDNDDETRATKADSVDV : :     EEDNVSEYSESSTSVSR AQRPEPQSDNDSSATCS   :     : FSQEHQDDDSQASPNPLDLPQLQHPNPLDLPQLQHPNPLDLPQLQHPNPLDLPQLQHPNPLDLPQLQHEQRQRQEG	ä – ë		io (
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ΟY	983	GTSKSPNREWEVLQPAPHQLITNLPEGV
qq	1867	TQSEERRSSIPTEETEHEDSHLIKETTTTTTVTREFYDEPENVEK 1911
Øχ	1040	FIMGGSISQGTPGTYLTSHNQAS-YTQETPKPSVGSISLGLPRQQESAK 109
qq	1912	LQDSQFSLSPSVAKQQEIPQ 1944
QY	60	15
g ·	e# 1	L 4
yo, da	1152	KISVESIPSLAGSITQGTPALPQTGIPTEAL-VKGSISRMPIEDSSPEKGREEAASKGHV 1210  S-KVIGFAKKAGWVAGGVVAAP-VALAAVARAAYDAIKKEDD-EEDOBERESL. 2045
ò	1211	127
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ογ	1271	GLICRALPRGSPHSDLKERTVLSGSIMQCTPRATTESFEDGLKYPKQIKRESPPIRAF 1328
QO	2081	HDQSSALPQESVSQPIEKESRTFNDESEFGVKSDHYTEDDQESLKSPKE 2129
QY	1329	EGAITKGRPYDGITTIKEMGRSIHEIPRQDILTQESRKTPEVVQSTRPIIE 1379
qq	2130	SGEAFSQFTSEKEQDRSDSPIHS-QKEDISQFQNESSPEDVKSEQPHDEEKPDLE 2183
Qy	1380	GQSAIKHNVKS
qq	2184	ROGSYSSGYSPKSPGGSITGLDEEKALSGVQEPEDRPENFAESHEKTE 2231
δy	1428	KVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTS 1480
ΟD	2232	ATSDENLFESDKYAPASPVPSEDSSNRVIETTTTTTTTTYTREHFEPEDDHS 2280
οy	1481	ARRIPVSYQNTMSRGSPMMNRTSDVTIPPNKSTNHERKSTLTPT-QRESIPAKSPVPGVD 1539
QQ	2281	YVVESQEYSSGSPVPSEKSVDRVIETTTTTTTTTTTTT- 2327
Qy	1540	PVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPS 1599
qq	2328	VESSHSPVPSEED 2345
Qy	1600	NLRPDVARGL
qq	2346	VHEQIQITITITITITITITISEHFVPDDEIDSEHMNESDKYASGSPVPSEEDSS 2394
οy	1654	IPGTQITEPPRPY
qa	2395	RVTETITITITITIEHFEPEDDHSPVVQTQEYSASESPVPSE 2435
ΟŶ	1710	EREKERERERIAAASSDLYI
qq	2436	TTVTREHE
οy	1746	GERPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTN 1779
qq	2493	PIQAYKQEESQEAF
QY	1780	GTSVITPLDPTAQLRIMPLPAG-GPSISQ
ΩD	2553	SDRAPLL
Qy	1808	GLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAVSEQQ 1864
qq	2613	KKAGMVAGGVVAAPVALAAVGAKAAYDALKKDDDEDENPDEQEKLLPKSPERQ 2665
Qy	1865	QLEQKTLEVEKRSVQCLYISSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELR 1920

	QY 347 PEIRKQREQQE-REQRVGQRGAGLSATIARSEHEISEIIDGL 387			Qy 448 FKDKFIQHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYKALV 491	QY 492 RRNYGKRRGRNQQIARPSQEEKVEEKEEDKAEKKEEEKKDEEEKDE540 :	QY 541KEDSKENTKEKDKIDGTAEETEEREQATPRGRKTANSGGRRKGRITR 587	OY 588	QY 603ATEEPPPPLPPPPPISTEPVETSRWTEEEMEVAKKGL-VEHGRNWAAIAKMYGT 656	QY 657 KSEAQCKNEYENYKRRHNLDNLLQQHKQKTSRKPREERDVSQCESVASTVSAQE 710	QY 711 DEDIEASNEEENPEDSEVEAVKPSEDSPENATSRGNTEPAVELEPTTETAPSTSPS 766  1397 SRSIASSVOSEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTPPPPPQTVQAKREVPK 1453	Qy 767 LAVPSTKPAEDESVETQVNDSISAETAEQMDVDQQEHSAEEGSVCDP 813	Qy 814 PPATKADSVDVEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRP 871		QY 922 PNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTPVSGYAL 959	QY 960	Db 1665 NELATGDGVRAGIQSGEFEKRDTIPTEGRSTDDAQKGKISSIVTPDLDDNKAEEGDILAE 1724  Qy 987 CRSSTSPCGTSKSPNREWEVLQPAPHQLITNLPEGVRLPTTRPTRPPPPLIPSSKTTVAS 1046		QY 1047 EKPSFIMGGSISQGTPGTYLTSHNQASYTQETPKPSVGSIS 1087 : :     : :     :     :     :     : Db 1785 TRVRKNTDSKVNVNTEETFSDNKDSKKPSLQTNAKAFNEKLPNNEDRVRGTFA 1837	QY 1088 LGLPRQQESAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVRGTAGAIQEGSIT-R 1146	QY 1147 GTPTSKISVESIPSLRGSITQGTPALPQTGIPT-EALVKGSIS 1188
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ολ	1189	RMPI	61
qq	1956		15
δγ	1220		28
ପ୍ର	2016	TPVCFSRNSSLSSLSIDSEDDLLQECISSAMPKKKRPSRLKSESEKQSPRKVGGILAEDL	7.5
g 2	1259	SMRESYSAPLEGLICRALPRGSPHSDLKERTVLGGSIMQGTPRATTESFEDGLKYPKOI 1311	81
ογ	1319		8.
Q	2129	SSDSDSILSLKSGISLGSPF	7.1
Oy Db	1379		34
δ	1435		94
g	2229		32
οy	1495	GSPMMNRTSDVIIPPNKSTNHERKSTLTPTQRESIPAKSPVPGVDPVVSHSPFDPHHR	52
g	2283		33
oy D	1553	GSTAGEVYWSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQT 161.	12
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g g	1613 2383	ILNDYITSQQMQVNLRPDVARGLSPREQPLGLPYPATRGIIDLINMPPTILVPHPGGTST 167:	72 13
ò.	1673	PPMDRITYIPGTOITFPPRPYNSASMSPGHPTHLAAAASAEREREREREKERERERIA : : : : : : : : : : : : : : : : : : :	30
g	2414	VELSRMS	57
δ	1731	AASSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITP-L::	37
q	2458	ESASFESLSPSSRPDSPTRSQAQTPVLSPSLPDMSLSTHPSVQAGGWRKLPPNL 2511	=
Š ć	1788	DPTAQLRIMPLPAGGPSISQGLPASRYNTAADALAALVDAAASAPQMDVSKTKES	12
Q C	7157	SPTIEINDGRPTKRHDIARSHSESPSKLPINRAGTWKREHS	2
8 6	1843	KHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSV	86
g	2553	KHSSSLPRVSTWRRTGSSSSILSASSESSEKAKSEDERHVSSM	35
ò	1899	VYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVIITRQIASDKDARERGSQSSDSS	. 86
qq	2596	PAPRQMKENQVPTKGTWRKIKESDISPTGMASQSAS 2631	31
ò	1959	SSLSSHRYETPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGPLHHYR	81
2	7607	SCAASCAESAFLIKUMAFFVSATEDVWVKLEDCFINNFR	2
δ d	2019	PQOESPSPQOUPPSQAEGMGQVPRTHRLITLADHI	55 5
9	7/97	SGKSPTGNTPPVLDSVSEKGSSSTKDSKDSKDTHGKQSVGSGSPVQTVGLETRLNSF	
ΟŽ	2056	CQIITQDFARNQVSSQTPQQPPTSTFQNSPSALVSTFKTSNRYSPESQAGSVHHQ	13
QQ	2728		73
y g	2114	RPGSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEPIS-PPQVPVVHEKQDSLLLL 2168 [1]	58
3 8	2169	SCROREDEDECTORIO NESTANOS DE LA CONTROLE DE LA COLONIA DEL COLONIA D	<b>*</b>
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Cyacession: T51023
Ryschulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu submitted to the Protein Sequence Database, July 2000
A; Reference number: 225286
A; Accession: T51023
A; Accession: T51023
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-2649 <SCH>A; Cross-references: EMBL: AL389901; GSPDB: GN00116; NCSP: B7F21.40
A; Cross-references: BAC clone B7F21; strain OR74A
A; Genetics:
A; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85;
                                                                                                                                                                                       C.Species: Neurospora crassa
C.Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|:| : :: || : |||: |||: 964 ERQLLAIPTVEEN-EETSFLRPEPQPKMEEMDTGGSGLPPLPTVEEHKVVDQDVDWVDVD 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1083 SGSVEHVRELSTIPPIDELPVFN----VKPWHQSSKVRKLSEQSPGFGAFFMGNIRDMAE 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1185 SGGKGHSGSDNHGKEGGRRTTSRFSTELDVEYAIQESIREAQEKKEREERAQREKYRTDK 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1305 KOWGKIAHELPNRDFHSVIQYYYAKKRELNLKERLKKOPRRRKKGRGKGKYNALVSELGN 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1139 ETAKEQHEAKQVYRTNYDAYL-------RFTLSDDPTAVKSRNQFSQSDKDKV 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1365 PENETTEDNOENGENSNGRROOPRRAAAPSWGHEATPNADSDGATPSATPGRRRAGTTTE 1424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 RPQERRTSYEPFHPGPSPVDHDSLESKRPRLEQVSDSHFQRVSAAVLPLVHPLPEGL-RA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 SADAKKDPAFGGKHEAPSSPISGQPCGDDQNASPSKLSKEELIQ----SMDRVDREIAKV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           909 QPQPQPQP-----QPQPQAQAQAQAQPQLLTEAEPKSVTEPEREREVEQEAETQEQAPT 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 EQQILKLKKKQQQLEEEAAKPPEPEKPVS------PPPPVEQKHRSIVQII----- 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255 EG------LGPKVELPLYNQPSDTKVYHENIKTNQVMRKK--LILFF-----KRR 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          354 -----EQQERFQRVGQRGAGLSATIARSEHEISEII-DGLSEQENNEKQMRQL---- 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----YDENRKKAEEAHKIF 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 457 KNFGLIASYLERKSVPDCVLYYYLTKKNENYKALVR---RNYGKRRGRNQQIARPSQEEK 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 PPHSVQYTFPNTRHQQEFAVPDYRSSHLEVSQASQLLQQQQQQQLRRRPSLLSEFHPGSD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297 NHARKQREQKICQR--YDQLMEAWEKKVDRIENNPRRKAKESKTREYYEKQFPEIRKQR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       401 -SVIPPMMF-DAEQRRVKFINMNGL--MEDPMKVYKDRQFMNVWTDHEKEIFKDKFIQHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VE-EKEEDKAEKTEKKEEEKKDEEEKDEKEDSKENTKEKDKIDGTAEETEEREQA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.4%; Score 429; DB 2; Length 2649; Best Local Similarity 18.0%; Pred. No. 5e-09; Matches 404; Conservative 267; Mismatches 873; Indels 698;
                                                                                                                                                          hypothetical protein B7F21.40 [imported] - Neurospora crassa
2825 TESSGAQSPKRH----SGSYL 2841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 -----
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A; Introns: 1619/3; 2584/1
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Mon Sep 10 08:14:28 2001

TPRGRKTANSQGRR 591 	9 ,	VQNFEWMFFRIFAELSAKVQNFMEDVFFGSMQFFLAFAQQIFLASFEKAFFILASITISE 1544 EPPPPLPPPPEPISTEPVETSRWTEEEMEVAKKGLVEHGRN 646		SEAQC	۰ 🖼	ERDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSEDSPENATSRGNTEPA 750	RYDVPSSSGHRPLAAAEAEEPQPAKSEAAPPANQPFSRFQVTPIQASPVLHTL 1717		VORSPTVMPAPLPPAPVAASASAAPSPQTPSRPGPAVSQTM-SPVPHPLRQPTATFVFT- 1775	QQEHSAEEGSVCDPPPATKADSVDVEVRVPENHASKVEGDNTKERDLDRASEKVEPR 856	-EREGEPIPVSQPPAQTQHQPVRISQKTAPVPSSSMPSASEAM-PR 1819	DEDLVVAQQINAQRPEPQSDNDSSATCSADEDVDGEPERQRMFPMDSKPSLLNPTGSILV 916 :	EANRPTPLLSQQHELR-EVREIREGRERQIRMEPLQPRE 1863	SSPLKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEQ 976	-OPRPMERPAMRFKQEPEOPLHHDPFQNFMPPQRSMQPRAEAAPMGRQ 1910	ROROBOIDLECRSSTSPCGISKSPNREWEVLOPAPHOLIINLPEGVRLPTTRPTRPPPPL 1036	DPPRSMAPSAPQSYTPPIQAQPVRNLLSESVPPQRTPPQL 1950	IPSSKITVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQETPKPSVGSISLGLPRQQES 1096	-AMERP1962	AKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVRGTAGAIQEGSITRGTPTSKISVE 1156	QRPMPTSMQEQYSANTSAAQPVPPPQAPPAIPPEPKKVS 2001	SIPSLRGSITQGTPALPQTGIPTBALVKGSISRMPIEDSSPEKGREBAASKGHVIYEGKS 1216	JONPPAPAPAPKRV-NDVASMPRAASTSTPPPQQMSAR 2045	EGNIK	PPQPPPPTTAVSASQRRDTEALGYSYARNPPSAAQAA 2082	GSPHSDLKERTVLSGSIMQGTPRATIESFEDGLKYPKQIKRESPPIRA 1327	MPSLKPYHTQSPQPPHMNVARSSMGSGMEPQVSAAGDNREFYSRHQYQPQ 2132	FEGAITKGKPYDGITTIKEMGRSIHEIPRQDILTQESRKTPEVVQSTRPIIEGSISQGTP 1387	HQPGASNSPVPHQVHHYSQSAQHPQQHLQQPQMAYPSQQQYQP. 2175	IKFDNNSGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVKAGETVRSR 1447	TSQALAASPTPQYAAHPSSISGRREAQSAREE 2209	VTI 150	~	PPNKSTNHERKSTLTPTQRESIPAKSPVPGVDPVVSHSPFDPHHRGSTAGEVYWS 1562
TTPRG     PKNDSGAEKPEG		VQNFEWMPPAIP!	 VMAPPSLRPEPP	WAAIAKMVGTKS	WSAIANHMGTKT(	ERDVSQCESVAS	RYDVPSSSGHRP	VELEPTTETAP-	VQRSPTVMPAPL	QQEHSAEEGSVCI	EREGEPIPVS	DEDLVVAQQINA( :	SAGWIPEA	SSPLKPNPLDLP	QPRPMERP	RQRQEQIDLECR:	DPPRSMAPSAPQ;	IPSSKTTVASEK	SPAMER	AKSATLPYIKQEI	QRPMPTSMQE	SIPSLRGSITQG	SIFSILNDDNPPAPA	GHILSYDNIKNA	1	LPR	MPSLKPYHTQSP	FEGAITKGKPYDO		IKFDNNSGQSAI	YA	HTSVVSSGPSVL:	wsstoogoaav-	PPNKSTNHERKS
568	2 1	909	1545	647	1605	m	1665	751	1718	800	1776	857	1820	917	1864	211	1911	1037	1951	1097	1963	1157	2002		2046	1277	2083	1328	2133	1388	2176			1508
Oy Dp	ò d	a õ	g	Qy	q	ογ	QQ	Qy	g	οy	q	Qγ	Q	δλ	g	ογ	β	οy	qq	οy	qq	ογ	QQ	δŏ	qq	ογ	οp	οy	С	Οy	Q	δ	a	ò

QΩ	D 2263 -PSKSSQASVPSQTAWAAQHGPNVQAKPPQMGSAMSQQQHSWQ	II : I GSAMSQQQHSWQ 2304
δλ	2y 1563 HLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITSQQ	RQTILNDYITSQQ 1622
qq	OD 2305 ATPTQQPHALGLREPAPRGQAVFSAHEAQSPTGSVVSHQHHRSLDG-	
QY	1623 MQVNLRPDVARGL	PTILVPHPGGTST 1672
qq	OD 2352 SQFPPMPDPRDRQNLRRGEPVPPQGQPYVRYVNIPG	3PGHGGPGG 2395
οy	1673 PPMD 	
QQ	OD 2396 PPGOVPGRGEAPADLRMQOMSQARSYTPGPVGAGFEGMGPPPSSSLGYPEQIRDAQ	SSLGYPEQIRDAQ 2451
δō.	1720 REKERERERIAAASSDLY	17
QQ Q	2452	
δλ	1778 TNGTSVITPLDPTAQLRIMPLPAGGPS	-
q	Ob 2493QHAAQFQAQQQHGVPAN	AAHPQHIQV 2518
۲۵ و	2y 1838 KTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSS 2y 1838 KTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSS 3y 1838 KTKESKHEAARLEENLRSRSAAVSEQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSS 3y 1838 KTKESKHEAARLEENLRSRSAAVSEQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSS 3y 1838 KTKESKHEAARLEENLRSRSAAVSEQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSS 3y 1838 KTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSS 3y 1838 KTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	SAFPSGKPQPHSS 1897 ::        :: 0100VVD0HHOG 2561
3 8	ACHT KOM KKIKHIKA	1 .
g 5	27 1896 VVISEAGKUKGPPREKKIEEELKIRGKITITAANLUVIITUQIADUKDAKEKGSQSSUS 25 2562 GMMARQLRPQHQYDQQGHGPGPANVMGADTIALATLRKGNTDGIFTSNKRHGQDG	CDAREKGSQSSUS 1957   SIFTSNKRHGQDG 2616
οy	2y 1958 SSSLSSHRYETPSDAIEVISPA 1979	
qq	:	
RESU B486 Cell	RESULT 12 B48666 cell proliferation antigen Ki-67, short form - human C. Species: Homo sapiens (man)	
C; Da	.May-1994	#text_change 07-May-1999
C; Ac R; Sc	C;Accession: B48666 S;Schlueter, C.; Decker, M.; Wohlenberg, C.; Becker, M.F	M.H.G.; Key, G.; Flad, H.D.; Ge
A;Ti	l antigen of	antibody Ki-67: a very large, u
ins. A;Re A;Ac A;St		
A; Mo A; Re	A:Molecule type: mRNA A:Residues: 1-2897 <sch></sch>	
A; Cr	A.Cross-references: EMBL:X65551 S.Superfamily: kinase interaction domain homology	
C; Ke F; 29	C;Keywords: alternative splicing; cell cycle control; nucleu F;29-91/Domain: kinase interaction domain homology <kih></kih>	leus; tandem repeat
On Be Ma	Query Match 3.3%; Score 415; DB 2; Length Best Local Similarity 18.3%; Pred. No. 2e-08; Matches 527; Conservative 368; Mismatches 1099; Inde	ngth 2897; Indels 882; Gaps 129;
QY	19 RYPPHSVQYT	JOGQQQQDERRRP 69
QQ	D 96 RYENESLQNGRKSTEFPRKIREQEPARRVSRSSFSSDPDEKAQDSKAYSKITEGKVSGNP	: :::   !SKITEGKVSGNP 155
οy	2y 70 SLLSEFHPGSDRPQERRTSYEPFHPGPSPVDHDSL2y	-ESKRPRLEQVSD 116
qq	OD 156 ELFDENLPPNTPLKRGEAPTKRKSLVMHTPPVLKKIIKEQPQPSGKQESG	KEQPQPSGKQESG 205
QY	2y 117 SHFQ-RVSAAVLPLVHPLPEGLRASADAKKDPAFGGKHEAPSSPISGQPCGD-	SSPISGOPCGD- 167
qq	DD 206 SEIHVEVKAQSLVISPPAPSPRKTPVASDQRRRSCKTAPASSSKSQTEVPKRGGERVATC	: svpkrggervatc 265

δ	168	-DQNASPSKLSKEELIQSMDRVDRE1AKVEQQILKLKKKQQQ 208
qq	266	LQKRVSISR-SQHDILQMICSKRRSGASEANLIVAKSWAD
δλ	209	-LEEEAAKPPEPEKPVSPPPVEQKHRSIVQIIYD 241
qq	325	SMNKRQRRPATPKKPVGEVHSQFSTGHANSPCTIIIGKAHTEKVHVPARPYRVLNNFISN 384
ΟY	242	ENRKKAEEAHKIFEGLGPKVELPLYNOPSDTKVYHENIKTNOVMRKKLI 290
g	385	QKMDFKEDLSGIAEMFKTPVKEQPQLTSTCHIAISNSENLIGKQFQGTDSGEEPLL 440
ΟŻ	291	EFEKRNHARKQREQKICQRYDQLMEAWEKKVDRIENNPRRKAKESK 337
qq	441	PTSESFGGNVFFSAQN-AAKQPSDK-CSASPPLRRQCIRENGNVAKTPRNTYKMTSLETK 498
٥ý	338	
qq	499	TSDTETEPSKTVSTVNRSGRSTEFR
οχ	395	KQMRQLSVIPPMMFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHEKEIF 448
qq	544	CILKRGQKATLLQQRREGEMKEIERPFETYKENIELKENDE 584
ογ	449	
q	585	KMKAMKRSRTWGGKCAPMSDLTDLKSLPDTELMKDTARGON 625
ογ	505	IARPSQEEKVEEKE
QQ	626	L.C. TO THE TELETICATION OF THE TRANSPORT OF THE TRANSPOR
οy	544	SKENTKEKDKIDGTAEETEEREQATPRGRKTANSQGRR 581
QQ	989	TRISGETTHTHREPAGDGKSIRTFKESPRQILDPAARVTGMKKWPRTPKEEAQSLEDLAG 745
ογ	583	KGRITRSMTNEAAAASAAAAATEEPPP
QQ	746	FKELFQTPGPSEESMTDEKTTKIACKSPPPESVDT-PTSTKQWPKRSLR 793
Qy	629	
qq	794	:
οy	989	
qq	852	-
οy	737	
QQ	606	RPKRSIRKADVEGELLACRNLAPSAGKAMHTPKPSVGEEKDIIIFVGTPVQKLDLTEN 966
δy	789	
Q	196	LTGSKRRPQTPKEEAQALEDLTGFKELFQTPGHTEEAVAAGKTTKMPCESSPPESADTPT 1026
οy	824	VEVRVPEABEKVEPR 856
QQ	1027	STRROPKIPLEKRDVQKELSALKKLTQTSGETTHIDKVPGGEDKSINAFRETAKQKLDP- 1085
οy	857	DEDLYVAQQINAQRPEPQSDNDSSATGSADEDVDGEPERQRMFPMDSKPSLLNPTGSILV 916
g	1086	AASVTGSKRHPKTKEKAQPLEDLAGWKELFQTPVCTDKPTTHEKTTKIAC 1135
ογ	917	SSPLKPNPLDLPQLQH
QQ	1136	RSQPDPVDTPTSSKPQSKRSLRKVDVEEEFFALRKRTPSAG
οy	950	IGTPVSGYALYQRHIKAMHESAL
QQ	, 1194	AFMGTPVQKLDLTENLTGSKRRLQTPKEKAQALEDLAGFKELFQTRGHTEESMTNDKTAK 1253
Qy	985	LECRSSTSPCGTSKS 999

1594 TPGYPSO--YQLYAMENTRQT-ILNDYITSQQMQVNLRPDVARGLSPREQPLGLPY---- 1646 : |:|| 1254 VACKSSQPDLDKNPASSKRRLKTSLGKVGVKEELLAVGKLTQTSGETTHTHTEPTGDGKS 1313 1447 ----LDQPGNLP-----GSNRRL------OTRKEKAQ-------ALEELT 1474 1380 GSISQGTPIKFDNNSGQ----SAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVERGKY 1435 1436 EDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSAR--RTPVSYQNTMS 1493 --RGSPMMNRTSDVTIPPNKSTNHERKSTLTPTQRESIPAKSPVP-GVDPVVS--HSPFD 1548 1824 TPKGKAQPLEDLAGLKELFQTPVCTDKPTTHEKTTKI---ACR--SPQPDPVGTPTIFKP 1878 : | : | : | 1879 QSKRSLRKADVEEESLALRKRIPSVGKAMDTPKPAGGDEKDMKAFMGTPVQKLDLP---- 1934 ---GNLPG------SKRWPQTPKEKAQALEDL-AGFKELFQTPGTDKPTTDEKTTK 1980 1754 V--RSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIM--PLPAGGPSISQGL 1809 1981 IACKSPQPDPVDTPASTKQRPK-----RNLRRADVEEEFLALRKRTPSAGKAMDTPK 2032 1861 SEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHS-SVVYSEAGKDKGPPPKSRYEEE- 1918 2091 TEESMIDDKITEVSCKS-------PQPESFKTSRSSKQRLKIPLVKVDMKEEP 2136 -----LRTRGKTTITAANFIDVIITRQIASDKDARERGSQSSDSSSSLSSHR----- 1965 PNREWEVLQPAPHQLI ---TNLPEGVRLPTTRPTRPPPPLIPSSKTTVASEKPSFIMGGS 1056 ----MKAFMESPKQILDSAASLTGSKRQLRT-----PKGKSEVPEDLAGFI---E 1356 ISQGTPGTYLTSHNQASYTQE-TPKPS-----VGSISLGLPRQQESAKSATLPYIKQ 1107 LFQ-TP----SHTKESMTNEKTTKVSYRASQPDLVDTPTSSKPQPKRSLRKAD----TE 1406 EEFSPRSQNSQPEGLLVRAQHEGVVRGTAGAIQEGSITRGTPTSKISVESIPSLRGSITQ 1167 1168 GTPALPQTG-IPTEALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIK 1226 1227 NAREGTRSPRIAHEISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGS---PH 1283 1334 ------KGKPYDGITTIKEMGRS---IHEIPRQDILIQESRKTPEVVQSTRPIIE 1379 ---TSGKTTQT-HRETAGDGKSI--KAFKESAKQMLDPANYGTGMERWPRTPKEEAQSLE 1715 1716 DLAGEKELFQTPD------HTEEST-TDDKTTKIACKSPPPESMDTPTSTRRPKT 1764 1549 PHHRGSTAGEV-----YWSHLPTQLDPAMPFHR----ALDPAAAYLFQRQLSP 1593 1647 PATRGI-----IDLINMPPTI----LVPHPGGTSTPPMDRITYIPGTQITFPPRPY 1693 1694 NSASMSPGHPTHLAAAASAEREREREREKERERERIAAASSDLYLRPGSEQPGRPGSHGY 1753 PA----SRYNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRS-----RSAAV 1860 PAVSDEKNINTEVETPVQKLDLLGNLP--GSKRQPQTPKEKAEALEDLVGFKELFQTPGH 2090 1284 SDLKERTVLSGSIMQGTPRATTESFEDGLKYPKQIKRESPPIRAFEGAIT------1577 GSKRRPQTPKEKAKALEDLAGFKELFQTPGHTEESMTDDKITEVSCKSP---1000 1357 1108 1407 1520 1662 1494 1935 2033 1919 1057 1810 1314 qq QQ 셤 qq QΥ Q Ω g ŏ Db δý g δý ద δ ద δ QQ Qγ qq ò qq δ Q δ g 셤 8 οŽ ŏ δ δ à ò

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R;Chan, W.; Kordeli, E.; Bennett, V.
J. Cell Biol. 123, 1463-1473, 1993
A:Title: 440-kD ankyrinB: structure of the major developmentally regulated domain and
A;Reference number: A49462; MUID:94075409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1793 KTERHST------PSAKT 1830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1873 PSGKIDKRPPVSPSGRT-----EKHPPVSPGRTEKRLPV--SPSGRIDKHQ 1916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2035 VRVSSIGVKKEDAAGGKEKVLSHKIPEPVQSVPEEESHR-------ESEVPKE 2080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1917 PVSTAGKTEKHLPVSPSGKTEKQPPVSPTSKTERIEETMSVR--ELMKAFQSGQDPSKHK 1974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1975 TGLFEHKSAKQKQPQEKGKVRVEKEKGPILTQREAQKTENQTIKRGORLPVTGTAESKRG 2034
                                                                                                                                                                                                                                                                                                                                          :Cross-references: EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQQQQQQLRRRPSLLSEFHPGSDRPQERRTSYEPFHPGPSPVDHDSLESKR-----P 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RLEQVSDSHFQRVSAAVLPLVHPLPEGLRASADAKKDPAFGGKHEAPS-SPISGQPCGDD 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QNASP----SKLSKEELIQSMDRVDREIAKVEQQILKLKKKQQQLEEEAAKPPEPEKPVS 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-----PPVEQKHRSIVQIIYDENRKKAEEAHKIFEGLGPKVELPLYNQPSDTKVYHE 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    278 NIKTNQVMRKKLILFFKRRNHAR-----KQREQKICQRYDQLMEAWEKKVDRIEN- 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGLSATIARSE------HEISEIIDGLSEQENNEKQMRQLSVIPPMMFDAEQRRV 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 4q25-4q27
(Superfamily: ankyrin; ankyrin repeat homology
C;Keywords: alternative splicing
C;Keywords: alternative splicing
F;2-3924/Product: ankyrin 2, long form #status predicted <WAZ>
F;2-1443,3585-3924/Product: ankyrin 2, short form #status predicted <WAZ>
F;63-95/Domain: ankyrin repeat homology <a href="https://www.naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.com/naid.co
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18.7%; Pred. No. 3.9e-08;
tive 357; Mismatches 946;
                                                                                                                                                                                                                Status: preliminary; nucleic acid sequence not shown; Molecule type: mRNA
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F;793-825/Domain: ankyrin repeat homology
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Matches 493; Conserv
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A;Title: Isolation and chromosomal localization of a novel nonerythroid ankyrin gene. A;Reference number: A40334; MUID:92009921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N;Alternate names: ankyrin B, 440K splice form; ankyrin-B; brain ankyrin; non-erythroid N;Contains: ankyrin 2, short form
2137 LAVSKLTRTSGETTQTHTE----PTGDSKSIKAFKESPKQILDPAASVTGSRRQLRTRK 2191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERSHVSSEPYEPISPPQVPVVHEKQDSLLLLSQRGAEPAEQRNDARSPGSISYLPSFFTK 2197
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C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 13-Aug-1999
C:Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2241 --VTTSGSVSSRGHSFADPASNLGLEDIIRKALMGSFDDKVEDHGVVMSQPMGVVPGTAN 2298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2532 RNVDAEDVIGSRRQPRAPKEKAQPLED-----LASFQE-----LSQTPGHTEELAN 2577
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A.Status: mRNA
A.Molecule type: mRNA
A.Residues: 1-3924 <CHA>
A.CCHA>
A.CCOSS-references: EMBL:226634; NID:g406287; PIDN:CAA81387.1; PID:g406288
EMBL:226634; NID:g406287; PIDN:CAA81387.1; PID:g406288
T.Stotto, E.; Kunimoto, M.; McLaughlin, T.; Bennett, V.
J. Cell Biol. 114, 241-253, 1991
A.Title: Isolation and characterization of cDNAs encoding human brain ankyz
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A;Residues: 463-474,'PE',477-495 <TSE>
A;Cross-references: GB:M37123; NID:g178647; PIDN:AAA62828.1; PID:g178648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2578 GAADSFTSAPKQTPDSGKPLKISRRVLRAPKVEPVGDVVSTRDPVKSQSKSNTSLP 2633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---TSVVTSGETRREEGDPSPHSGGVCK-PKLISKSNSRKSKSPIPGQGYLGTERP 2350
                                                                                                                                                                                                                                                                                                       ESKEELSAVERLTQTSGQSTHTHKEPASGDEGIKVLKQRAKKKPNPVEEEPSRRRPRAPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKAQPLEDLAGFTELSETSGHTQESLTAGKATKIPCESPPLEVVDTTASTKRHLRTRVQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKARALEDLVDFKELFSAPGHTEESMTIDKNTKIPCKSPPPELTDTATSTKRCPKTRPRK
                                                                                                                                                                                                                                                       ----HHYRPQQESPSPQQQLPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --FQNSPSALVSTPVRTKTSNR-YSPESQAQSVHHQRPGSRVSPENLVDKSRGSRPGKSP
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                                                                                                                                                                                                                                                                                                                                                                                                                    SQAEGMGQVPRTHRLITLADHICQIITQDFARNQVSSQTPQQPPTST----
                                                                                  -----PASSPAP----
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A;Reference number: S37431
A;Accession: S37431
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A; Residues: 1-1443,3585-3924 <OTT>
A;Cross-references: EMBL:X56958
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A;Molecule type: mRNA
A;Residues: 1-2077 <0T1>
A;Cross-references: GB:X56957
A;Accession: B39643
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δý	455 HPKN	HPKNFGLIASYLERKSVPDCVLYY-YLTKKNENYKALVRRNYGKRRGRNQQIA 506	
g	2139 SPFN	SPENTIFPLDYMKDEFLPALSLQSGALDGSSESLKNEGVAGSPCGSL 2185	
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<u>Ω</u>		MEGTPQISSEESYKHEGLAETPETSPESLSFSPKKSEEQTGETKESTKTETTTEIRSEKE 2245	
o o	547 NTKE : 2246 HPTT	NTKEKDKIDGTAEETEEREQATPRGRKTANSQGRRKGRITRSMTNEAAAASAAAA 601 :	
ά	602 AATE	AATEEPPPPLPPPPEPISTEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAKMVOTKSEAQ 661	
셤	2302 LAKETP	:	
ΩŸ	662 CKNF	CKNFYENYKRHHIDNILAQUKQKTSRKPREERDVSQCESVASTVSA 708	
q	2338 ESTA	ESTATSDETKALPLPEASVKTDTGTESKPQGVIRSPQGLELALPSRDSEVLSAVADDSLA 2397	
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e e	856 KDED    2565 FDEL	KUEDLYVAQQINAQKPEPQSDNDSSATCSADEDVDGEPEKQKMFPMDSKPSLLNP 910 	
ò	-	TGSITASSPLKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTP 953	
- <sub>4</sub>		: :   : :	
λά	954 VSGY	VSGYALYQRHIKAMHESALLEEQRQRQEQIDLECRSSTSPCGTSKSPNREWEVLQ 1008	
a	2681 VSKQ	VSKQYTFKWNEDTQEEPGKSEEEKDSESHL-AEDRHAVSTEAEDRSYDKLNRDTDQ 2735	
ρλ	1009 P	SSKTTVAS	
q	2736 PKIC	PKICDGHGCEAMSPSSSARPVSSGLQSPTGDDVDEQPVIYKESLALQGTH 2785	
γά		SATLPYIKQEEFSPRSQNS	
g	2786 EKDT	EKDTEGEELDVSRAESPQADCPSESFSSSSSLPHCLVSEGKELDEDI 2832	
λά	1118 QPEG	QPEGLLVRAQHEGVVRGTAGAIQEGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGI 1177	
q	2833	SAISSIQKTEVTKTDETFENLPKDCPSQDSSITTQTDRFSMD 2874	
ρλ	1178 PTEA	EDSSPEKGREEAASKGHVIYEGKSGHILS-	
g	2875	: :	
λά	1236 RTAH :	GNIKQGM	
음	2910 KTQT	KTQTDANHTTSFHSSEVYSVTITSPVEDVVVASSSSGTVLSKESNFEGQDIK 2961	
λά G	1288 ERTV	ERTVLSGSIMQGTPRATTESFEDGLKYPKQIKRESPPIRAFEGAITK-GKPYDGITTIKE 1346 .:   .:	

oy Oy	1347 MGRSIHEIPRQD ILTQESRKTPEVVQSTRPIIEGS-ISQGTPIKFD 1391 ::::
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g &	3078 MTRSGAIDMTKRSYADESFHFFQIGQESREFILSEDVKEGATGADPLPLETSAES 3132 1427 IKVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSAR 1482
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G &	G EIFI AEAVSYO IND 3 SHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYO 1
· qa	210SCPDSSEPAV
Qy	1603 LYAMENTRQTILNDYITSQQMQVNLRPDVARGLSPREQPL-GLPYPATRGI 1652
qa	3223 LDFSTLTRSVYSDRGDDSPDSSPEEQKSVIEIPTAPMENVPFTESKSK 3270
oy (	1653 IDLTNMPPTILVPHPGGTSTPPMDRITYIPGTQITFPPRPRNSASMSPGHPTHLAAAASA 1712
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g d	1/13 EKEREREKEKEKEKERTAAASSDLYLRFGSEQPGRPGSHQFTPLQQNF 1//2 :
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QQ	3328LSDLDTSVQKTVAPQQQDMASIAPDNRSKSESDASSLDSKTKCP 3371
QY	1833 QMDVSKTKESKHEBARLEBNLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKP 1892
qq	3372 VKTRSYT-ETETESRERABELELESEEGATRPKILTSRLPVKSRSTTSSCRGGTSPTKES 3430
Qy	GKDKGPPPKSRYEEELRTRGKTTIT :     :
qq	3431 KEHFFDLYRNSIEFFEEISDEASKLVDRLTQSEREQEI 3468
Qy	QSSDSSSSLSSHRYETPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEG 201
QQ	3469 VSDDESSSALEVSVIENLPPVETEHSVPEDIFDTRPIWDESIETLIERIPDENG 3522
Qy	013 PLHHYRPQOESPSPQOCLPPSSQAEGMGQVPRTHRLITLADHICQIITQDFARNQ 2
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δ, i	/ KSKGSKPGKSPEKSHVSSEPYEPISPPQVPVVHEKQDSLLLLSVKGAEPAECKNDAKSPG
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ΟŊ	2187 SISYLPSFFTKLENTSPWVKSKKQEIFR-KLNSSGGGDSDMAAAQPGTEIFNLPAVTTSG 2245
οp	3627ISHSYAEIEQTITLDHSEGFSVLQEELCTAQHKQKEEQAVSKESETCDHPPIVSEE 3682
ΟŻ	2246 SVSSRGHSFADPASNLGLEDIIRKALMGSFDDKVEDHGVVMSQPMGV- 2292
QQ	3683 DISVGYSTFQDGVPKTEGDSSSTALFPQTHKEQVQQDFSGKMQDLPEESSLEYQQEYFVT 3742
δλ	2293 VPGTANTSVVTSGETRREEGDPSPHSGGVCKPKLISKSNSRKSKSPIPGQGYLGTERPSS 2352
qa	3743 TPGTSTSETQKAMIVPSSPSKTPEE 3767
Qy	2353 VSSVHSEGDYHRQTPGWAWEDRPSSTGSTQFPYNPLIMRMLSSTPPTPIACAPSAVN 2409

OY 600 AAAATEEPPPPLPPPEPISTEPVETSRWTEEEWEVAKKGLVEHGRNWAAIAKWYGTKSE 659  1   1   1   1   1   1   1   1   1   1	521EDFTHPVKGAVAPIYDENYSRDGAIDRFPASTATPVFAQPS 712 EDIEASNEEENPEDSEVEAVKPSEDSPENATSRGNTEPAVELEPTTETAPS 713 EDIEASNEEENPEDSEVEAVKPSEDSPENATSRGNTEPAVELEPTTETAPS 714 EDIEASNEEENPEDSEVEAVKPSEDSPENATSRGNTEPAVELEPTTETAPS 715 EDIEASNEEENPEDSEVEAVKPSEDSPENATSRAPSGNDVDQQEHSAEEGSVCDPPATKA 763 TSPSIAVPSTKPAEDESVETQVNDSISAETAEQMDVDQQEHSAEEGSVCDPPATKA 764 TSPSIAVPSTKPAEDESVETQVNDSISAETAEQMDVDQQEHSAEEGSVCDPPATKA 765 TSPSIAVPSTKPAEDESVETQVNDSISAETAEQMDVDQQEHSAEEGSVCDPPATKA 766 TSPSIAVPSTKPAEDESVETQVNDSISAETAEQMDVDQQEHSAEEGSVCDPPATKA 767 TSPSIAVPSTKPAEDESVETQ	ASEDLNAPSPFIQUEQRYATMPVPINTHVEEPFILSQEELDHIARITAMATE- DSVDVEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDS  :  :     ::     ::     ::     ::       ::	QY 880 SATCSADEDVDGEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVI 937	998 KSPNREWEVLOPAPHOLITNLPEGVRLPTRPTRPPPPLIPSSKTTVASEKPSFIMGGSI :	1058 SQGTPGTYLTSHNQASTTQETPKPSVGSISLGLPRQQESAKSATLPYIKQEE	1110 FSPRSQNSQPEGLLVRAQHEGVVRGTAGAIQEGSITRGTPTSKISVESIPSLRGSITQ	GTPALPQTGIPTEALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIKN	1228 AREGIRSPRIAHEIS-LKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGS	1027 QHHEPTISSAFFGIGEGEKKKYGDDAVEQQKLENYEEEEKTKSSSREAFDGFFT			OY 1392 NNSGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVRAGETVR 1445 :: :    :	QY 1446 SRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRG 1495   1250 PPSSQIPTRSPSVMSSSIMSELPPGLDDLSDDERMKIMAVMAEADMONVRRPIARG 1305	QY 1496 SPMANRTSDVTIPPN
Db 3768 VSTPAEEEKLYLQTPTSSERGGSPIIQEPEEPSEHREESSPRKTSLVIVESADN 3821 Qy 2410 Q 2410 Db 3822 Q 3822	RESULT 14 T25752 hypothetical protein F45E4.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T25752 R;Wilson, R.	submitted to the Emb Date initially, September 1990 A;Description: The sequence of C. elegans cosmid F45E4. A;Description: T2575. A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA	A; Residues: 1-2361 <wil> A; Cross-references: EMBL:U70852; PIDN:AAB09135.1; GSPDB:GN00022; CESP:F45E4.4 A; Experimental source: strain Bristol N2; clone F45E4 C; Genetics: A; Gene: CESP:F45E4.4 A; Map Position: 4 A; Map Position: 4 A; Ill (2): 939/3; 977/2; 998/1; 1021/1; 1125/3; 1140/3; 1157/2; 1173/2; 131</wil>	Query Match 3.2%; Score 409.5; DB 2; Length 2361; Best Local Similarity 18.6%; Pred. No. 2.5e-08; Matches 523; Conservative 374; Mismatches 975; Indels 943; Gaps 138;	QY 79 SDRPQERRTSYEPFHPGPSPVDHDSLESKRPRLEQVSDSHFQRVSAAVLPLVHPLPEG 136                               1   1   1	QY 137 LRASADAKKDPAFGGKHEAPSSPISGQPGGDQNASPSKLSKEELIQSM 185	Qy 186 DRVDREIAKVEQQILKLKKKQQQLEEEAAKPPEPEKP 222	QY 223 VSPPPVEQKHRSIVQIIYDENRKKAEEAHKIFEGLGPKVELPLYNQPSDTKVYHEN 278 :           :       :       :         :         :	Qy 279IKTNQVMRKKLILFEKRNHARQREQKICQRYDQLMEAWEKKVDRIENNP 329  Db 233 GSSAHSQFGFSTPSISGFKIFFDKAKTATETLVKEIKDEVIVEVDKDKTETKP 285	Qy 330 RRKAKESKTREYYEKQFPEIRKOREQQERFQRVGQRGAGLSATIARSEHEISEIID 385	QY 386 GLSEQENNEKQ-MRQLSVIPPMMFDAEQRRVKFINMNGLMEDPMKVYKD 433	QY         434 RQFMNVWTDHEKEIFKDKFIQHPKN-FGLIASYLERKSVPDCVLYYYLTKKNENYKALVR 492           Db         365	SQEEKVEEKEEDKAEKTEKKEEEKDEEEKD   :    :      :    :    :    :    :	540 EKEDSKENTKEKDKIDGTAEETEEREQATPRGRKTANSOGRRKGRITRSMTNEAAAASAA

Oy Db	1528	SIPAKSPVPGVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAM 1572 : :    :   LMPPQQAIPIIPPGLEGLSDEERHTIMSVMAEAEFEESRSQVPSRQPSRSPSFVNPQQ 1422	
oy Db	1573	PEHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITSQQMQVNL 1627	
Oy Dp	1628	RPDVARGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRITYIPGT 1684 ::	
OY Db	1685	QITFPPRPYNSASMSPGHPTHLAAAASAEREREREREKERERERIAAASSDLYL 1738 :	
δγ	1739	RPGSEQPGRPGSHGYNSPSPSVRTQETMLQQRPSVFQGT MPPPLPOMSOPEITTGLEHSSSADMEFGRDSRSHOVIPPIGLENI.SFEROLINGSPROAMAHA	
0.7 Db	1779	NGTSVITPLDPTAQL-RIMPLPAGGPSISQGLPASRYNTAADALAALVDAAASAPQMDVS	
oy B	1838	KTKESKH	
Qy Db	1857	SAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFP	
λ δ	1889	SGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRIRGK	
δ d	1925	TITAANFIDVIITRQIASDKDARERGSQSSDSSSSLSSHRYE     :   :	
7 da	1968	TPSDAIEVISPASPAPPOEKLQTYQPEVVKANQAENDPTRQYEGPL	
Q Q	2015	HHYRPQOESPSPQQQLPPSSQAEGMGQVPRTHRLITLADHICQIITQDFARNQVSSQTPQ 2074 ::	
Oy Dp	2075	VRTKTSNRYSPESQAQSVHQRPGSRVSPENLVDKSRGS :   :         :	
oy Op	2132	RPG-KSPERSHVSSEPYEPISPPQVPVVHEKODSLLLLSQRGAEPAEQRNDARS 2184   :                     :	
oy Oy	2185		
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δŏ	2289	RREEGDPSPHSGGVCKPKLISKSNSRKSKS- ::  : :	
<u>a</u> 8	2212	BOTTDCWAMEDDDSSTCSTOEDY	
B 5	2254	SPR	
٥y	2386	NPLTMRMLSSTPPT	

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Ascession: T30826
A; Status: Differential splicing-in of a proline-rich exon converts alphaNAC into a muse (Species in Museulus (house mouse)
C; Species: Nus musculus (house mouse)
C; Accession: T30826
R; Yotov, W.V.; St-Arnaud, R.
Genes Dev. 10, 1763-1772, 1996
A; Title: Differential splicing-in of a proline-rich exon converts alphaNAC into a mus A; Reference number: Z20889; MUID: 96312450
A; Accession: T30826
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-2187 < x707>
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Map position: 10
A; Introns: 24/1; 1996/1; 2024/3; 2050/3; 2099/3; 2142/3; 2183/3
A; Note: differential splicing; DNA binding; transcription factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PISTE--PVETSRWTEEEMEVAKKGLVEHGRNWAAIAKMVGTKSEAQCKNFYF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -NYKRRHNLDNLLQQHKQKTSRKPREERDVSQ-----C---ESVASTVSAQEDEDIEASN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                719 EEENPEDSE-----VEAVKPSED--SPENATSRGNTEPAVELEPTTETAP----ST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               899
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1066	1159	1212	1272	1332	1389	1440 1325	1496 1368	1550 1426	1610 1443	1667	1716	1764 1610	1822	1880 1710	1940	2000	2060	165/
. :         :       :         :	PYIKOEEFSPRSONSOPEGLLVRAQHEGVVRGTAGAIQEGSITRGTPTSKISVESIP	SLRGSITQGTPALPQTGIPTEALVRGSISRMPIE-DSSPEKGREEAASKGHVIY	EGKSGHILSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPLEGL 	ICRALPRGSPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYPR     :    :	TKGKPYDGITTIKEMGRSIHEIPRQDILTQESRKT 	FDNNSGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVKA   S	GETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGS :  :          : :	PMMNRTSDVTIPPNKSTNHERKSTLTPTQRESIPA	HRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTR	QTILNDYITSQQMQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHP :	GGTSTPPMDRITYIPGTQIJFPPRPYNSASMSPGHPTHLAAAASAERERSTRAPTI		ETML-QORPSVFQGTNGTSVITPLDPTAQLRIMPLPAGGPSISQGLPASRYNTAADALA- 	ALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQC   :   :	LYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVIITRQ:	IASDKDARERGSQSSDSSSLSSHRYETPSDAIEVISPASSPAPPQEKLQTYQPEVVKAN :	QAE	
1017	1103	1160	1213	1273	1333	1390	1441	1497	1551 1427	1611	1668	1717 1551	1765 1611	1823	1881	1941	2001	2061
q	Oy Pp	Oy Dp	ço q	ç Q	oy Dp	oy Ob	Qy Db	O.y	Oy Op	Oy Dp	95 P	. yo	oy Op	oy Op	oy Oy	දු වූ	ે ઉ	3 6

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A;Map position: 2
A;Introns: 36/2; 92/2; 182/2; 272/3; 344/2; 426/2; 490/1; 541/2; 700/3; 770/3; 1286/3
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submitted to the EMBL Data Library, March 1996
A; Reference number: 220417
A; Accession: T27777
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-272 < WIZ>
A; Cross-references: EMBL: Z69904; PIDN: CAB54502.1; GSPDB: GN00020; CESP: F07A11.6b
A; Experimental source: clone ZK20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-2722 <WIL>
A;Cross-references: EMBL:266511; PIDN:CAB54211.1; GSPDB:GN00020; CESP:F07A11.6b
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                                                                                DMA-----AAQPGTEIFNLPAVT----TSGSVSSRGHSFADPA-SNLGLEDI--- 2266
                                                                                                                                                                                                                                                                     2004 DESVPELEEQDSTQTATQQAQLAAAAEIDEEPVSKAKQSRSEKKARKAMSKLGIRQVTGV 2063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C.Accession: T20532; T27777
                                               2121 PENLVDKSRGSRPGKSPERS-HVSSEPYEPISPPQVPVVHEKQDSLLLLSQRGAEPAEQR 2179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----ASIQTLRH-----QSVMFPPDVSIPPPI--PPTHDEMMAPR 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 VSDSHFQRVSAAVLPLVHPLPEGLRASADAKKDPAFGGKHEAPSSPISGQPCGDDQNA-- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 --SPSKLSKEELIQSMDRVDREIAKVEQQILKLKKKQQQLEEEAAKPPEPEKPVSPPPVE 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 QKHRSIVQIIYDENRKKAEEAHKIFEGLGPKVEL---PLYNQPSDTKVYHENIKTNQVMR 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 SSGYPPNQGAFSTEQSRYPPHSVQYTFPNTRHQQEFAVPDYRSSHLEVSQASQLLQQQQQ 62
                                                                                                                                    N-----DARSPGS----ISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGGG---DS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.2%; Score 405; DB 2; Length 2722; Best Local Similarity 18.1%; Pred. No. 4.4e-08; Matches 442; Conservative 340; Mismatches 823; Indels 836;
1858 VSPAKGSDCLHSPKGPYGSQ-----VATPLAAFTSDKVPPEAVSASV---
                                                                                                                                                                                                                                                                                                                                                     2064 TRVTIRKSKNILF-----VITKP-DVYKSPASDTYIVFGEAKIED 2102
                                                                                                                                                                                                                                                                                                                      2267 ----IRKALMGSFDDKVEDHGVVMSQPMGVVPGTANTSVVTSGETRREE 2311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F07All.6b - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Palmer, S. submitted to the EMBL Data Library, October 1995 A; Reference number: 219287 A; Accession: T20532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: clone F07A11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: CESP: F07A11.6b
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1678 -	1336 K	1719 -	. 1395 G	1759 A	1446 S		1506 T		1563 H		1623 M	1681 I		1716 R	2021 R	1767 M	2077 L	1827 A	2127 P.	1887 F	2159 -	1947 A	2197 -	Z007 T	2232 -	2058 I		2108 Q	2346 S	2161 K	2395 K	2211 E	2450 S	RESULT 17
qq	Qy	qa	QY	QQ	ÓΣ	qq	Qy	QC	δō do	an i	y g	λŏ	' 셤	Qy	qq	QY	qα	δλ	đ	Qy	q	Qy	qО	QY	đ	Οy	Ф	Οy	qa	Qy	ф	QY	QQ	RE
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287 KKLILFFKRRNHARKQREQKICQRYDQLMEAWEKKVDRIENNPRRKAKESKTREYYEKQF 346   1   1   1   1   1   1   1   1   1   1	NGCTTV TOGINAGINISCIAL TOTTEGETGETGETT THE TOTTEGETGETT TOTTEGETGETGETGETGETGETGETGETGETGETGETGETG	941 PSTPVVRDAGSDIVAONASHADANITARSEBELSELLUSESEQENNRAQMAKUSYLPFM 400 941 PSTPVVRDAGSDIVAONASHONNIN	MEDAEORRVKFI NANGLMEDPMKVY KDROFMNVWTDHEKEJ FKDKFJOHPKNEGLI ASYL.		467 ERKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEKVEEKEEDKAEKTE 526	:     :     :     :     :     :     :     :     :     :       :       :	527 KKEEEKKDEEEKDEKEDSKENTKEKDKIDGTAEETEEREQATPRGRKTANSQGRRKGRIT 586	:: :  ::: ::       : :   :   :   :   :	587 RSMINEAAAAAAAAAATEEPPPPPPPPPPPPPTSTEPVETSRWIEEEMEVAKKGL 640	1112 LDVRK	641 VEHGRNWAAIAKMVGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRKPREERDVSQCE 700	1140 IE 1170	SVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSEDSPENATSRGNTEPAVELEPTTETA	IESSDDEGGKDGDKGNSSNGEESDSEKADLPP	761 PSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDVDQQEH 803	**************************************	004SAEEGSVCLPFFRAIANSVDVEVKYFENHASKVEGUNIKEKULDKASERVEFKUEDL 800 1263 AXSSDEGGEFKRVPRKRKEDSEDAAKHFGWSAKD-DOKOKRKEEHR 1310	VVAQQINAQRPEPQSDNDSSATCSADEDVDGEPERQRMFPMDSKPSLLNPTGSI	1311RSSEDESKKNAKRDFRDIPHEDVSDEEFTEDGSRSRRQSTSST 1353	NIPIGTPVSGYALY	:::   ::   ::   ::   :: : : : : : : : :	OBUTYANDEATT BEODODODOT DE BOOGCHES CONDENDATO ON THAIT DE	CONTINUATE STATES OF THE CONTINUATE STATES OF	1021 GVRLPTTRPTRPPPPLIPSSKTTVAS-EKPSFIMGGSIS 1058	:     : 1443KPLSPPVTAKSSVSSIDDPSIRDEFSMNSAADSPMSTIGRPWVLTKAAM 1491	1059QGTPGTYLTSHNQASYTQETPKPSVGSISLGLPRQQESAKSATLPYI 1105		1106 KOEEPSPRSONSOPECLLVRACHEGVVRGTACAIOEGSTTRGTPTSKISVEST 1158	ASDNGSPENVVVETPSIVSOTPREPETISEOSSESE	PSLRGS1TOGTPALPOTGIPTEALVKGSISRMP1E-DSSPEKGREFAASKCHVIYEGKSG	PEAVPECPEASVEPQMETSQNVEPVSEEHEDSHEHGDSEVAVES	HILSYDNIKNAREGIRSPETAHEISLKRSYESVEGNIKOGMSWRESPVSAPIEGLICRAL	OQQPLEHQEEKEELENKILDVAAEHHEEQVQGDEDSVESSIPAPSD	1278 PRGSPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYPKQIKRESPPIRAFEGAITKG 1335
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Db	1678	-
οy	1336	MGRSIHEIPRQDILTQESRKTPEVVQSTRPIIEGSISQGTPIKFD-N
qq	1719	NEKTDLLFSPSS
ογ	1395	HAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVKAGETVR 144
QQ	1759	SELVVMEKEVPMEQVIAQEVHVPSEPSPMEEEV
οy	1446	SVLRSTLHEAPKAQLSPGIYDDTSARRIPVSYQNTMSRGSPMMNRTSDV 150 :  : : :  : : :  :
qq	1811	LETSPVPKEEPIKMEESPEGTPTPDLISNNESQDTPGAVNNHLHE 1855
ΟŊ	1506	TIPPNKSTNHERKSTLIPTQRESIPAKSPVPGVDPVVSHSPFDPHHRGSTAGEVYWS 1562
QQ	1856	NHDAVQTPIQLQPASQHQVAQPSPRPAVAPDSQQNGPV 1893
δλ	1563	YPSQYQLYAMENTRQTILNDYITS
QQ	1894	LVSQQSQPSPMSSQQSDMAQNLILSSK 1920
δ	1623	LPYPATRGI
qq	1921	-DINDLAAKLHKNPEALAQATRGDCSGIFQHLLLHAQGNGQNMTPEMLQL 1969
δλ	1681	IPGTQITFPPRPYNSASMSPGHPTHLAA
QQ	1970	KAAFFAQQGENEANQMMQAKMKQQTINKDRIKEQERVKRMYEENERKVEED 2020
QY	1716	REREREKERERERIAAASSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQET 1766
QQ	2021	REKEKORKEEEERQRLAAAATMATQKAAEALKQKQEVPRHGFQHVLSMMTPEARS 2076
δλ	1767	
ΟD	2077	LYEQFPGLSSYINRDSIGAINGVLHLPTQSIQRPSSTASTSSNPPKAPLQ 2126
δλ	1827	SKTKESKHEAARLEENLRSRSAAVSEQQQLEQKT
qq	2127	PSASVNQNTIDPAEIEEIRVQRWFYKPLKMSA- 2158
Qy	1887	FPSGRPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVIITRQIASDKD 1946
qq	2159	EEAATVMAVASSDPNPPATSTVDLAAMLQQLQAAQAA 2196
δλ	1947	ARERGSQSSDSSSSLSSHRYETPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQAENDP 2006
QQ	2197	: :   :
οy	2007	TROYEGPLHHYRPQQESPSPQQQLPPSSQAEGMGQVPRTHRLITLADHICQ 2057
qq	2232	GALNPLSMLALTSSLNQSSPVYQGIARVLLTMNMGQMLATHQTSELLATMNQQET 2286
οy	2058	IITQDFARNQVSSQTPQQPPISTFQNSPSALVSTPVRTKTSNRYSPESQA 2107
QQ	2287	III : III : III : III I I I I I I I I I
οy	2108	OSVHHQRPGSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVHE 2160
qq	2346	SCPLHAMIGGGQQPPPPQQPMQAVAPAPPRSP-SPPRKSMFENLPPEMKE 2394
δλ	2161	KQDSLLLLSQRGAEPAEQRNDARSPGSISYLPSFFTKLENTSPMVKSKKQ 2210
QQ	2395	KNEMERKEILRRLDIILLEELGAEDEEDGKPDLKQIPTSEEDTDDSKADSMGAEG 2449
δλ	2211	EIFNI
QQ	2450	SAFREILSRSTMGNNSGSPSASGTTSPSTSSSISS 2485

Oy 632 EMEVAKKGLVEHGRNWAAIAKWGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRKPR   1119 LRQAAE	Otransmitte  Qy 913 SILVSSPLK	Db 1415 PSTSTIHSYGQPPTTANYGSQTEELPHAPSGPPGSGRAPREKPLSGGDSEVGAPQ Qy 1030TRPPPPDLIPSSKTTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQETPKP	Db 1570 SQTRMVHASASTSPLCSPTDSQPTSHSYSQTTPP	Db 1717 LVINLNAQEQTHTPLATATTVSITWASSVLMAQQKQPVYGDPFQSRLDFGGGSGSPVCL Qy 1316 KQIKRESPPIRA-'FEGAITKGKPYDGITTIKEMGRSIHEIPRQDIL	QY         1389
Hassoon protein - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000 C; Accession: T42730 R; Dieck, S; Sanmarti-Vila, L; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, J. Cell Biol. 142, 499-569; Hugge CAG/Glutamine-repeat protein selectively A; Reference number: 22249; MuID: 98345363 A; Reference number: 222249; MuID: 98345363 A; Retaus: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-3942 CIB> A; Cross-references: EMBL: 17034; NID: 93413809; PIDN: CAA76598.1; PID: 93413810 A; Expérimental source: strain 129 SVJ A; Map position: 9F1 A; Introns: 72/2; 208/3; 505/3; 675/3; 2889/3; 3582/1; 3851/3; 3886/1; 3930/1 A; Note to bassoon	A; Description: may be involved in cytomatrix organization at the site of neural bases component of the presynaptic cytoskeleton C; Keywords: coiled coil; zinc finger C; Keywords: coiled coil; zinc finger Query Match 3.2%; Score 405; DB 2; Length 3942; Best Local Similarity 18.8%; Pred. No. 7.1e-08; Matches 569; Conservative 328; Mismatches 1070; Indels 1060; Gaps 13 Qy 52 QASQLLQQQQQQUERRPSLLSEFHPGSDRPQERRTSY-EPFHPGPSPVDHDSLESKRPR 110		228 VEOKHHSIVQIIXDENRKKABERKIREGIGPKVELPLYNQPTOTRYFENI   1   1   1   1   1   1   1   1   1	OY 364 QRCAGLSATIARSEHEISEIIDGLSEQENNEKQMRQLSVIPPMMFDA 410  BY VSGRGLAKHSAQKASARPRPESSQEPKRLPHNATTGYEELLSEAGPAEPTDS 930  QY 411 EQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHEKEIFKDKFI 453  DD 931 SGALQGGLRFKTIELNSTGSYGHELDLGGGPDPNLDREPELEMESLT 978  QY 454 QHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEK 513  DD 979 GSPED	514 VEEKEDRAEKTEKKEEEKKDEEKDEKEDSKENTKEKDKIDGTAEETEEREGATPRG  1035 ARHSHGPLLPTIEDSSEEEELREEEELLREGEKMREVBQQRIRSTARKTRRD  572 RKTANSQGREKGRITRSMINEAAASAAAAATEEPPPPLPPPPEPISTEPVETSRWIEE  1088 KEELRAQRRKERSKI

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2016 DSAVDLSSLKHSYSLGFADGRYLGGGLQYGSFTDLRHPTDLLSHPLPLRRYSSVSNIYSD 207	1505 VTIPPNKSTNHERKSTLTPTQRESIPAKSPVPGVDPVVSHSPFDPHHRGSTAGEVY 1560	1561 WSHLPPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMBNTR-QTILND 1616 1	1617 YITSQQMQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTN 1657	1658 MPPTILVPHPGGTSTPPMDRITYIPGTQITFPPRPYNSAS 1697	1698 MS 1712 ::	1713EREREREREREREKERERIAAASSDLYLR 1739	1740 PGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQL 1793 :	1794 RIMPLPAGGPSISQGLPASRYNTAADALAALVDAAASAPQMDVSKTKES 184	1843 KHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHS 189 1	1897SUVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVIITRQIASDKDA 1947	1948 RERGSQSSDSSSIEVISPA- 1979 	1980SSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGPLHHYRP 2019 1:   :     :	2020QQESPSPQQQLPPSSQAEGMG-QVPRTHRLITLADHICQI 2058 2158 IVTPGALGRFEKKKPDPLEIGYQAHLPPESLSQLVSRQPPKSPQVLXSPVSPLSPHRL 2815	2059 ITQDFARNQVSSQTPQQPPTSTFQNSPSALVSTPVRTKTSNRY 2101 :	2102 SPESQAQSVHHQRP-GSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEP 2149   ::	2150ISPPQVPVVH	2191 LPSFFTKLENTSPMVKSKKQEIFRKLNSSGGGDSDMAAAQPGTEIFNLP 2239	2240 AVTISGSVSSRGHSFADPASNLGLEDIIRKALMGSFDDKVEDHGVVMSOPMGVVPGTANT 2299
đ	Qy Db	Oy Op	QY Db	Q. Db	O.Y D.b	Qy Db	Oy Dp	Qy Dp	Qy Db	Qy Db	Oy Dp	Oy Db	Oy Db	QY Db	Oy Db	Qy Db	OY Db	Qγ

C;Accession: A48666
R;Schlueter, C.; Duchrow, M.; Wohlenberg, C.; Becker, M.H.G.; Key, G.; Flad, H.D.; Ge J. Cell Biol. 123, 513-522, 1993
A;Title: The cell proliferation-associated antigen of antibody Ki-67: a very large, u 128; A; Accession: A48666
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-3256 cSCH>
A; Cross-references: EMBL:X65550; NID:g415818; PIDN:CAA46519.1; PID:g415819
C; Superfamily: kinase interaction domain homology
C; Keywords: alternative splicing; cell cycle control; nucleus; tandem repeat
F; 29-91/Domain: kinase interaction domain homology <KIH> cell proliferation antigen Ki-67, long form - human C;Species: Homo sapiens (man) C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 08-Oct-1999 2300 SVVTSGETRREEGDPSPHSGGVCKPKLISKSNSRKSKSPIPGQGYLGTERPSSVSSVHSE 2359 : :|| | : | | : | | : 3073 TAGSSGPT--ONGFPAHQA-----PTYTGPSTYPAPTYP-PGTGYPAEPGLPSQPAFHPT 3124 --- PTAFQQPR-FPPAAPQY 3072 97 SPVDHDSL------ESKRPRLEQVSDSHFQ-RVSAAVLPLVHPLPEGLRASA- 141 592 SDQRRRSCKTAPASSSKSQTEVPKRGGERVATCLQKRVSISR-SQHDILQMICSKRRSGA 650 651 SEANLIVAKSWADVVKLGAKQTQTKVIKHGPQRSMNKRQRRPATPKKPVGEVHSQFSTGH 710 --SPPPV-----EQKH-----RSIVQIIYDENRKKAEEAHKIFEGLGPKVELPLYNQ 268 Gaps 142 -----DAKKDPAFGGKHEAPSSPISGQPCGD--DQNASPSKLSKEELIQSMDRVDRE-- 191 PSDIKVYHENIKTNQVMRKKLI-----308 767 PQLTSTCHIAISNSENLLGKQFQGTDSGEEPLLPTSESFGGNVFFSAQN-AAKQPSDK-C 824 825 SASPPIRRQCIRENGNVAKIPRNIYKMISLEIKTSD------TETEPSKIVSIVNR 874 RGAGLSATIARSEHEISEIIDGLSEQENNE-----KQMRQLSVIPPMMFDAEQRRVKFI 418 419 NMNGLM---EDPMKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNFGL----IASYLERKSV 471 46 SHLEVSQASQLLQQQQQQLRR-----RPSLLSEFHPGSDRPQERRTSYEPFHPGP 96 309 QRYDQLMEAWEKKVDRIENNPRRKAK----ESKTREYYEKQFPEIRKQREQQERFQRVGQ 364 2360 GDYHRQTPGWAWEDRPSSTGSTQFPY-----NPLTMRMLSSTPPT--PIACAPS Indels 882; Length 3256; 192 -----IAKVEQQILKLKKKQQQ------LEEEAAKPPEPEKPV--Query Match
3.2%; Score 404; DB 2; L.
Best Local Similarity 18.1%; Pred. No. 6.1e-08;
Matches 516; Conservative 368; Mismatches 1083; 2407 AVNQAAPHQONRIWEREPAPLLSAQYE 2433 3178 VTMSSAPPETG----YSGPAVSGSYE 3199 A; Reference number: A48666; MUID: 94043435 3046 A-----SAAVPATPSG--269 224 셤 ЭĠ ŏ g à g ò δ ò 셤 ò g δ 셤 οy g ŏ 셤 δ ò

970 524 1011 562 1071 601 1131	1177 708 1235 763 1292 798 1352 830	1464 1464 932 1519 968 1579 1990 11639	1695 1082 1736 1134 1193 1819 1253 1817
919GEMKELERPFETYKENIELKENDEKMKAMKRSRTWGQKCABMSDLTDLKSL. 472 PDCVLYYYLTKKNENYKALVRRNYGKRRGRNQOIARPSOEKVEEKEEDKAEK 1	1132	H	LPTTRPTRPPPLIPSSKTTVASEKPSFINGGSI
9	99 99 111 99 111 99 99 99 121 99 99 121 99 99 121 99 99 121 99 99 121 99 99 121 99 99 121 99 99 121 99 99 121 99 99 121 99 99 121 99 99 99 121 99 99 99 121 99 99 99 99 99 99 99 99 99 99 99 99 99		
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Ор	1858	LCKSPQSDPADTPINTKQRPKRSLKKADVEEEFLAFRKLTPSAGK 1902
δy	1311	GLKYPKQIKRESPPIRAFEGAIT
QO	1903	AMHTPKAAVGEEKDINTFVGTPVEKLDLLGNLPGSKRRPQTPKEKAKALEDLAGFKELFQ 1962
δλ	1350	SIHEIPRQDILIQESRKTPEVVQSTRPIIEGSISQGTPIKFDNNSGQSAIKHN 1402
qq	1963	TPGHTEESMTDDKITEVSCKSPQPDPVKTPTSSKQRLKISLGKVG 2007
60	1403	VKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVRAGETVRSRHTSVVSSGPSVLRST 1462
ò	1463	151 AND TEACH TO THE STANDARD
g Q	2042	
δŏ	1519	STLTPTQRESIPAKSPVP-GVDPVVSHSPFDPHHRGSTAGEVYWSHLP 1565
QQ	2092	ST-TDDKTTKIACKSPPPESMDTPTSTRRPKTPLGKRDIVEELSALKQLTQTTHTDKVP 2150
οy	1566	TQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQT-ILNDY 1617
QQ	2151	GDEDKGINVFRETAKOKLDPAASVTGSKRQ-PRTPKGKAQPLEDLAGLKELFQTPVCTDK 2209
οy	1618	ITSQQMQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPPTI 1662
Dp	2210	PITHEKTIKIACRSPQPDPVGTPIIFKPQSKRSLRKADVEEESLALRKRIPSVGK 2264
ογ	1663	LVPHPGGTSTPPMDRITYIPGTQITFPPRPYNSASMSPGHPTHLAAAAASAERERERER 1720
ф	2265	AMDTPKPAGGDEKDMKAFMGTPVQKLDLPGNLPGSKRWPQTPK 2307
δλ	1721	EKERERERIAAASSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGT 1778
qq	2308	EKAQALEDL-AGFKELFQTPGTDKPTTDEKTTKIACKSPQPDPVDTPASTKQRPK 2361
δλ	1779	NGTSVITPLDPTAQLRIMPLPAGGPSISQGLPASRYNTAADALAALVDAAASAP 1832
qq	2362	RNLRKADVEEEFLALKKRTPSAGKAMDTPKPAVSDEKNINTFVETPVQKLDLLGNLP 2418
δŽ	1833	QMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAF 1887
QQ	2419	GSKRQPQTPKEKAEALEDLVGFKELFQTPGHTEESMTDDKITEVSCKS 2466
٥y	1888	PSGKPQPHS-SVVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVIITR 1939
g	2467	
Οý	1940	QIASDKDARERGSQSSDSSSSLSSHRYETPSDAIEVIS 1977
q	2518	:
ογ	1978	Ä:
qq	2578	IDKNIKIPCKSPPPELIDIAISIKRCPKIRPRKEVKEELSAVERLIQISGQSIHIHKEPA 2637
δλ	2015	HHYRPQQESPSPQQQLPPSSQAEGMGQVPRTHRLITLADHICQIIT 2060
QQ	2638	SGDEGIKVLKQRAKKKPNPVEEEPSRRRPRAPKEKAQPLEDLAGFTELSETSGHTQESLT 2697
οy	2061	ODFARNQVSSQTPQQPPTSTFQNSPSALVSTPVRTKTSNR-YSPE 2104
QQ	2698	AGKATKIPCESPPLEVVDTTASTKRHLRTRVQKVQVKEEPSAVKFTQTSGETTDADKEPA 2757
οy	2105	SQAQSVHHQRPGSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVHEKQDS 2164
Dp	2758	GEDKGIKALKESAKQTPAPAASVT-GSRRRPRAPRESAQAIEDLAGFKDPAAGHTEES 2814
οy	2165	LILLSQRGAEPAEQRNDARSPGSISYLPSFFTKLENTSPMVKSKKQEIFRKLNS 2218
QO .	2815	MTDDKTTKIPCKSSPELEDTATSSKRRPRTRAGKVEVKEELLA 2857

Db 512 GRKEGEAEAEBEBVEKEBAEBAEVEBAEAEETEAAAAEEEBEAEGEBEAAAGEE 569  Qy 581 -RKGRITRSMTNEAAAAAAAAAATEEPPPPLPPPPPPISTEPVETSRWTEEBMEVAKKG 639  ;	THE PRAYELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISA-ETAEQMOVQOEHSAE	RESULT 20 T42717 DNA-binding protein Rc - mouse NA-binding protein Rc - mouse NA-lternate names: Ig kappa chain gene enhancer Recognition component C; Species: Mus musculus (house mouse) C;Date: 11-3an-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000 C;Accession: T42717 R;Wu, L.C.; Liu, Y.; Strandtmann, J.; Mak, C.H.; Lee, B.; Li, Z.; Yu, C.Y. Genomics 35, 415-424, 1996 A;Title: The mouse DNA binding protein Rc for the kappa B motif of transcription and ew family of large transcriptional proteins. A;Reference number: 222238; MUDD:97001141 A;Accession: T42717 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-2282 <wul> A;Residues: 1-2282 <wul> A;Residues: 1-2282 <wul> A;Cross-references: EMBL:L46815; NID:g1377885; PID:g1377886; PIDN:AAB40884.1 A;Experimental source: strain BALB/C; clone T1; thymocyte, brain C;Genetion: C;Genetion: binds V(D)J recombination signal sequence and kappa B motif C;Superfamily: HIV-EP2 enhancer-Dinding protein C;Superfamily: HIV-EP2 enhancer-Dinding protein C;Superfamily: HIV-EP2 enhancer-Dinding protein C;Keywords: DNA recombination; transcription</wul></wul></wul>
Qy         2219 SGGGDSDMAAAQPGTEIFNLPAVTTSGSVSSRGHSFADPASNLGLED         2265           I	RESULT 19 15-1116 NF-180 - sea lamprey C; Species: Petromyzon marinus (sea lamprey) C; Species: Petromyzon marinus (sea lamprey) C; Species: Petromyzon marinus (sea lamprey) C; Species: Petromyzon marinus (sea lamprey) C; Species: Detromyzon marinus (sea lamprey) C; Species: 15-6ep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000 C; Accession: 151116 R; Jacobs, A.J.; Kamholz, J.; Selzer, M.E. Brain Res. Mol. Brain Res. 29, 43-52, 1995 A; Title: The single lamprey narrofilament subunit (NF-180) lacks multiphosphorylation re A; Reference number: 151116; MUID:95287814 A; Residues: 151116 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Residues: 151110 c.Jac> A; Cross-references: EMBL:1110 c	OY 253 IFEGLGPRIVELPLYNOPSDTKVYHENIKTNOVMRKKILLFFKRNHARKOREGKIC 308  187 I.REKTDDEVRLRNETEALINAFRKNYDDTSLYRMEMDKRTQSLL 230  QY 309 QRYDQLMEAWEKVURIENNPRRAKESKTREYYEKQFPEIRKQREQQE357  DD 231 DEITFLKRNHEEFUDELLAQIOSSTVVERKOFP-PEITAALREIRGQLEGGSAR 285  QY 358

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Query Match 3.1%; Score 391.5; DB 2; Length 2282; Best Local Similarity 18.8%; Pred. No. 1.2e-07; Matches 468; Conservative 294; Mismatches 886; Indels 843; Gaps 115;	2 SSSGYPPNQGAFSTEQSRYPPHSVQYTFPNTRHQQEFAVPDYRSSHLEVSQASQLLQQQQ 61	62 QQQLRRRPSLLSEFHPGSDRPQERRTSYEPFHPGPS 97	98 PVDHDSLESKRPRLEQVSDSHFQRVSAAVLPLVHPLPEGLRASADAKKD 146	147 PAFGGKHEAPSSPISGQPCGDDQNASPSKLSKEELIQS	185	210 EEEAAKPPEPEKPVSPPPVEQKHRSIVQIIYDENRKKAEEAHKIFEGLGPKV 261	262ELPLYNQPSDTKVYHENIKTNQVMRKKLILFFKRNHARKQREQKICQRYDQLME 316   1	317 AWEKKVDRIENNPRRKAKESKTREYYEKQFPEIRKQREQQERFQRVGQRGAGLSATIAR- 375 392 SAEQOVSPPNTNAKSYAEIIFGKCGRIGQRTSMLASTSTQP 432	376SEHEISEIIDGLSEQEN-NEKQMRQLSVIPPMMFDAEQRRVKFINM 420	421 NGLMEDPMKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNFGLIASYLERKSVPDCV 475	476 LYYY	501 RNQQIARPSQBEKVEEKEEDKAEKTEK	534 DEEKDEKDEKEDS	556	590 TNEAAAASAAAAAATEEPPPPL	612	651 AKMVGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRKPREERDVSQCESVASTVSAQE 710 
S # B	Oy Dp	oy Dp	Qy	Qy Dp	Oy Dp	Qy Dp	Oy Dp	Oy Dp	Qy Op	Oy Dp	Qy Db	Oy Dp	Qy Dp	Qy Dp	Q <b>y</b>	Oy Db	oy Og

KPSEDSPENATSRGNTEPA 750                     HPAREMRRSASEQSPNVPHSSHMTETR 991	YVNDSISAETAEQMDVDQQEHSA 805 	EGDNTKERDLDRASEKVEPRDEDLVVAQQ 865   :: :            -GGKSQMQDRPPLGSS-PPYTEALQVFQP 1106	-PERQRMFPMDSKPSLLNPTGSILVSSP 919	PPWVSCTPCNIPIGTPVSGYALYQRHIKAMHESA 971 	EWEVLQPAPHQLITNLPEGVRLP 1025	-EKPSFIMGGSISQGTP-GTY 1065	ONRGYQTPYLRVPERKGTSLSSEGILSL 1385	SATLPYIKOEEFS1111 : :    : -    VKEEEASKADEKLELVSTCSVV 1438		SIPTEALVKGSISRMPIEDSSPEKGREE 1203	AREGTRT 1237 :	SAPLEGLICRALPRGSPHSDLKERTVLSGSIM 1297	-SFEDGLKYPKQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIH- 1352  :	RPIIEGSISQGTPIKFDNNSGQ 1396    : : : : : : : : : :	GMPPLEIVPENIKVVERGKYEDVKAG 1441 :	TLHEAPKAQLSPGIYDDTSARRTPVSYQ 1489	MNRTSDVTIPPNKSTNHERKSTLTPTQRESIPAKSPVPGVDPVVSHSP 1546
DEDIEASNEEENP-EDSEVEAV	VELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDVDQQEHSA 	EEGSVCDPPPATKADSVDVEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQ 	INAGRPEPQSDNDSSATCSADEDVDGEPERQRMFPMDSKPSLLNPTGSILVSSP :	LKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTPVSGY 	LLEEQRQROGOIDLECRSSTSPCGTSKSPNREWEVLQPAPHQLITNLPEGVRLP 	-TTRPTRPPPPLIPSSKTTVASEKPSFIMGGSISQGTP-GTY 	LTSHNQASYTQETPKPS	VGSISLGLPRQQESAKSATLPYIKQEEF     :     :   : :  :  :  :  :  :  :  :	PRSQNSQPE-GLLVRAQHEGVVRGTAGA1QEGSITRGT   : :     : :   : :   : :     LTSTEDRKKTEKPHVGGQGRSRREAETLSSLSSDVSDPKELSPLSHSTLSHGTAPGSEAL	PTSKISVESIPSLRGSITQGTPALPQTGIPTEALVKGSISRMPIEDSSPEKGREE  :   :  :  :  :  :  :  :  :  :  :  :  :	AASKGHVIYEGKSGHSPRTLSYDNIKNAREGTRSPRT i :	AHEISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIM	QGTPRATTESFEDGLKYPKQIKRESPPIRAFEGAITKGKPY :	EIPRODILTQESRKTPEVVQSTRPII- :   :	SAIKHNVKSLITGPSKLSRGMPPLEIV  :	ETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTS- 	NTMSRGSPMMNRTSDVTIPPNKSTNHERKSTLTPTQRESIPAKSP 
7111	751 992	806	866 1107	920	972	1026 1266	1066	1083	1112	1149,	1204	1238	1298 1667	1353	1397	1442	1490
Qy	QY	oy Op	Qy Dp	Qy Dp	Qy	Qy Dp	Qy	oy G	oy Op	දු පු	S G	S G	o d	oy ep	Oy Dp	Qy Dp	Qy Db

QY   96 -PSPVDHDSLESKRPREQVSDSHFQRVSAAVLPLVHPLPEGLRASADAKKDPAFGG   151	Qy   321 KVDRIENNPRRAKESKTREYYEKQFPEIRKQREQOERFQRVGRGAGLSATIAR 375   1   1   1   1   1   1   1   1   1	483 KNENYKALVRRNYGKRRGRNQOIARPSQEEKVEEKEEDKAEKTEEKKEEEKKDEEEKDE	1   1   1   1   1   1   1   1   1   1	QY         829         PENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQREPGSDNDSSATCSADE- 887           Db         1085
Db 1932 WSPSKEAGSRPSYTRKHSLTKNDSSPQGCSPAREAQASYTSTPG-PQM 1978  Qy 1607 ENTROTILNDYITSQQMQVNLRPDVARGLSPREQPLGLPYPATRGI 1652	1826 DAAASAPQMDVSKTKESKHEAARLEENIRSRSAAVSEQQQLEQKTLEVEKRSVQCLXTSS :	\$15053  Ni Alternate protein YCR033w - yeast (Saccharomyces cerevisiae)  Ni Alternate names: hypothetical protein YCR592  Cispecies: Saccharomyces cerevisiae  Cispecies: Saccharomyces cerevisiae  Cispecies: Saccharomyces cerevisiae  Cispecies: Saccharomyces cerevisiae  Cispecies: Saccharomyces cerevisiae  Cispecies: Saccharomyces cerevisiae  Cispecies: Saccharomyces cerevisiae  Cispecies: Algoria: S15053; S19445; S40918  Rijia, Y.; Slouimski, P.P.; Herbert, C.J.  Yeast 7, 413-424, 1991  Airitle: The complete sequence of the unit YCR59, situated between CRY1 and MAT, reveals  A; Reference number: S15052; MUID:91335897  A; Accession: S15053  A; Accession: A; Accession: S15053  A; Accession: A; Accession: A; Accession: A; Accession: A; Accession: A; Accession: A; Accession: A; Accessi	A; CLC C.J.; Jia, Y.; Sloninski, P.P.  submitted to the Protein Sequence Database, March 1992  A; Reference number: \$19445  A; Reference number: \$19445  A; Rocession: \$19445  A; Molecule type: DNA  A; Residues: 1-1226 (*RIER)  A; Cross-references: EMBL: X59720; NID: 91907116; PIDN: CAA42300.1; PID: e264374; PID: 9190717  K; Wicksteed, B.L.; Roberts, A.B.; Sagliocco, F.A.; Brown, A.J.P.  A; Ritle: The complete sequence of a 7.5 kb region of chromosome III from Saccharomyces of A; Reference number: \$40917; MUID: 92133166  A; Reference number: \$40917; MUID: 92133166  A; Rocession: \$40918  A; Rocession: \$1304, A, 306-374, S', 376-403, Q', 405-434, VV, 436-441, N', 443-481, E', 483-51	A;Cross-references: EMBL:S78624; NID:g244237; PIDN:AAB21259.1; PID:g244239 C;Genetics: A;Map position: 3R  Query Match Best Local Similarity 20.2%; Pred. No. 6.2e-08; Matches 222; Conservative 181; Mismatches 368; Indels 326; Gaps 52; Authore Statement 181; Mismatches 320; Gaps 52; Authore Statement 181; Mismatches 320; Gaps 52; Authore Statement 181; Mismatches 320; Gaps 52; Authore Statement 181; Mismatches 320; Authore Statement 181; Mismatches 320; Authore Statement 181; Mismatches 320; Authore Statement 181; Mismatches 320; Authore Statement 181; Mismatches 320; Authore Statement 181; Mismatches 320; Authore Statement 181; Mismatches 320; Mismatches 320; Authore Statement 181; Mismatches 320; Mismatches 320; Mis

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992 RIVNPQTYSQVKISHSQHVETQHPNSETTTYQPLDLEFAINLQPTPKE---NFAQTFQDT 1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          971 ALLEEQRQRQEQID----LECRSSTSPCGTSKSPNREWEV-LQPAPHQLITNLPEGVRLP 1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --PPHPTVPQQTIIVHPPEHPLVIHSEQVYTQHPNPTEAIIQPLDLELTITPQPTAEGEL 1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---IEDSSPEKGREEAASKGHV-IYEGKSGHILSYDNIKNAREGTRSPRTAHEISLKRSY 1247
                                 KPVDIKLKITSEPIKVESSLYEEETPTQTPGPFVEAKLFPSQQ------QQPAETSETP 355
                                                                                                                                                                                                                 374 ARSEHEISEIIDGLSEQENNEKQMRQLSVIPPMMFDAEQRRVKFINMNGLMED----- 426
                                                                                                                                                                                                                                                                     EEGESSGIDLESSVHPQEDSE----EIGPLPTLQEDVSQ-----HLGPVLEDESSLSEL 405
                                                                                                                                                                                                                                                                                                                          --PMKVYKDRQFMNVWTDHEKEIFKD----KFIQHPKNFGLIASYLER--KSVPDCVLYY 478
                                                                                                                                                                                                                                                                                                                                                           -EKTEKKEEEKKDEEEKDEKEDSKENTKEKDKIDGTAEETE-EREQATPRGRKTANSQGR 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              631 SDQQGVLSQSLEPILYDSLSQQEYTTGISQISECGEPFPTQQETPEHSVGMHTEEVAQPP 690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            773 KPAEDESVETQVNDSISAETAE----QMDVDQQEHSAEEG------SVCDPPPATKAD 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---KHEDLALTITPEPSLEDGSILFPQEDLLQPIDSTGQGEFSHIKTSTLSKPPYVSNTK 840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SCTPCNIPIGTPVSGYALYQRHIKAMHES 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSAFQETMSETTY-----NSKQVDLSSTHLKTSELPPDYTMGLEPSLYQQITQSSPKSL 894
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                                                                                                              KKVD---RIENNP---RRKAKESKTREYYEKQFPEIRKQREQQERFQRVGQRGAGLSATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IQPTQNEDY ------GYQLPNVTVRPVDVALTVTSEPVKETESFLAPQEFPVHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASNEEENPEDSEVEAVKPSEDSPENATSRGNTE---PAVELEPTTETAPSTSPSLAVPST
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                                                                                                                                                                                                                                                                                                                                                                                                                             479 YLTKKNENYKALVRRNYGKRRG-----RNQQIARPSQEEKVEEKEEDKA--
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J. Biol. Chem. 263, 19159-19165, 1988
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R;Peeters, B.; Heyns, W.; Bossyns, D.; Rombauts, W.
J Biol. Chem. 258, 14206-14211, 1983
A;Title: Proline-rich polypeptides bound to rat prostatic binding protein. The primary A;Reference number: A94675; MUID:84061859
A;Accession: B20593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: A single 12.5-kilobase androgen-regulated mRNA encoding multiple proline-rich
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C; Superfamily: rat prostatic proline-rich peptides 637K precursor
C; Keywords: prostate; tandem repeat
C; Keywords: prostate; tandem repeat
F; 1-26/Domain: signal sequence #status predicted <SIG>
F; 27-5761/Product: prostatic proline-rich peptides 637K proprotein #status predicted
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proline-rich peptides 637K precursor, prostatic - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-May-1992 #sequence_revision 13-May-1992 #text_change 05-Nov-1999
C;Accession: A42663; A41819; A31966; B20593; A20593
R;De Clercq, N.; Hemschoote, K.; Devos, A.; Peeters, B.; Heyns, W.; Rombauts, W.
J. Biol. Chem. 267, 9884-9894, 1992
A;Title: The 4.4-Kilodalton proline-rich polypeptides of the rat ventral prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                           3
                                                                                                                                                                                                                                                                                                                                                                   A Experimental source: ventral prostate
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:100347, NCBIP:100348)
R;De Clercq, N.; Hemschoote, K.; Devos, A.; Peeters, B.; Heyns, W.; Rombauts, submitted to the Protein Sequence Database, April 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 2822-2859 <PE2>
A;Note: this peptide, designated proline-rich polypeptide IV, can be found at
C;Genetics:
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                                                                                                                                                                                                                                                                                                                       <DE2>
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A;Residues: 2020-2057 <PBE>
A;Note: this peptide, designated proline-rich polypeptide V, can
A;Accession: A20593
                                                                                                                                                                                                                                                                                         A;Molecule type: DNA; mRNA
A;Residues: 1-3706,'I',3708-4077,'F',4079-4155,'S',4157-5761
A;Cross-references: GB:M86514
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A;Status: not compared with conceptual translation
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                                                                                                                                                                                                                                          A; Reference number: A42663; MUID:92250652
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A; Residues: 3372-3540 <HEM>
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A; Residues: 1-5762 <DE1>
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g	1164 PQ	PQTLQDSTTQIIEPPTVVVGPVPIYEEVTVQTTSQDQAEYPPSPTVSFQSL-DLELTISP	1222
λ	1248 ES	ESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLS-GSIMQGTPRATTE	1306
q	1223 EA	EATRESYHPSILQQTTIVNPPEHPLVIHSEQVHTQHPNLTEATVQPLDPDLTTTPQPTTE	1282
λ	1307 SFI	SFEDGLKYPKQIKRESPPIRAFEGAITKGKPYD-GIT	1342
q	1283 G-	ELPQTLQDSTSQIIIEPPIKVVALVPVYQEVSQDQAEYTTSSTVSFQPLDQELT	1337
74 74	1343 TIH	TIKEMGRSIHEIPRQDILTQESRKTPEVVQSTRPII               : :	1378 1397
χ̈́		EGSISQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSRGMPLEIVPENIKVVERGKYEDV	1438
e e	1398 EG		1429
<b>≿</b> &	1439 KAC 1430 TVC	KAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGS	1496 1473
۲۵ م	14971	PMANRTSDVTIPPNKSTNHERKSTLTPTQRESIPAKSPVPGVDPVVSHSPFDPHHRGSIIIII     :     :   :     :   :	1554
}			1 + 6 +
% q	1555 TAC : 1518 LS(	TAGEVYWSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTIL	1614 1567
27		NDYITSQQMQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGG	1669
ą	1568 EL	ELTVTSEPTKEAYHSTISKNSLAINPQXVHIQHPNPAEATVQPLDLELTISSSLQPTAEG	1627
સ્ત્ર ક	1670		1717 1685
à		REREKERERERIAAASSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPS	1773
ą	1686 LS	::         : :         : :	1745
č	1774 V	FQGTNGTSVITPLDPTAQLRIMPLP	1799
q	1746 İEI		1805
λ	1800	-AGGPSISQGLPASRYNTAADALAAL	1836
ą	1806 TI	TIHSHSPGWTQQHANLKESKGHTTGKILLDYAEPNMEIELKHHGLFLLKTTEATT	1860
λć		SKTKESKHEAARLEENLRSRSAAVSEOQOLEQKTLEVEKRSVQCLYTSSAFPSG	1890
<u>a</u>		SENTNŲMIKSLAŲVTALFIŲNKKSMLPALVESŲDESŲPPPNMSLŲPLDŲBLILSSŲPHG	1920
ž g	1891 1921 WVE	KPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVITTRQIAS WVPHIPNTPEKIYLHY AEPPTGPFWEPPELFFLKTTKSRPYQGTAQWAAS	1943 1971
Ϋ́		DKDARERGSQSSDSSSSLSSHRYETPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQAE	2003
ą	 1972 PKI		2019
ζ	2004	NDPTRQYEGPLHHYRP	2019
ą	2020 GW	GWIPHPPNTHGKIYLHYAEPPTGPFVEPPDLFFLKTTKSKPVEWTLTRTDKSRKEMVSQS	2079
<u> </u>	2020	QQESPSPQQQLPPSSQAEG-MGQVPRTHRLITLADHIC	2056
. ;			, () ;
≿ &	2138	OLITODEAKNQVSSQTFQQPFISTFQDSPSALVSTPWR TKTSNRYSPESQAQSV 	2110 2177

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2215 <WUX>
A;Residues: 1-2215 <WUX>
A;Cross-references: EMBL:U39653; NID:g1049397; PID:g1049401; PIDN:AAB52495.1; GSPDB:G
A;Experimental source: strain Bristol N2; clone T13H2
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: CESP:T13H2.4
A;Map position: X
A;Introns: 112/2; 136/1; 167/1; 196/1; 649/1; 696/1; 757/1; 850/1; 882/1; 985/1; 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein T13H2.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C;Accession: T16871
R;Wu, X.
submitted to the EMBL Data Library, October 1995
A;Description: The sequence of C. elegans cosmid T13H2.
A;Reference number: 218593
A;Accession: T16871
                                                      --VSSEPYEPI-SPPQVP 2156
                                                                                                                                                                                                                                                                               2230 -----DKIYL---HYAEP-----PTGPFVEPPDLFFLRTTKSKPVQGTTTEMAKSP 2272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2330 G-------KIYLHSI--EPPGPFVKPTDLILVKTTTKSKPAEWTPRRIDKL 2372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2359 EGDYHRQTPG---WAWEDRPSSTGSTQFPYNPLTMRMLSSTP----PTPIACAPSAVNQA 2411
                                                                                                                                                                                                                                                                                                                                                                             2209 KQEI----FRKLNSSG-GGDSDMAAAQPGTEIFNLPAVTTSGSVSSRGHS-FADPASNL 2261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2373 LKEMVPHS-----PEYEEAVFPAHGEGODESGSPPNMPLQPLDQELTLSSQPHG 2421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | | | : : | | | : | | 1.1 | | 1.1 | | 1.1 | | 1.2 | | 1.2 | | 1.2 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.3 | 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224 SPPPVEQKHRSIVQIIYD---ENRKKA-----EEAHKIFEGLGPKVELPLYNQPSDTK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                274 VYHENIKTNQVMRKKLILFFKRRNHARKQREQKICQRYDQLMEAWEKKVDRIENNPRRKA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 KESKTREYYEKQFPEIRKQREQQERFQRVGQRGAGLSATIARSEHEISEIIDGLSEQENN 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       394 EKQMRQLSVIPPMMFDAEQRRVKFIN-MNGLMEDPMKVYKDRQFMNVWTDHEKEI--FKD 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 741; Gaps
                                                                                                                                                                                      2157 VVHEKQDSLLLLSQRGAEPAEQRNDARSPGSISYLPSFF----TKLE----NTSPMVKSK
                                                                                                                                                                                                                                                                                                                                                                                                                                              2262 GLEDIIRKALMGSFDDKVEDHGVVMSQPMG-VVPGTANTSVVTSGETRREEGDPS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2316 ----PHSGGVCKPKLISKSNSRKSKSPIPGQGYLGTERPSSV----
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2111 HHQRPGSRVSPEN--LVDKSRGSRPGKSPERSH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2412 APHQQNRI-----WEREPAP 2426
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354	507	387	556 439	616 481		514		774			883	934	772			876	1043		986	1125 1056	1182	1109	1242	1147			0181
2PTNLTAEEAQAMFYTYLNYTQQDFGKIGNLLHSEHKQLQPFLN	KFIQHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYKAL		8 PSQEEKVEEKEEDKAEKTEKKEEEKKDEE	7 TAEETEEREQATPRGRKTANSQGRRKGRITRSMTNEAAAAAAAAAATEEPPPPLPPPE 	PISTEPVETSRWTEEEMEVAKKGLVEHGRNWAAJAKWYGTKSEAQCKNFYFNYKR	Z FVHNDVGFFVVFSETANK	: : :     : : :       GPSNPQQLNNPETTRKSVPSPLQRSMSTPASEATDEDLIAFLREPLALA	0 EENPEDSEVEAVKPSEDSPENATSRGNTEPAVELEPTTETAPSTSPSLAVPSTKP :	AEDESVETOVNDSISAETAEQMDVDQQEHSAEEGSVCDPPFATKADSVDVEVRV		5 KVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATC :   :	4 SADEDVDGEPERQRMFPMDSKPSLLNPTGSI-LVSSPLKPNPLDLPQLQHRA	0 MQDPAPPL.PPKKAAPKRKKPTKAEIEAAGGNVSSVEKPKKPRAFSKKKAQGTV		Wenymismismodolist nykonysinyksky	4 EEUKUMAEULDLE	0 APHQLITNLPEGVRLPTTRPTRPPPPLIPSSKTTTRPPPPLIPSSKTT		GIYGGYEDVSNNQFQQPDYPPLSVESQVSCHSQESNITYHSSMPVTPISQQANNG	O LPRQQESAKSATLFYIKQEEFSPRSQNSQPEGLLVR 	AQHEGVVRGTAGAIQEGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGIPT	:   :   :   :   :   :   :   :   :   :	3 VKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIKNAREGIRSPRIAHEIS : : :   ::   ::   ::	O MSNRVIKTPSSETHPOSYANVQYVPMNPSLPVSSHSES		QVKSTRKLPSNFKEDDIRHSTCPDNCNKCVSEKSN	/
31	451	355	388	557		674		720			835	884	720	935		9/4	1010	-		1090	1126	1057		1110			1971
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a	170B	LEUUKGVEULAATUDEUICIVKILPHEISHINLGRFRUUSKFSGVGVNGISHGLINUGFP 126/
Qy Dp	1311	GLKYPKQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHEIPRQDILTQESRKT 1367         : : :
δλ	36	VOSTRPIIEGSISQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSRGMP 1
qq	1304	PEVSIGKLIKQQHLNRPNQFNNISGQSQIDLATLQQSVMLSP-KLQRYSE 1352
Qy Db	1419	PLEIVPENIKVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHE 1465   :
QY	1466	AP-KAQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTSDVTIPPNKST 1513
qq	1412	MKQQIKLTSLQSNKTSQ
Qy dc	1514	-NHERKSTLTPIQRESIPAKS-PVPGVDPVVSHSPFDPHHRGSTAGEV 1559
2 0	1560	YPSQYQLYAMENTRQTILN 161
qq	1519	TMNE
δŏ.	1616	DYITSQQMQVNLRPDVARGLSPREQ-PLGLPYPATRGIIDLTNMPPTILVP 1667
qq	1568	NPMSEQOVOMNYQTSIVQQTSVEQQGPLQLQNQIQVTNQ-QTHRVQYQHHPVQHN 1621
Qy	1668	GGTSTPPMDRITYIPGTQITFPPRPXNSASMSPGHPTHLAAAASAERERERE 1720
qq	1622	QRNGPTKAAPRKRTPKPAPVQSRSVALHERAQMIVDFAKTQPADQEDQTVQ 1672
ΟŊ	-	KIAAASSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFGGTNG 178 :   :   :   :   :   :   :   :   :   :
g	1673	LQDHEHQrnsqqqprnsqqqp1712
δy	1781	QGLPASR
ДQ	1713	QHQAQQELAENQGSMGMATQQQQCRQSQLQQQLQQPPQ-QQMQIQQQY 1759
λŏ	1841	
q	1760	181
δς P	1897	SVVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVIITRQIASDKDARER 1950  1
1 8	197	00L
h 2	1872	QUADVASCOLO SENTE CONTRACTOR CONT
οy	1993	OPEVVKANDAENDPTRQYEGPLH 2027
qq	1932	
δy	2028	QQLPPSSQAEGMGQVPRTHRLITLADHICQIITQDFARNQVSSQTPQ 2074
QQ	1992	KRKPTNNHTNGMHTPDASPAGGISSGQSSSSGMQSQSLSITTGMSSSSS 2040
οy	2075	QPPTSTFQNSPSALVSTPVRTKTSNRYSPESQAQSVHHQRPGSRVSPENLVDKSRGSRPG 2134
qq	2041	SPPASDEDISTHLITPPQEHSSPLTTPPIINHEYVQQVSSPVDIFSQPSTSEPG 2094
οy	2135	KSPERSHVSSEPYEPISPPQVPVVHEKQDSL 2165
OD	2095	PSSRPIRTGVHHREEAL 2111

RESULT 24 T42761

Qy         642         EHGRNWAATAK	1424	SPCGTSKSPNREWEVLQPAPHQLITNILPEGVRLPTTRPTRPPPPLIPSSKTTVASE            :	QY         1121 GLLVRAQHEGVVRGTAGAIQEGSITRGTPTSKISVESIPSLR         1162           BD         1800 QVTPLARRDILITQMGTAQSVSLKPGPVPEPGAEPHRATP-AELRAHALPGTRKPHTVVV 1858           QY         1163GSITQGTPALPQTGIPTEALV	OY 1256 OGMSMRESPVSAPLEGLICRAL-PRGSPHSDLKERTVLSGSIMOGTPRA 1303  1956 PGPHEEQRPYPQGLPGRLYSSMSDTNLAERGLNYHAQRIGGLFQGPGRDSAVDLSSLKHS 2015  QY 1304 TTESFEDGLKYPKQIRRESPPIRAFEGAITKGRPYDGITTIKEMGR 1349  1 1
Bassoon protein - rat N;Alternate names: brain-specific synapse-associated protein C;Species: Rattus norvegicus (Norway rat) C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000 C;Accession: T42761 R;Dieck, S.; Sanmarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex, J. Cell Biol. 142, 499-509, 1998 A;Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localized A;Reference number: Z2249; MUID:98345363 A;Accession: T42761 A;Accession: T42761 A;Accession: T42764 A;Molecule type: mRNA A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-3938 ADIE> A;Cross-references: EMBL:16563; NID:93413503; PIDN:CAA76287.1; PID:93413504 A;Cross-references: EMBL:2100 Dawley; brain C;Function: may be involved in cytomatrix organization at the site of neurotransmitte	e presynaptic cytoskeleton ; zinc finger 3.0%; Score 380.5; DB 2; Length 3938; 18.8%; Pred. No. 6.3e-07; vative 330; Mismatches 1086; Indels 1029; C LRRRPSLLSEFHPGSDRPGERXTSTE-PFHPGPSPVDHDSLESKRPFI :		310RYDQLMEAWEKKVDRIENHOPRRKAKESKTREYJEKQFPEIRKQREQQDJAESSDU 310RYDQLMEAWEKKVDRIENHOPRRKAKESKTREYJEKQFPEIRKQREQ-QERFGRVG	н н .

qq	2173 LLPSTATVRAADGMIXSTIN-TPIAATLPITTQPASVLRPMVRGGMXRPYG 2222	Db 3066 QNGFLAHQAPTYTGPSTYPAPTYPPGTS
ç 9	1502 TSDVTIPPNKSTNHERKSTLTPTQRESIPAKSPVPGVDPVVSHSPFDPHHRGST 1555  :	3126 FPVQA
ò	AGEVYWSHI PTOLDDAMPEHRALDDAAAAYLEOROI SPTBGYPSOYOI VAMENTROTTI.N	Qy 2422 REPAPLLSAQYE 2433
; 음		Db 3176 GPAVSSYE 3184
οy	1616 DYITSQQMQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPM 1675	RESULT 25
qq	2291RPELPAG-GAREEPLSTAPPAVIKEAPVAQAPAP- 2324	hypothetical protein T13H2.3 - Caenor! C.Species: Caenorhabditis elegans
ે દે		C; Accession: T16870
3 8	DD	K;Wu, X. submitted to the EMBL Data Library, Oc
B 5	1/19 ER :	A; Description: The sequence of C. eleg A; Reference number: 218593 A; Accession: T16870
ôy		A; Status: preliminary; translated from A; Molecule type: DNA
qq	2432 FALGREQLAQORLQLEQIQQLQQQLQQQLEEQKQRQRQRAFPATCEAPSRGPP 2483	A; Residues: 1-2447 <wux> A; Cross-references: EMBL: U39653; NID:</wux>
ογ	1811 ASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAVSE 1862	A; experimental source: strain Bristol C; Genetics:
g	2484 PAATELAQNGQYWPPLTHTAFIAVAGTEGPGQAREPVLHRGLPSSASDMSL 2534	A; Welle: Charillon: A A; Map position: A A: Tat pose: 18/2: 135/2: 176/2: 406/1.
οy	1863 QOQLEQXTLEVEKRSVQCLYISSAFPSGKPQPHSSVVYSEAGKDKGPPFKSR 1914	C;Superfamily: RING finger homology F:58-207 / December of the control of the con
qq	2535 QTEEQWEAGRSGIKKRHSMPRLRDACEPESGPDPSTVRRIADSSVQTDDEEGEGR 2589	First to the company tringer items of the company o
Oy Op	1915 YEEELRTRGKTTITAANFIDVIITRQIASDKDARERGSQSSDSSSLSSH 1964 	Query Match 3.0%; Scor Best Local Similarity 19.1%; Prec Matches 492; Conservative 309; A
δy	1965 RYETPSDAIEVISPASSPAPPOEKLOTYQPEVVKAN 2000	LEQVSDSF
q		Db 199 PTCRQNLGSKRELQQDPRFDQLIYC
δ	QA	Qy 158 SPISGQPCGDDQNASPSKLSKEELIQSN :             ::
g	SA	Db 256 GSDWNKRYGIDPNSKLKAPRPLKS
Oy Dp	2026 PQQQLPPSSQAEGMG-QVPRTHRLITLADHICQIITQDFARNQ 2067                 :: :     :: ::   ::	QY 208 QLEEEAAKPPEPEKI  :  :  :  :   308 PKEDDINYLENDKEGTSVAAEKEVLEEG
Qy	2068VSSQTPQQPPTSTFQNSPSALVSTPVRTKTSNRYSPESQAQSVHHQRP-G 2116	QY 254 FEGLGPKVELPLYNOPSDTKN
qq	2817 SPQKQFIADSTLRQQTLPRPMKTLQRSLSDPKPLSPTAEESAKERFSLYQHQGGLG 2872	:
ð á	2117 SRVSPENLVDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVHE 2160	301
3 8	SQVSALFFNGLVKKVKKTLFSFFFEERHLFLAGGVFVSQLYASLLQKGLAGFTTVPAT	424 SNESFDEDASG
6 G	ZIOI NÜDƏLLILƏQRGABFARQVANDARSFGSISILPSFFTKLENTSFMYKSKKQELFKKLNSSG 2220 	QY 324RIENNPRRAKESKTF
Qy	2221 GGDSDWAAAQPGTEIFNLPAVTTSGSVSSRGHSFADPASNLGLEDIIRKALM 2272	Oy 371 ATIARSEHEISEIIDGLSEQENNEKOMF
đ	2975 LGTYQRKESLAKDRVGRDYPPLRGLGEHRDYLS 3007	Db 535IHVISDDSNSEHESDEAEDF
S G	2273 GSFDDKVEDHGVVMSQPMGVVPGTANTSVYTSGETRREEGDPSPH 2317 3008 DSELNOLBLOGCTTPAGOVUDYDASAAVDANTPSGEPTAFOODREDDAATONSTAGSSGEPT 3065	Qy 431 YKDRQFMNVWTDHEKEIFKDKFIQHPKN
ογ		484 NENYKALVRR

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91049397; PID:91049400; PIDN:AAB52494.1; GSPDB:G N2; clone T13H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 693/1; 816/1; 1053/1; 1131/3; 1181/3; 1308/3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       re 376.5; DB 2; Length 2447;
d. No. 4.9e-07;
Mismatches 892; Indels 881; Gaps 119;
                                                           : |:| : || : || : || invevisspays
SYPAEPGLPSQPAFHPTGHYAAPTPMPTTQSAP 3125
                                  PMRMLSSTPPTPIACAPSAVNQAAPHQQNRIWE 2421
                                                                                                                                                                                                                                                                        n 20-Sep-1999 #text_change 02-Sep-2000
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:: |:::||::||:
ESDNDSRDNELQKKKRKM--KRKNVPKTDGSDV 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4DR-----VDREIAKVEQQILKLKKKQQ 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : || : || AGRKKIRWFHESDEDGSVRKVME----SKKGA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSPPPVEQKHRSIVQI-IYDENRKKAEEAHKI 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | | : |: |
3RPKKKFAPELIEGDIPTPSEDSLTSSDEERDD 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGLIASYLERKSVP-----DCVLYYYLTKK 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVLPLVHPLPEGLRASADAKKDPAFGGKHEAPS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PR----YDQLMEAWEKKVD 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLSVIPPMMFDAEQRRVKFINMNGLMEDPMKV 430
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                                                                                                                                                                                                                                                                                                                          ctober 1995
gans cosmid T13H2.
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DVKQSAITSKPGETSPDSSSKIEEKPDKVSEEVSDDEMTPEHIT 638  SKENT	-IKHKVFYDSANRMPSKSNLDFTGRRNAREIPMEEISRLAEEQVAHEEYKIHRRRQVVLE 867VSAQEDEDIEASNEEENPEDSEVEAKPSEDSPENATSRGNTEPAVEL 753	SILNPTGSILVSSPIKPNPLD	DSLTRPNTLADNSHLGESQQIPVIESIQSSTSEALKESENYKDMPILTPASTVSSKSSAP 1390  I - EDSSPEKGREEAASKGHVIYE - GKSGHILSYDNIKNAREGTRSPRTAHEISLKRSY 1247
DVKQSALTSKPGETSPDSSSKIEEKPDKVSEEVS SKENTKEKDKIDGTAEETEEREQATPRGRKTAN- :	-IKHKVFYDSANRMPSKSNLDFTGRRNAREI	-AQRPEPQSDNDSSATCSADEDVDGEPERQRMFPMDSKP-	DSLTRPNTLADNSHLGESQQIPVIESIQSSTSEALKES  I - EDSSPEKGREEAASKGHVIYE - GKSGHILSYDNI
595 544 639 639 699 614 759	809 706 868 912 912 789 972 843	868 1091 927 1141 984 1193 1038 1231 1098 1271	1331 1192 1391 1248 1431 1307 1468
00 00 00 00 00 00 00 00 00 00 00 00 00	2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	

-	:  :  :  :  :	2281	qq
		2188	δλ
2280	. ::       :     :       :	2224	QΩ
2187		2128	οy
2223		2174	Q
2127		2068	Οy
2173	SQQAVQQGMPAGIQGMPTGMGMQQLQGLGMPGMQULPQQAGQSQ	2131	qq
2067	QQQLPPSSQAEGMGQVPRTHRLITLADHICQIII	2027	Qγ
2130	RMIQSGQPLSMQQMQQLQQMSQVQMQHAQQVQQMQQMQMQQLQMQQFAARMQQGTPKPAV	2071	qq
2026	VISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGPLHHYRPQQESPSP	1975	οy
2070	EQEMRVRQAQAAQTQAAQAQAQAQAQAQAQTQAHAQNQAQTQAIVEIQ	2031	QQ
1974	EEELRTRGKTTITAANFIDVIITRQI	1916	QY
2030		1981	Op
1915	RSAAVSEQQQLEQKTLEVEKRSVQCLYISSAFPSGKPQPHSSVVYSEAGKDRGPPPKSRY	1856	Qγ
1980		1933	QQ
1855		1796	Qy
1932	PGQVNVPMPAQMLNQGNPQMAVNPAQAQMMDERRKMEEVNAVYHL	1888	QQ
1795	PGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRI	1748	Qy
1887	. GMYTAAQLQAMQAAVAQTAQAAQAAYAABAAYQAQVAQQARAAPPQQLVQRQVPVGH	1831	QQ
1747		1693	ΟŸ
1830		1778	QQ
1692	PYPATR	1645	Qy
1777	: :	1741	QQ
1644	YLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITSQQMQVNLR	1585	ΟŸ
1740	K	1716	QQ
1584	KSPVPGVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRAL	1532	Qy
1715	HKKRETRKKKNIFVPNIPPKIRRKYVDKKIEMERAKYRARIKSQKMASIRIAVPQ	1661	QQ
1531	VSYQNTMSRGSPMMNRTSDVTIPPNKSTNHERKSTLTPTQRESIPA	1486	Qy
1660	IGETDEDDDVEEEPEFTVDQLELAKKILKQRQGLESSEDSDSDEDMYYDNVDGSVIRRAP	1601	qq
1485	SPGIYDDTSARRTP	1463	Qy
1600		1541	g S
4	00	4	2

RESULT 26
T02345
Typotherical protein KIAA0324 - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C;Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 05-Nov-1999
C;Accession: T02345
R;Ricke, D.O.; Bruce, D.; Mundt, M.; Doggett, N.; Munk, C.; Saunders, E.; Robinson, D

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75;
re, J.; White, S.; Ueng, S.; Tatum, O.; Campbell, C.; Fawcett, J.; Deaven, L. submitted to the EMBL Data Library, March 1998
A:Description: Sequencing of human chromosome 16p13.3.
A;Reference number: 214664
A;Accession: T02345
A;Accession: T02345
A;Molecule type: DNA
A;Residues: 1-1791 CRIC>
A;Cross-references: EMBL:AC004493; NID:q2996648; PIDN:AAC08453.1; PID:q2996650
C;Genefics:
A;Map position: 16
A;Introns: 1610/2; 1706/2
A;Note: KIAA0324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       976 QRQRQEQIDLECRSSTSPCGTSKSPNREWEVLQ----PAPHQLITNLPEGVRLPTTR--- 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------GSI 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1117 SQPE--GLLVRAQHEGVVRGTAGAIQEGSITRGTPTSKISVESIPSLRGSITQGTPALPQ 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1175 TGIPTEALVKGSI-----SRMPIEDSSPEKGREEAASKGHVI-YEGKSGHILSYDNIKN 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1228 -----AREGTRS-----PRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPLEGL 1272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1273 ICRALPRGSPHSDLKERTVLSGSIMQGTP------RATTESFEDGLKYPKQIKR 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1321 ESPPIRAFEGA-----ITKGKPYDGITTIKEMGRSIHEIPRQDILTQESRKTPEVVQS 1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             413 HSSSELSPDAVEKAGMSSNQSISSPVLDAVPRTPSRERSSSASSPEMKDGLPRTPSRRSR 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             473 SGSSPGLRDGSGTPSRHSLSGSSPGMKDIPRTPSRGRSECDSSPEPKALPQTPRPRSRSP 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 ALPTSSODEELMEVVEKSE------EPAGQILSHLSSELKEMSTSNFESSPEVEE 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 LRENSFGSPLEFRNS-GPLGTEMNTGFSSEVKEDLNGPFLNQLETDPSLDMKEQSTRSSG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         583 AS-POERSESDSSPDSKAKTRTPLRORSRSGSSPEVDSKSRLSPRRSRSG---SSPEVKD 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  639 KPRAAPRAOSGSDSSPEPKAPAPRALPRRSRSGSSSKGRGPSPEGSSSTESSPEHPPKSR 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----DEDIEASNEEEN 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 QEKSKDSLVQSCPGSLSLCAGVKSSTPPGESYFGVSSLQLKGQSQTSPDHRSDTSSPEVR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 723 PEDSEVEAVK-PSEDSPENATSRGNTEPAVELEPTTETAP------STSPSL--- 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         768 AVPSTKPAEDESVETQVNDSIS-----AETAEQMDVDQQEHSAEEGSVCDPPPATK 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 MSPEQSRFQSDSSSYPTVDSNSLLGQSRLETAESKEKMALPPQ----EDATASPPRQKDK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        879 SSATCSADEDVDGEPERQRMFPMDSKPSLLNPTGSIL--VSSPLK----PNPLDLPQLQH 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAAV------IPPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEE 975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  819 ADSVDVEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309 RPAVSLTLDQSQSQASLEAVEVPSMASSW-----GGP-----HFSPEHKELSNSP
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.0%; Score 376; DB 2; Length 1791; Best Local Similarity 19.9%; Pred. No. 3.5e-07; Matches 396; Conservative 222; Mismatches 803; Indels 566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        681 QHKQKTSRKPREERDVSQCESVASTVSAQE----
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qq	758	RSPSVSSPEPAEKSRSSRRRRSASSPRTKTTSRGRSPSPKPR-GLQRSRSRSREKTRT 816
Qy	1374	SLITGPSKLSRGMPPLEIV
q	817	TRRRDRSGSSGSTSRRRQRSRSRSRVTRRRRGGSGYHSRSPARQESSRTSSRR 869
Qy	1434	KYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIY 1476
QO	870	RGRSRTPPTSRKRSRSRTSPAPWKRSRSRSRASPATHRRSRSRTPLISRRRSRSRTSP-VS 928
δλ	1477	DDTSARRIPVSYQNTMSRGSPMMNRTSDVTIPPNKSTNHERKSTLTPTQRESIPAKSPVP 1536
QO	929	RRRSRSRTSVTRRRSRSRSRSPVSRRRSRSRTPPVTRRRSRSRTPTTRRRSRSRTP 983
οy	1537	GVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPG 1596
QO	984	PVTRRR
ογ	1597	YPSOYQLYAMENTRQTILNDYITSOQMQVNLRPDVARGLSPREQPLGLPYPATRGIIDLT 1656
QQ	1012	RRSRSRTSPVTRRRSRSRTSPVTRRRSRSRTSP-VTRRRSRSRTPPAIRRR 1061
Qy	1657	DRITYIPGTQITFPPRPYNSASMSPGHPTHLAA
QO	1062	SRSRIPLLPRKRSRSRSPLAIRRRSRSRIPRIARGKR 1098
Qy	1717	EREREKERERERIAAASSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQ 1776
QQ	1099	SLIKSPPAIRRKSASGSSSDRSRSATPPAIRNHSGSRTPPVALNSSRMSCFSRPSMSP 1156
δλ	1777	GTNGTSVITPLDPTAQLRIMPLPAGGPSISQGLPASRYNTAADALAALVDAAASAPQMDV 1836
qa	1157	TPLD
δy	1837	SKTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHS 1896
QO	1192	GPRIPDHQRISVPENHAQSRIALALTAISLGTARPPPSM 1231
Qy	1897	SVVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVIITRQIASDKDARER 1950
qa	1232	SAAGLAARMSQVPAPVPLMSLRTAPAANLASRIPAASAAAMNLASARTPAIPTAVNLADS 1291
δy	1951	GSQSSDSSSLSSHRYETPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQY 2010
οqα	1292	RIPAAAAAAMNLASPRIAVAPSAVNLADPRIPIAPAVNLAGARIPAALAALSLIGSGI 1348
Qy	2011	EGPLHHYRPQQESPSPQQQLPPSSQAEGMGQVPRTHRLITLADHICQIITQDFARNQVSS 2070
qa	1349	11PPTAANYPSSS 1359
Qy	2071	QTPQQPPTSTFQNSPSALVSTPVRTKTSNRYSPESQAQSV 2110
QQ	1360	RIPOAPASANLVGPRSAHATAPVNIAGSRTAAAIAPASLISARMAPALSGANLISPRVPL 1419
Qy	2111	-HHQRPGSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVHEKQDSLLL 2167
Ф	1420	SAYERVSGRISPP-LLDRARSRIPPSAPSQSRMTSERAPSPSSRMGQAP 1467
Oy	2168	LSQRGAEPAEQRNDARSPGSISYLPSFFTKLENTSPWYKSKKOEIFRKLNS 2218
qa	1468	-SQSLLPPAQDQPRSPVPSAFSDQSRCLIAQTTPVAGSQSLSSGAVA 1513
Οy	2219	SGGGDSDWAAAQPGTEIFNLPAVTTSGS 2246
Dp	1514	TTTSSAGDHNGMLSVPAPGVPHSDVGEPPASTGAQQPSALAALQPAKERRSSSSSSSSS 1573
07	2247	VSSRGHSFADPASNLGLEDIIRKALMGSFDDKVEDHGVVMSQPMGVVPGTANTSVVTSGE 2306
QQ	1574	SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS
Οy	2307	CO .
qa	1617	GRPP

407 MFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNFGLIASYL 	QY 467 ERKSVPDCVLYXXLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEKVEEKEEDKAEKTE 526	QY 527 KKEEEKKDEEEKDEKEDSKENTKEKDKIDGTAEETEEREQATPRGRKTANSQ 578	Qy 579 GRRKGRIIRSMINEAAAAAAAAEEPPPPLPPPPEPISTEPVETSRWIEEEMEVAKK 638 : : : : : : : : : : : : : : : : : : :	Qy 639 GLVEHGRNWAAIAKWVGTKSEAQCKNFYFNYKRHNLDNLLQQHKQKTSKKPREERDVSQ 698 : ::   ::   :   :	QY 699 CESVASTVSAASN 718	QY 719 EEENPEDSEVEAVKPSEDSPENATSRGNTEPAVELEPTTETAPSTSPSL 767 :   :     :	QY 768 AVPSTKPAEDESVETQVNDSISAETAEQMDVDQQEHSAEEGSVCDPPPATKADS 821	OY 822 VDVEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSA 881 :   :   :   :   :   :   :   :   :   :	QY 882 TCSADEDVDGEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAÄV 936   1   1   1   1	Qy 937 IPPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEQRQRQEQI 983	QY 984DLECRSSTSPCGTSKSPNREWEVLQPAPHQLITNLPEGVRLPTTRPTRPPPPLIPSS 1040	KTTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQETPKPSVGSISLGLPRQOESAKSA:	-TLPYIKQELVRAQHEGVVRGTA 	QY 1137 GAIQEGSITRGIPTSKISVESIPSLRGSITQGIPALPQTGIPTE 1180  DD 1906 TPFLREKLFINEGSAEEPADLFAGSPTRKVVSTDSPFTDSGSGDIDVITESATLTSVPSR 1965	QY 1181 ALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIKNAREGTR 1233 ::: : : : : :	Qy 1234 SPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLS 1293	QY 1294 GSIMQGTPRATTESFEDGLKYPKQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHE 1353
QY 2361 DYHRQTPGWAWEDRPSSTGSTQFPYNPLTMRMLSSTPPTPIACAPSAVNQAAPHQQNRIW 2420 	Oy 2421 EREPAPL 2427 	SUL	A4/1/1 chondroitin sulfate proteoglycan PG-M core protein - chicken C;Species: Gallus gallus (chicken) C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000	C;Accession: A47171 R;Shinomura, T.; Nishida, Y.; Ito, K.; Kimata, K. J. Biol. Chem. 268, 14461-14469, 1993 A;Title: cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed during	A;Reference number: A47171; MUID:93300846 A;Accession: A47171 A;Status: preliminary A;Molecule type: nucleic acid	Residues: 1-3562 <shi> Cross-references: GB:D13542; NID:g391643; PIDN:BAA02742.1; Experimental source: stage 22-23 developing limb buds Note: sequence extracted from NCBI backbone (NCBIN:134456,</shi>	C; Superfamily: chicken chondroitin sulfate proteoglycan PG-M core protein; C-type lecting F; 166-243/Domain: link protein repeat homology <lnk1> F; 264-345/Domain: link protein repeat homology <lnk2> F; 264-345/Domain: profe homology <lnk2> F; 364-345/Domain: profe homology <lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk2></lnk1>	F;3296-3327/Domain: EGF homology <egf>F;3296-3327/Domain: C-type lectin homology <lch>F;334-3454/Domain: C-type lectin homology <lch>F;3461-3517/Domain: complement factor H repeat homology <fhd></fhd></lch></lch></egf>	Query Match 3.0%; Score 374.5; DB 2; Length 3562; Best Local Similarity 18.1%; Pred. No. 9.5e-07; Matches 511; Conservative 379; Mismatches 1102; Indels 833; Gaps 118;	TEQ-SRYPPHSVQYTFPNTRHQQEFAVPDXRSSHLEVSQASQL 56 : :::		98PVDHDSLESKRPRLEQVSDSHFQRVSAAVLPLVHPLPEGLRA	QY 140 SADAKKDPAFGGKHEAPSSPISGQPCGDDQNASPSKLSKEELIQSMDRVDREIAKVEQQI 199	QY 200 LKLKKKQQQLEEEAAKPPEPEKPVSPPVEQKH 232   1   1   1   1   1   1   1   1   1	QY 233 RSIVQIIYDENRKKAEEAHKIFEGLGPKVELPLYNQPSDTKVYHENIKTNQVMRKKL 289	OY 290 ILFFKRRNHARKQREQKICQRYDQLMBAWEKKUDRIENNPRRKAKESKTREYYEKQF 346	OY 347 PEIRKOREQOERPORVGORGAGLSATIARSEHEISEIIDGLSEQENNEKOMROLSVIPPM 406 

: :   ;   ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	:     EKLLGSHFSFFDQGS	TLHEA-PKAQLSPGIYDDTSARTPVSY-QNTWSRGSPWMNRTSDVTIPPNKS 1512       :     :     GEAETLTESFTKASVSPTGKPEPQEQYGRKTVSMPSAVVHAYTAEPNELVTS 2218	TNHERKSTLLPTQRESIPAKSPVPGVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQL 1568	DPAMPEHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTIL- 1614   :::::::::	NDXITSQQMQVNLRPDVAR-GLSPREQPLGLPYPATR	PYNSASMSP  ::  :  PFHPASVGP		NLSIUNIQVEESSSIUSNAEINEEIIIIAAELIEIAISMAISSKALEEESSSHSNSNUNU 2464 PSPSVRIQEIMLQQRPSVFQGINGISVIIPLDPIAQLRIMPLPAGGPSISQGLPASRYNT 1816	ITHYFLVIEDPYNKEMDHRKGENGTSRPLPTPGDVSLEESSHML 2528	AADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAVSEQQ 1864   : :	QLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRGK 1924 	מ א			:  : ::   : :    - :   ::    :  -  :	RNQVSSQTPQQPPTSTFQNSPSALVSTPVRTKTSNRYSPESQAQSV 2110 	PISPPOVPVVHEKO	:	DSLLLLSQRGAEPAE-QRNDARSPGSISYLPSFFTKLENTSPMVKSKKQEIFRKLN 2217   ::   ::   ::	LGLEDIIRKAL		KVEDHGVVMSQPMGVVPGTANTSVVTSGETRREEGDPSPHSGGVCKPKLISKSNSRKS 2335
: :   KDLETAEVT SRGMPPLEIVP-	KKGKGSFSAVSI	TLHEA-PR     :   GEAETLTESFTK	TNHERKSTLT    :    :  TEHDITSLQTVT	DPAMPFHRALDF   : :: LPKATES	NDYIT	GIIDLTNMPPT-	GHPTHLAAP	PSPSVRTQETMI	: ITHYFLVIEDPY			TTITAANFII         :  : TVITGLASLETE	SHRYET	EGPLHHYRPQOE	:  : :: DSILNFSTVEEN	RTTVLNELGIFLE	HHQRPGSRVSPE	J	-	SSGGGDSDMAAA 1	SVSQNPKSSVTV	KVEDHGVVMSQF
Db 2072 Ov 1414		Qy 1462 Db 2167	Qy 1513 Db 2219	Oy 1569	1615		Oy 1701		Db 2485	Oy 1817 Db 2529	Qy 1865 Db 2589	Qy 1925			Db 2744	Qy 2065 Db 2804	2111	Db 2858	Oy 2163 Db · 2906	2218	2956	Qy 2278

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A;Map position: 2
A;Introns: 36/2; 92/2; 182/2; 272/3; 344/2; 426/2; 490/1; 541/2; 700/3; 770/3; 1286/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ricajadsty. S. submitted to the EMBL Data Library, March 1996 submitted to the EMBL Data Library, March 1996 submitted to the EMBL Data Library, March 1996 sheerence number: 220417 sheesesion: T27776 sheesesion: T27776 sheesesion: T27776 sheerences: DNA sholecule type: DNA sheesidues: 1-2526 shills sheesidues: 1-2526 shills sheesidues: EMBL: 269904; PIDN: CAB54501.1; GSPDB: GN00020; CESP: F07A11.6a shipmental source: clone ZK20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-2526 <WIL>
A; Residues: 1-2526 <WIL>
A; Cross references: EMBL:266511; PIDN:CAB54210.1; GSPDB:GN00020; CESP:F07A11.6a
A; Experimental source: clone F07A11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apportetical protein F07A11.6a - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999 C;Accession: T20531; T27776
R;Palmer, S.
submitted to the EMBL Data Library, October 1995
A;Reference number: Z19287
A;Reference number: Z19287
                                                                                                                                                                                                                      3055 EETESSVNDLIIEENATVSGDSPSIH---DY---PTAFWNFGERTSTDVPKLSTIEVEFSS 3109
                                                          2336 KSPIPGQGYLGTERPSSVS----SVHSEGDYHRQTPGWAWEDRPS-----STGSTQFP- 2384
                                                                                                                                                                                  2385 ---YNP-----LIMRMLSSTPPTPIACAPSAVNQAA--PHQONRIWEREPAPLLSAQYE 2433
3004 VSSDMAATYKPPTTDLDTTVSSLLVFSPEPESESISTESTPH------FNKFVTERS 3054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 LKLKKKQQQLEEE-----AAKPPEPEKPVSPPPVEQKHRSIVQIIYDENRKKAEE---- 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 LRARSTKPQFEDSIEYKISAYIPEPTQN-SPIP-EFPSESTACVVYEIQSGSTPERDLFE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 ---AHKIFEGLGPKVELPLYNOP--SDTKVYHENIKTNOVMRKKLILFF----KRRNHARK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 QREQKICORYDQLMEAWEKKVDRIENNPRRKAKESKTREYYEKOFPEIRKQREQQERFQR 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 SGEQK----HYRRRFES 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         362 VGQRGAGLSATIARSEHEISEIIDGLSEQENNEKQMRQLSVIPPMMFDAEQRR---VKFI 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 YGQ---VIDVDMVKSNDNKAFAVVQFTNIDDAQKALQDTNIPKPMSYQSRPSHRIIIFYL 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    419 NWNGLMEDPMKVYK-------DRQFMNVWTDHEKE--IFKDKFIQHPKNFGLI 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : |: | : : | | | 347
290 PIECTNEEIMLIIRSLSDRIVDICVDWWDRSAVITLDDWEPANLLLKRWKLVGRNNFG-- 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                463 ASYLERKSVPD-C---VLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEKVEEKE 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348 ----EHKVAVDFCSDRFNLYFINRKKENIEVAARSSSPTSKSENDGSSSPSSRDRQNL 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.9%; Score 372; DB 2; Length 2526; Best Local Similarity 18.2%; Pred. No. 7.7e-07; Matches 467; Conservative 343; Mismatches 898; Indels 860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
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Oy Db	519		
δγ	576	NSQGRRKGRITRSMTNEAAAAAAAAAATEEPPPPLPPPPEPISTEPVETSRWTEEEMEV 635  : :  VSEEKRH	
δ δ	636	AKKGLVEHGRNWAAIAKWVGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRKPREERD 695   :   :	
oy Do	696	QCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSEDSPENATSRGNTE :	
Qy Db	749	PAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMD 797 	
oy Op	798	뮹 :	
à à	848	RASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDVDGEPERQRM 898	
2 6	899		
8 6	929		
3 & 2	980	PHQLITNLPEGVRLPTTRPTRPPPPLIPS	
7 A	1040	PGTYLTSHNQASYTQETPKPSVGSISIGLPRQOESAKS	
Pb Qy	1100	ATLPYIKQEBFSPRSQNSQPBGLLVRAQHBGVVR-GTAGAIQEGSITRGTPTSKI 1153 	
Qy Db	1154	SVESIPSLRGSITQGTPAL 1172	
Oy Dp	1173	PQTGI	
Oy Dp	1197	PEKGREBAASKGHVIYEGKSGHILSYDNIKNA 1228  :	
O D	1229	REGTRSPRTAHEISL	
yo 4	1252	GNIKOGMSMRESPVSAPLEGLICRALPRGSPHSDLKER 1289	
QY	1290	132	
qa à	, 1226	GELTTSSDDEDHNDAGEIHQORLTEDRENRKROKSLTAYSSDEQGERKNVPKRMRRDD 1283	
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1689 --PDSQQNG-PVLVSQQSQPSPMSSQQSDMAQNLILSSKDINDLAAKLHKNPEALAQATR 1745 2084 IMNQOETLMALLAARNGLPFAMPQONQOPOMPAQGGFA-IPTVLPHMSLKRNAKDQLSVG 2142 :1 : :1 | : :1 | : :1 | : :1 | : :1 | : :1 | : :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | ----YDD------TSARRIPVSYQNTMSRGSPMMNRTSDV----TIPPNKSINHERK 1518 1568 LDPAMPFHRALDPAAAAYLFQRQLSPT-PGYPSQYQLYAMENTRQTILNDYITSQQMQVN 1626 1604 SEP-----SPMEEEVKLETSPVPKEE-------PIKMEESPEQTPTP--DLIS---- 1642 --- LQQRP-SVFQGTN 1779 1826 ------DAAASAPOMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEK 1875 1899 VYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVIITR-----QIASDKDARERGS 1952 1972 ASSDPNPPATSTVDLAAMLQQLQAAQAAQQAPVVTTASTP-NPLSNLETLLSTASLA 2030 2031 NLATG-----GALNPLSMLALTSSLNQSSPVYQGIARVLLTMNMGQMLATHQTSELLA 2083 | | | : | : | : | : | 1284 S----EDAAAKHPGWSAKDDQKQRRRKLEHRRSSEDESKKNAKRDFRDFREDVSDEE- 1337 1365 RKTPEVVQSTRPIIEGSISQGTPIKFDNNSGQSAIKHNVKSLITGPSKLS-RGMPPLEIV 1423 PE-NIKVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEA---PKAQLSPGI---- 1475 1519 STLTPTQRESIPA-----KSPVPGVDPVVSHS--PFDPHHRGSTAGEVYWSHLPTQ 1567 1627 LRPDVARGLSPREQPLGL---PYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRITYIPG 1683 1684 TOITFPPRPYNSASMSPG-----HPTHLAAAASAERERERERERERERERIAAASSDLY 1737 1643 -----nnesqdtpgavnnhlhenhdavqtpiqlqpasqhqvaqpsprpava---- 1688 1780 GTSVITPLDPTAQLRIMPLPAGG-----PSISQGLPASRY----NTAADALAALV--- 1825 -----FPSGKPQPHSSV 1898 1918 ASTSSNPPKAPLOPS-----ASVNONTIDPAEIEEIRVORWFYKPLKMSAEEAATVMAV 1971 2155 -VPVVHEKQD-----SLLLLSQRGAEPAEQRNDARSPGSISYLPSFFTKLENTSP 2203 1509 SIFDEEEADEFPQYPDFGISTNEKEVSGKDP---HNIKPTEPLNNGHT--DLLFS----: 1858 QKQEVPRHGFQHVLSMMTPEARSLYEQFPGLSSYINRDSIGATNGVLHLPTQSIQRPSST 1953 QSSDSS-----SSLSSHRYETPSDALEVISPASSPAPPQEKLQTYQPEVVKA 2000 NQAENDPTROYEGPLHHYRPQQESPSPQQQLPPSS-----QAEGMGQVPRTHRLITLAD 2054 HICQ---IITQDFARNQV----SSQTPQQPPTSTFQNSPSALVSTPVRTKTSNRYS--2103 --PESQAQSVHHQRPGSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEPISPPQ----2143 GVSDRKKSCPLHAMIGQGQOPP-----PPQQPMQAVAPAPPRSP-SPPRKSMFEN 2204 MVKSKKQEIFRKL--NSSGGGDSDMAAAQPGTEIFNLPAVTTSGSVSS 2249 1738 LRPGSEQPGRPGSHGYVRSPSPSVRTQETM-----1876 RS-----VQCLYTSSA-----1476 g g ò Db ò Q δ ΩŽ g ò g ò a ò q οy a δ q ò ογ g δy 요 δy g ŏ g ò g ολ ò g

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981 PSIESYSEDDESKFCSYGQYPADLAHKIHSANHMDDNDGELDTPINYSLKYSDEQLNSGR 1040
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                                                                                           --EISEIIDGESEOENNEK 395
                                                                                                                                                                                                                                                396 QMRQLSVIPPMMFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHE--KEIFKDKFI 453
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            648; Gaps
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            Indels
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            807;
            Mismatches
                                                                                       347 PEIRKQREQQE-RFQRVGQRGAGLSATIARSEH-
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1542 PKESNENQEKEAEKTIDSEKDLL----
            Conservative 288;
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            Matches 409;
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A. Residues: 1506-1525 AMIX>
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A. Residues: 1506-1525 AMIX>
A. Residues: 1506-1525 AMIX>
A. Residues: 1506-1525 AMIX>
A. Molecule extracted from NCBI backbone (NCBIN:78214, NCBIP:78218)
A. Molecule extracted from NCBI backbone (NCBIN:78214, NCBIP:78218)
A. Spirio, L.; Olschwang, S.; Groden, J.; Robertson, M.; Samowitz, W.; Joslyn, G.; Gelber C. A. Spirio, L.; Olschwang, S.; Groden, J.; Robertson, M.; Samowitz, W.; Joslyn, G.; Gelber A. Reference number: A49319; MUID:94073973
A. Reference number: A49319
A. Accession: A49319
A. Residue; preliminary; translated from GB/EMBL/DDBJ
A. Molecule type: mRNA
A. Residues: 'G', 143-171, 'P', 173-179 < SRI>
A. Residues: 'G', 143-171, 'P', 173-179 < SRI>
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A; Residues: 1-2843 <KIN>
A; Residues: 1-2843 <KIN>
A; Cross-references: GB:M74088; NID:g182396; PIDN:AAA03586.1; PID:g182397
B; Joslyn, G.; Carlson, M.; Thliveris, A.; Albertsen, H.; Gelbert, L.; Samowitz, W.; Grod
arrington, J.; McPherson, J.; Wasmuth, J.; Le Paslier, D.; Abderrahim, H.; Cohen, D.; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-183, 'L', 185-969, 'N', 971-1308, 'G', 1310-1324, 'SS', 1326, 'HSTLE', 1332-1354, 'P' A; Cross-references: GB:M73548; NID:g190163; PIDN:AAA60354.1; PID:g190164
R; MiXi, Y.; Nishisho, I.; Horii, A.; Miyoshi, Y.; Utsunomiya, J.; Kinzler, K.W.; Vogelst Cancer Res. 52, 643-645, 1992
A; Title: Disruption of the APC gene by a retrotransposal insertion of L1 sequence in a day. Reference number: A44928; MUID:92119623
                                                                                                                                                                                                                                                                                                                                                                                                             Smith
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Cell 66, 601-613, 1991
A;Title: Identification of deletion mutations and three new genes at the familial polypo
A;Reference number: A39658; MUID:91330307
A;Accession: B39658
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A:Note: mutations of this gene can result in familial adenomatous polyposis or sporadic
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Hum. Genet. 90, 560-562, 1993
A;Title: Identification of an alternative 5' untranslated region of the adenomatous
A;Reference number: I54271; MUID:93186137
                                                                                                                                                                                                                                                                                                                                                                                                         D.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                               I.; Nakamura,
                                                                                                                                        RHUAPA
adenomatous polyposis coli protein - human
N.Alternate names: polyposis coli locus protein DP2.5; tumor suppressor APC
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Ju1-2000
C;Accession: A37261; B39658; A44928; A49319; I54271
R;Kinaler, K.W.; Nilbert, M.C.; Su, L.K.; Vogelstein, B.; Bryan, T.M.; Levy, Icul, S.F.; Horii, A.; Ando, H.; Miyoshi, Y.; Miki, Y.; Nishisho, I.; Nakamur. Science 253, 661-665, 1991
A;Title: Identification of FAP locus genes from chromosome 5q21.
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C;Keywords: cancer; familial adenomatous polyposis; tumor suppressor
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DSMGAEGSAFRRILSRSSTMGNNSGSPSASGT----TSPSTSSSISS 2289
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Pred. No. 1.7e-06;
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Best Local Similarity
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ISRMPIEDSSPEKGREEAASKGHVIYEGKSGHI	RSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTWSRGSPMANRTSI	YIPGTQITFPPRPYNSASMSPGHPTHLAAAASAEREREREREKERERE	DKGPPKSRYEEELRTRGKTTITAANFIDVILTRQIASDKDARERGSGSSDS  HSSSLPRVSTWRRTGSSSSILSASSESSEKAKSEDEKHVNSISGTKQSKENQVSAKGT  SSSLSSHRYE-TPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGPLHH  SSSLSSHRYE-TPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGPLHH  WRIKENBEFSPTNSTSQTVSSGATNGAESKTLITQMAPAVSKTEDVWYLEDCPINN  YRPQGESPSPQQQLPPSQABGCMGQVPRTHALITLADHIC
1187 1969 1220 2029 1271 2089 1331 2141 1391	2184 1445 2228 1505 2253 1563 2306 1623	1680 2366 1728 2418 1788 2450 1848	1906 2554 1958 2612 2017 2669 2057 2724 2115
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hypothetical protein W06A7.3c - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C; Accession: T26216
R; Ainscough, R.
Submitted to the EMBL Data Library, August 1996
A; Reference number: Z20173
A; Accession: T26216
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Accession: T26216
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-2484 <WIL>
A; Cxoss-references: EMBL: Z78066; PIDN: CAB51467.1; GSPDB: GN00023; CESP: W06A7.3c
C; Genetics: A; Gene: CESP: W06A7.3c
A; Mpp position: 5
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A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2
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Oy Op	1071	QASYTQETPKPSVGSISLGLPRQDESAKSATLPYIKQEEFSPRSONSQPEGLLVRAQHEG 1130 
S S	1131	VVRGTAGAIQEGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGIPT 1179 
oy eb	1180	TEAFGDAEHYSYLDANIEKLVAMADEPLPVDELVSIEERREEVARKGHVIYEGKSGHIL 1220 
yo d	1221	LEGLICRALPR 1
ر م	1280	KRESPPIRA
දු දු		ITTIKEMGRSIHEIPRODILT
γ̈́ο		
<u>გ</u>	1006	STNDENPEAVSMVENVLPVNTEGLDESKEDNPDAPTAEAHSGEKNLRNDKTTDTRERDPE 1065
Oy Dp	1421	EIVPENIKVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQ-LSPGIYD 1477
δy	1478	DTSARRIPVSYQNTMSRGSPMMNRTSDVTIPPNKSTNHERKSTLIPPTQRESIPAKSPVPG 1537
g	1104	HAG
ò	1538	TQLDPAMPFHRALDPAAAAYLFQRQLSPTPGY 159
9	1143	TQPENAESHILQETGGASELKDDQNQPEEFSAEHQGKFEVSAEPDQ 1188
9 P	1598	PS-OYQLYA-MENTRGTILNDYITSQQMQVNLRPDVARGLSPREQPLGLPYPATRGIIDL 1655     ::
ογ	1656	TNMPPIILVPHPGGTSTPPMDRITYIPGTQITFPPRPYNSASMSPGH 1702
q	1249	KELETQELSSKEIKTSGQPETVPETSEAFVSDPEIFQRVKRASSTEPKTGKTEPHA 1304
ά	1703	175
g	1305	PIFIVGQSTEDDEQSIANVIDELVHEDDEKKVPEVTANISVSASENIDDSTTANAVPKTE 1364
0y Db	1754	VRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMPLPAGGPSISQGLPASR 1813 
οy	1814	YNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEEN 1852
g	1415	::  :  :   :  - :
ογ	1853	EKRSAAVSEOQQLEQKTLEVEKRSVQC 1880
qq	1466	
φ	1881	LYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVIITRQ 1940
qq	1526	
οý	1941	IASDKDARERGSQSSDSSSSLSSHRYETPSDAIEVISPASSPAPPQEKLOTYQPEVVKAN 2000
qq	1568	VYTESEISEMAPQVSESTCPIPEPLADLKLPVEDDEKTPEPEPVVPG 1614

	::     : :   :   :		85	qa
	EETEEREQATPRGRKTANSQGRRKGRI 585		559	Qy
	PVSSAKVIALESSGDCEEGNIKISANENSVEPDGADKPA 84	SDQESSENKEPDASENVEETE	25	7 점
95;	320; Mismatches 937; Indels 686; Gaps 9	428; Conservat	atches	<b>2</b> .
	Score 361; DB 2; Length 2607; Pred. No. 2.1e-06;	Match 2.9%; Local Similarity 18.1%;	Query Ma Best Loc	Oπ
2586,	; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2; 258	tion: 5 1827/1; 1866/3	A; Introns:	A;r A;I
		55P:W06A7.3a	Generics: Gene: CES	
/ . 3a	CIOSS-Tererences: EMBL:2/8006; PIDN:CABUISZZ.Z; GSPDB:GNUUUZ3; CESP:W05A/:3A Experimental source: clone W06A7	ererences: EMBL:Zental source: clo	xperime	<b>₹ ₹</b> (
•		s: 1-2607 <wil></wil>	esidue:	E E (
	translated from GB/EMBL/DDBJ	preliminary; tra	tatus:	8 X
	<b>6</b>	se number: Z20173 on: T26215	eferenc ccessic	A; A
	a Library, August 1996	Jn, K. to the EMBL Data	mitted	sut
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c	a - Caenorhabditis elegans egans	protein	hypothetical r C;Species: Cae	hyr C;S
		-	RESULT 31	RES
		HDEVDNFL-RREPTPPFET	2126	g dd
Ω.	VRE-AEKQLPESPVPEKIETPEPLVDIHDTVDKV 212		2070	අු
1	GDYHRQTPGWAWEDRPSSTGSTQFPYNPLTMRMLSSTPPTPIACAPSAVNQA 2411	VHSE	2356	٥٧
on	: :       :       :       :       :         :		2010	qq
r.	235	HSGGVCKPKI	2317	Qy
on	:     : :   : :   : :   : :   :   : :   :   :   : :   :   : :   :   :   : :   :   : :   :   :   :   :   :   :   :   :   :   : :   :	 FGSLGSDDMKP	1955	. <u>a</u>
· w	231		2272	ò
4	:   :  :  SPNAPPVGFENTAQFLEKLQQEDRPSAEGSIDSSGFEKVDHEGLDEFAAPPVHDPMQKSV 1954		1895	qq
7	227	IFNLPAV	2235	QY
4	:	:       DSFSSISSFGDRQKFF	1835	ΩD
4	223		2180	Qy
4		I:     :   :   :   III	1775	qq
6	217	ISPPOVPVVHEKO	2150	Oy
4	:  : : : :           DMQSVPHSPQEKQEEIEALSEIIEEPQAMKEVEKPVESAPEKDNESLEAPEI 1774	: : :   :   DMQSVPHSPQEKQEEI	1723	đ
6	KSRGSRPGKSPERSHVSSEPYEP 214	TKTSNRYSPESQAQSVHH-	2095	Oy
2	:       :	: :      EEQQKELVESLERPLTIITQ	1672	q
4	DFARNQVSSQTPQQPPTSTFQNSPSALVSTPVR 209	RLITLADHICC	2047	Qy
1 0	HIRTOGESPERGUET FOSGABGAGG : 10   1   1   1   1   1   1   1   1   1	. н	1615	ž 8
ď	PSSOAEGMG	OAEND PTROYEGPI	2001	ò

οy	286	TRSMTNEAAAPPPP	610
QQ	145	:	204
δ	611	LPP PPEPISTEPVETSRWTEEMEV	635
q	205	IPNVFTPEVANDETVETFSVTAEEASIPVVVELEPIGDEXEFQRPVENFSEPSDNINLEE	264
δy	636	GRNWAAIAKWGTKSEAQCKNFYFNYKRHNLDNLLQQHKQKTSR     :       : :   : :	688
g	265	NMFTPLDELEPQQKILNEKAEHIEIEASGDEFIKDHPFPVEN	316
Qγ	689	SEENPEDSEVEAVKPSEDSPEN	740
qq	317	THE TO THE THE THE THE THE THE THE THE THE THE	376
Qγ	741	ATSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISA	190
q	377	LVEAREIITESKDAYSTDVPESRKTVSDVIGLEEAGDKIVSNNVSNVMGN	426
οy	791	EGSVCDPPPATKADSVDVEVRVPENHASKVEGDNTKERDLDRAS	850
g	427	PDESQLALEQADNVPELPIENSEQETVAVKATESCOHVVDSQKTLERASSLEE	479
οy	851	EKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDVDGEPER	895
g G	480	:   :   :	537
οy	896	ORMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTP	953
qq	538	VLELDDRVQNKNPESEVTAVDASKTEGDFSDSPDSRATETFWEKLVTVTENLLFAGDK !	595
δλ	954	RSSTSPCGTSKSPNREWEVLOPAPHO	1013
qq	296	LSEERIQEIRENETISQPGKEEDDLENANDPDDE-TIVEKIVSM (	638
δy	1014	ASEKPSFIMGGSISOGTPGTYLTSHN	1070
qq	639	AESSLPIEBAVISTEDGGTSDQPAQNAIPDSEETTVDDSQTEEIFTDDN	989
δy	1071	QASYTQETPKPSVGSISLGLPRQQESAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEG	1130
ΩD	687	VKKSKENTPKAENDTEINYLPGGEEGPEDNAEKRNEAVSPNDETSEIKQDLEN	739
Qγ	1131	VVRGTAGAIQEGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGIPT ]	1179
g	740	LENGASGPDNNVQVDEAAQEDPTDPETVDETTSKISENMPKAPDTEDDNATEFIEAGLET	799
δy	1180	VIYEGKSGHIL	1220
g	800		855
δ	1221	SYDNIKNAREGIRSPRTAHE-ISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPR	1279
QQ	856	REDRRIVSLIGIGDQNAPIQVIFVGDGDENPDANADQFR	894
ογ	1280		1327
qa	895	TSEHNELIESDKESEEAITKNEEDVOQDPIQSEEPLISQEGESSIGNKIVA 9	945
QY	1328		1361
Q	946	VVGSVLLGGAVIPYGVLASNENEDAHADREVEETGDSTRDRPEEETFVSKLTSMVENILP	1005
οy	1362	QESRKTPEVVQSTRPIIEGSISQGTPIKFDNNSGQSAIKHN-VKSLIIGPSKLSRGMPPL   : :     : :     : :       : :	1420
д	1006	RNDKTTDTRERDPE	1065
о <sub>ў</sub>	1421	YEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQ-LSPGIYD	1477
g	1066	EETILNKLVENALPTGVTGSFTEVSAPDAQELDETVVD 1	1103

οy	1478 DTSARRTPVSYQNTMSRG	SPMMNRTSDVIIPPNKSTNHERKSTLTPTQRESIPAKS
QQ	1104 HAG	VEDAPEKSAGGTVIEKFTSMIESILPVQ
οy	1538	STAGEVYWSHLPT
qq	1143 TOPENAESHIDOETGG	ASE
δλ	1598 PS-	OYOLYA-MENTROTILINDY ITSQOMQVNLRPDVARGLSPREQPLGLPYPATRGIIDL 1655
q	1189	ESAEFQLEAKKDQDKETIENSEDAKKETVMEKLVSLVENILPVEAVLPSDSTVTKNSEDK 1248
δy	1656	TNMPPILLVPHPGGTSTPPMDRITYIPGTQITFPPRPYNSASMSPGH 1702
Op	1249 KELETQELSSKEIKTSGQP	TSGQPEYVPETSEAFVSDPEIFQRVKRASSTEPKTQKTEPHA 1304
Qy	1703	EREREKERERERIAAASSDLYLRPGSEQPGRPGSHGY 1753
QQ	1305	PIFIVGQSTEDDEQSIANVIDELVHEDDEKKVPEVTANISVSASENIDDSTTANAVPKTE 1364
Qy	1754 VRS	PSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMPLPAGGPSISQGLPASR 1813
qq	1365 VSSEQLQVATVEFELESAPE	ILESAPEEESAAIPEVQEPLEKVEVQPDLSQNSPAPH 1414
δλ	1814 YNTAADALAALVDAAASAPQMD	AASAPQMDVSKTKESKHEAARLEEN 1852
qq	1415	KIIDLHFNIPKDHEDYGNDYVPFGTESSEESQKADGNQENQEEEDVVAELN 1465
οy	1853	188
qq	1466	FHPIRQWRDEDVISLQSLKSLVAEVGCITDVDASDVNEQDEESTLKILKVVPSEPSLLEL 1525
ΟŊ	1881	VVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVIITRQ 1
g	1526 DFTNDPKVIHVPIPLME	'LMEPATMYLEEMVEWIIADAVKEVSEME 1567
δλ	1941	SHRYETPSDAIEVISPASSPAPPQEKLQTYQPEVVKAN 200
qq	1568 VVTESEISEMAPOVSESTCPIP	SESTCPIPEPLADLKLPVEDDEKTPEPEVVPG 1614
δλ	2001 QAEND-	-PTRQYEGPLHHYRPQQESPSPQQQLPPSSQAEGMGQVPRTH- 2046
QQ	1615 QVQERIIPIEVEQAPT-	PTIPORPPRAPKSELPKVAKPLDDSKSRVRFAPLNIKLGRTYS 1671
οy	2047	DFARNQVSS
qq	1672 EEQQKELVESLERPLTIIT	LTIITQQKPPEKPTEDIGALSPLSPNTLAEYEEVPMM 1722
δλ	2095 TKTSNRYSPESQAQSVHH	QRPGSRVSPENLVDKSRGSRPG
οp	1723 DMQSVPHSPQEKQEEIEAL	EIEALSEIIEEPQAMKEVEKPVESAPEKDNESLEAPEI 1774
Qy	2150	DSLLLLSQRGAEPAEQR 2179
qq	1775	
Οy	2180 NDARSPGS	SFFTKLENTSPMVKSKKQEIFRKLNSSGGGDSDMAAAQPGTE 2234
qq	1835 DSFSSISS	FGDRQKFRTAIENIRQDLLPFQSSVSQYLRSSPNPSQQLLVTNLSMDSPSDL 1894
Οy	2235 IFNLPAV	TTSGSVSSRGHSFADPASNLGLEDIIRKAL 2271
qa	1895	SPNAPPVGFENTAQFLEKLQQEDRPSAEGSIDSSGFEKVDHEGLDEFAAPPVHDPMQKSV 1954
Qy	2272 MGSFDDK	VEDHGVVMSQPMGVVPGTANTSVVTSGETRREEGDPSP 2316
QQ	1955 FGSLGSDDMKPGSQDDGFV	DDGFVFIERNEANEATLKKNQKMSSHHNDVIEKNYFNDNAP 2009
Qy	2317 HSGGVCKP	-KLISKSNSRKSKSPIPGQGYLGTERPSSVSS 2355
QQ	2010	TAALLESPIAEEARKLVQDAVESASEYKKQAVDSGDEIGRELLDNVEQKIEQVKEPIVDS 2069
ΟŊ	2356 VHSEGDYHRQ	-GDYHRQTPGWAWEDRPSSTGSTQFPYNPLTMRMLSSTPPTPIACAPSAVNQA 2411

Db 1957 KVSEILKKDVCVDNKGSPKSDKG 1982  Qy 335 ESKTREYYEKQFPEIRKQREQQERFQRVGQRGAGLSATIARSEHEISEIIDGLS 388	2043 SSSLTNLKYKFEDAKKDGEGGQKRVLKPAIALQEHKLKMPPASM 438 NVWTDHEKEIFKDKFIQHPKNFGLIASYLERKS	Db 2087 RISTS-EKELCKMADSFFGTDTILESPDDFSQHDQDKSPLSDSGFETRSEKTPSAPQSAE 2145 Qy 471VPDCVLYYYLIKKNENYKALVRRNYGKRRGRNQQIARPSQEEKVEEKE 518 Db 2146 TIGEKPLEHEVPIPPYITETRIEVVHVIRSYDEAGDVPOROPEPPYSPKP 2196	519EDKAEKTEKKEEEKKDEKEDSKENTKEKDKI     :     :	Qy 555DGTAEETEEREQATPRGRKTANSQGRKRGRITRSMTNEAAAASAAAA 601 	Qy 602 AATEEPPPDLPPPPEPISTEPVETSRWTEEBMEVAKKGLVEHGRNWAAIA 651 :	QY         652 KMVGTKSEAQCKNFYENYKRRHNLDNLLQQHKQKTSKRPREERDVSQCESVASTVSAQED 711           ::          : <t< th=""><th>QY 712 EDIEASNEEENPEDSEVEA-VKPSEDS-PENATSRGNTEPAVELEPTTETAPSTSPS 766   1:                                  </th><th>Qy 767 LAVPSTKPAEDESVETQVNDSISAETAEQMDVDQQEHSAEEGSVCDPPPATKAD 820   1   1   1   1   1   1   1   1   1  </th><th>QY 821 SVDVEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSS 880 :   :   :   :   :     D</th><th>OY 881 ATCSADEDVDGEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVIPPM 940   1   1   1   1   1   1   1   1   1  </th><th>QY 941 VSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEQRQRQEQIDLECRSSTSPCGTS 997 : :: :: ::  ::  Db 2552KHAMMMRFTEDRLDRGREKLIYEDRVDRTVKEA 2584</th><th>QY 998 KSPNREWEVLQPAPHQLITNLPEGVRLPTTRPTRPPPPLIPSSKTTVASEKPSFIM 1053  1</th><th>OY 1054 GGSISQGTPGTYLTSHNQASYTQETPKPSVGSISLGLPRQQESAKSATLPYIKQEEFSPR 1113  1                                    </th><th>Qy 1114 SQNSQPEGLLVRAQHEGVVRGTAGAIQEGSITRGTPTSKISVESIPSLRGSITQG-TPAL 1172   1   1   1   1   1   1   1   1   1  </th><th>QY 1173 PQTGIPTEALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIKNA 1228                                      </th><th>Qy 1229 REGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDL 1286 : </th></t<>	QY 712 EDIEASNEEENPEDSEVEA-VKPSEDS-PENATSRGNTEPAVELEPTTETAPSTSPS 766   1:	Qy 767 LAVPSTKPAEDESVETQVNDSISAETAEQMDVDQQEHSAEEGSVCDPPPATKAD 820   1   1   1   1   1   1   1   1   1	QY 821 SVDVEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSS 880 :   :   :   :   :     D	OY 881 ATCSADEDVDGEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVIPPM 940   1   1   1   1   1   1   1   1   1	QY 941 VSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEQRQRQEQIDLECRSSTSPCGTS 997 : :: :: ::  ::  Db 2552KHAMMMRFTEDRLDRGREKLIYEDRVDRTVKEA 2584	QY 998 KSPNREWEVLQPAPHQLITNLPEGVRLPTTRPTRPPPPLIPSSKTTVASEKPSFIM 1053  1	OY 1054 GGSISQGTPGTYLTSHNQASYTQETPKPSVGSISLGLPRQQESAKSATLPYIKQEEFSPR 1113  1	Qy 1114 SQNSQPEGLLVRAQHEGVVRGTAGAIQEGSITRGTPTSKISVESIPSLRGSITQG-TPAL 1172   1   1   1   1   1   1   1   1   1	QY 1173 PQTGIPTEALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIKNA 1228	Qy 1229 REGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDL 1286 :
	plice form	N. Alternate names: anfyInt of C. Species: Homo sapiens (man) C. Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 20-Sep-1999 C. Accession: A55575 R. Kordeli, E.; Lambert, S.; Bennett, V. J. Biol. Chem. 270, 2352-2359, 1995	A;Title: Ankyrin-G. A new ankyrin gene with neural-specific isoforms localized at the ax A;Reference number: A5575; MUID:95138209 A;Accession: A55575 A;Status: preliminary	A; Molecule - type: Invad. A; Residues: 1-4377 <kor> A; Cross-references: GB:U13616; NID:g608024; PIDN:AAA64834.1; PID:g608025 C; Genetics:</kor>	Gene: GDB:ANNA Gene: GDB:ANNA Map position: 10q21-10q21 Superfamily: unassigned anyrin repeat prof	Reywolds: alternative spiiting; peripher 73-105/Domain: ankyrin repeat homology 106-138/Domain: ankyrin repeat homology 139-171/Domain: ankyrin repeat homology	172-200/Domain: ankyrin repeat homology 201-233/Domain: ankyrin repeat homology 234-266/Domain: ankyrin repeat homology 267-299/Domain: ankyrin repeat homology	300-32//omaln: ankyrin repeat nomology 330-35//omaln: ankyrin repeat homology 366-398//omaln: ankyrin repeat homology 399-431//omaln: ankyrin repeat homology 399-431//omaln: ankyrin repeat homology	45.4.94/DOMAIN: ankyrin repeat nomology 45.4.99/Domain: ankyrin repeat homology 498.530/Domain: ankyrin repeat homology 531.563/Domain: ankyrin repeat homology 531.563/Domain: ankyrin repeat homology	504-394/Obmaln: ankyrin repeat nomology 597-629/Domaln: ankyrin repeat homology 630-662/Domaln: ankyrin repeat homology 663-695/Domaln: ankyrin repeat homology 663-695/Domaln: ankyrin repeat homology 663-730/maln: ankyrin repeat homology	729-7 729-7 762-7 795-8	Query Match  2.8%; Score 359; DB 2; Length 4377;  Best Local Similarity 18.3%; Pred. No. 4.9e-06;  Matches 473; Conservative 312; Mismatches 861; Indels 860; Gans 122;	PRIEDVSDSH-FORVSAAVL-PLVHPLPEGIRASADAKKDPAFGGKHEAPSSPI 160     :::     :	161 SGQPCGDDQNASPSKLSKEELIQSMDRVDREIAKVEQQILKLKK-KQQQLEEEAAKPPEP		280 KTNQVMRKKLILFFKRRNHARKQREQKICQRYDQLMEAWEKKVDRIENNPRRKAK    :::::  :: :: : : : : : : : : : : : :

<u>γ</u> α	1287	7KERTVLSGSIMQGTPRATTESFEDGLKYPKQIKRESPPIRAFEGAITKGKP 1337	
٠.	1338	YDGITTIKEMGRSIHEIPRQDILTQESRKTPEVVQSTRP	
<u>a</u> >	1377	/ WUKKVFKTWESSGATNNKSOKEKLSHVLVHDVRENH1GHPESKSVDOKNEFMSVTEKEKK 2906 / II-EGSISOGTPIKFDNNSGOSAIKHNVKSL-ITGPSKLSRGMPPLEIVPENIKVVERGK 1434	
ą	2907		
<u></u>	1435	S YEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTS 1480  :   .   .	
. >	1481	ARRIPVSYQNTMSRGSPMMNRTSDVII-PPNKSTNHERKSTLTPTQRESIP	
ð	3000	) SKET-VETOHFNSIEDEKVTYSEISKVSKHQSYVGLCPPLEETETSPTKSPDSLEFSP 3056	
<u>≽</u> 9	1531	L AKSPVPGVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAA 1584	
<b>≱</b> 1	1585	S YLFOROLSPTPGYPSQYQLYAMENTRQTILNDYITSQQMQVNLRPDVARGLSPREQPL-G 1643	
ą	3105	:	
<u>*</u>	1644	LPYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRIFYIPGTQITFPPRPYNSASMSPGHP 170	•
ō	3156	VSFLDSSGKSPLTPETPSSEEVSYEFTSKTPDSLIAYIPGKPSPIPEVSEESEEEEQAKS 3215	
<u>&gt;</u> , 4	1704	THLAAAASAEREREREKERERERIAAASSDLYLRPGSEQPGRP	
9 3	1740	1 SLAVALI VEBIRAVEREMENDOVSANDSNYRFANNRYALI LEFFFFFFLUALDĀLESVSANDSNYRFANNRYALI LEFFFFFFLUALDĀLESVSANDSNYRFANNRA PARAMATER PAR	
<u>.</u> 9	3268	GENETATION TO THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF T	
≿	1803	3PSISQGLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHBAARLEENLRSRSAA 1859	
ą	3318	3 SDDESIYQPVPVKKYTPKLKEVDDEQKEKPXASAEK 3353	
<u>≯</u>	1860	) VSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVYSEAGKDKGPPPKSRYEEEL 1919	
ð	3354	ASNOKELESNQNEI 3382	
Δ	1920		
ð	3383	3 AQNGNNDQSITECSIATTAEFSHDTDATEIDSLDGYDLQDEDDGLTESDSKLPIQAM 3439	
<u>ک</u> ج	3440	EVISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGPLHHYRPQGES 2023	
. ≥	2024	PSPOOOL PPSSOAEGMGOVPRTHRITTADHICOITTODEARNOVSSOTPOOP PTSTF	
, <u>,</u>	3485	:   :   :   :   :   :   :   :   :   :	
<u></u>	2082	QUSPSALVSTPVRTKTSNRYSPESQAQSVHHQRPGSRVSPENIVDKSRG 2130	
ą	3521	:   :	
Δ·	2131		
ð	3578	3 TIPDTIPARIPIDESTPISEPNPFPFHEGKMFEMIRSGAIDMSKRDFVEE 3627	
≱.	2191		
ą	3628	3628 RLOFFOIGEHTSEGKSGDQGEGDKSMVTATPQPQSGDTTVETNLERNVET 3677	

3678 PTDEPUREITPSGECOEGIEGSAAAATNISKYDEKLAFPIKMGISASTWTMKKEG 373 2273 -GSFDOKVVEDHGVVANSOMEVPGTANTSVATSGETREEGDFBEH 2317 37.38 PGETTDKIEAVMTSCOGLENETITHISNIANSOMGVPBH 3776 44.44 44.45 44.	Ž	PAVITSG
TYSOVITSGETRREEGDPSPH 2317  ITELIMISNIANSOMGYRPH 3776  ITELIMISNIANSOMGYRPH 3776  IN 29-Oct-1999 #text_change 18-Feb-2000  IN 29-Oct-1999 #text_change 18-Feb-2000  IN 29-Oct-1999 #text_change 18-Feb-2000  IN 29-Oct-1999 #text_change 18-Feb-2000  IN 29-Oct-1999 #text_change 18-Feb-2000  IN 20-Oct-1999 #text_change 18-Feb-20	рр	PTSGECQEGTSSSGSLEKSAAATNTSKVDPKLRTP
ETITMISNIANSQMGVRPH 3776	οy	3 -GSFDDKVEDHGVVMSQPMGVVPGTANTSVVTSGETRREEGDPSPH 231
Part	QQ	PGEITDKIEAVMISCOGLENETITMISNIANSOMGVRPH 377
nr 29-Oct-1999 #text_change 18-Feb-2000 nr 29-Oct-1999 #text_change 18-Feb-2000 nr 29-Oct-1999 #text_change 18-Feb-2000 nr 29-Oct-1999 #text_change 18-Feb-2000 nr Calone K06A9. 1:Ac70890.1; GSPDB:GN00028; CESP:K06A9.1a 1:Ac70890.1; GSPDB:GN00028; CESP:K06A9.1a 1:Ba/2; 222/1; 1088/1; 1367/1; 2039/1; 2049/1; 1:Ba/2; 222/1; 1088/1; 1262	RESU T344	
m GB/EMBL/DDBJ  m GB/EMBL/DDBJ  in GB/EMBL/DDBJ  in GB/EMBL/DDBJ  in GB/EMBL/DDBJ  in GB/EMBL/DDBJ  in GB/EMBL/DDBJ  in GB/EMBL/DDBJ  in GB/EMBL/DDBJ  in GB/EMBL/DDBJ  in GB/EMBL/DDBJ  in GB/EMBL/DDBJ  in GB/EMBL/DDBJ  in GB/EMBL/DDBJ  in GB/EMBL/DBB 2; Length 2232;  in GB/EMBCHOREDEPAVELEP 755  in GB/EMBCHOREDEPAVELP 755  in GB/EMBCHOREDEPAVELP 755  in GB/EMBCH	hyp C; St C; De	orhabditis elegans on 29-Oct-1999 #text_change 18-Feb-
### GB/EMBL/DDBJ  ##################################	C; AC	1
### GB/EMBL/DDBJ  1: AAC70890.1; GSPDB:GN00028; CESP:K06A9.1a  NZ; clone K06A9  158/2; 222/1; 1088/1; 1367/1; 2039/1; 2049/1;  ###################################	A; De	gans cosmid
158/2; 222/1; 1088/1; 1367/1; 2039/1; 2049/1;     158/2; 222/1; 1088/1; 1367/1; 2039/1; 2049/1;     158/2; 222/1; 1088/1; 1367/1; 2039/1; 2049/1;     16. No. 2.5e-06;     17. Mismatches 797; Indels 484; Gaps 80;     18. Mismatches 797; Indels 484; Gaps 80;     19. Mismatches 797; Indels 484; Gaps 80;     19. Mismatches 797; Indels 484; Gaps 80;     19. Mismatches 797; Indels 484; Gaps 80;     19. Mismatches 797; Indels 484; Gaps 80;     19. Mismatches 797; Indels 484; Gaps 80;     19. Mismatches 797; Indels 484; Gaps 80;     19. Mismatches 797; Indels 484; Gaps 80;     19. Mismatches 797; Indels 484; Gaps 80;     19. Mismatches 797; Indels 872     19. Mismatches 797     19. Mismatches 797; Indels 872     19. Mismatches 797     19.	A; A;	Ē
158/2; 222/1; 1088/1; 1367/1; 2039/1; 2049/1;  tre 357; DB 2; Length 2232;  d. No. 2.5e-06;  Mismatches 797; Indels 484; Gaps 80;  EDSEVEAVESEDSPEN-ATSRGNTEPAVELEP 755    :	A A A A A A A A A A A A A A A A A A A	:AAC70890.1; GSPDB:GN00028; CESP:K06A9.1 . N2; clone K06A9
Duery Match  2.8%; Score 357; DB 2; Length 2222;  Matches 385; Conservative 220, Mismatches 797; Indels 484; Gaps 697 SQCESVASTVSAGEDEDIEASNEERPEDSEVEAVRYEEDSPEN-ATSRCNTEPAVELEP 755 [11] [1] [1] [1] [1] [1] [1] [1] [1] [1	C; G¢ A; G¢ A; Iï	158/2; 222/1; 1088/1; 1367/1; 2039/1; 2049/1;
10   1   1   1   1   1   1   1   1   1	M M O	2.8%; . Score 357; DB 2; Length 2232; imilarity 20.4%; Pred. No. 2.5e-06; ; Conservative 220; Mismatches 797; Indels 484; Gaps
466 SSSAGTAŠTISGSTGSTAJIVPGSSSSVGSSTGSASPSSPGTMSTVSGPTGSTUTVVP 523  756TTETAPSTSPSLAVPSTKPAEDESVET-OVNDSISAETAEQMDVDQGEHSAEEGSVCD 812  1	οy	SQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSEDSPEN-AISRGNTEPAVELEP 75
756TTETAPSTSPALAVPSTKPAEDESVET-QVNDSISAETAEQMDVDQQEHSAEEGSVCD 812	g	SSSAGTASTISGSTGSTATIVPGSSSSVGSSTQSASPSSPGTMSTVSGPTGSTVTVVP 52
### ### ### ### ### ### ### ### ### ##	b oy	TTETAPSTSPSLAVPSTKPAEDESVET-QVNDSISAETAEQMDVDQQEHSAEEGSVCD
	ô	PPPATKADSVDVEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPE 87
1   1   1   1   1   1   1   1   1   1	o Q	
622 P-SMNPSSST	Οy	PQSDNDSSATCSADEDVDGEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQH 93
933 RAAVIPPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEGRQRQEQIDLECRSSTS 992	ор	P-SMNPSSST
993 PCGTSKSPNREMEVLQPAPHQLITNLPEGVRLPTTRPTRPPPP 103   1   1   1   1   1   1   1   1   1   1	yo q	RAAVIPPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEQRQRQEQIDLECRSSTS 99
1036 LIPSSKTTVASEKPSFINGGSISQCTPGTTLTSHNOASYTQESGRQSTLTTPSPN 723 1036 LIPSSKTTVASEKPSFINGGSISQCTPGTYLTSHNOASYTQEPSSTQSSGRQSTLTTPSPN 723 1036 LIPSSKTTVASEKPSFINGGSISQCTPGTYLTSHNOASYTQETPKPSVGSISLGLPRQOE 109 104 -PSQSTSSLESSTSGATTSSGSAGTTWTSPSQSSSVG 759 1096 SAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVRGTAGAIQEGSITRGTPTSK 115 1096 SAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVRGTAGAIQEGSITRGTPTSK 115 1097 SAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVNRGTAGAIAGSGTTRGTPTSK 115 1098 SAKSATLPYIKQEFSPRSQNSQPEGLLVRAQHEGSVSTARALITSTQQSVSTNSPGST 115 1099 SAKSATLPYIKQEFSPRSQNSQPEGLLVRAGISRMPIEDSSPEKGREEAASKG 120 1153 ISVESIPSLRGSTTGGTPALPQTGIPTALVKGSISRMPIEDSSPEKGREEAASKG 120 1151	3 8	COLUMN TO THE TOTAL OF THE TOTA
1036 LIPSSKTTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQETPKPSVGSISLGLPRQOE	S &	PSGSSLGTQSTNSSPSPSSLSPS-TSGMSTLITSEPSPSSTQSSGAQSTLTTPSPN 723
724PSQSTSSLESSTSGATTSSGSACTTMTSPSQSSSVG	δý	LIPSSKTTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQETPKPSVGSISLGLPRQQE 109
1096 SAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVRGTAGAIQEGSITRGTPTSK	qq	
760 SSOGSTSPAASTTSGEMTSGGSTQTPGSSVSTSAAILTSTQGSVSTNSPGST 1153 ISVESIPELGSITQGTPALPQTGIPTEALVKGSISRMPIEDSSPEKGREEAASKG 1154 ISVESIPELGSTTGGTPALPQTGIPTEALVKGSISRMPIEDSSPEKGREEAASKG 1155 ISVESIPELGSTTGGTPALPQTGIPTEALVKGSISRMPIEDSSPAPSTSGNPNPSTSSG 1109 HVIYECKS-GHILSYDNIKNAREGTRSPRTAHBISLKRSYESVEGNIKOGMSMRE	οy	SAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVRGTAGAIQEGSITRGTPTSK 115
1153 ISVESIPSLRGSITQGTPALPQTGIPTEALVKGSISRMPIEDSSPEKGREEAASKG ::   ::   :	qq	SSQGSTSPAASTISGEMISQGSTQTPGSSVSTSAAILTSTQQSVSTNSPGST
1209 HVIYEGKS-GHILSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRE	oy D	ISVESIPSLRGSITQGTPALPQTGIPTEALVKGSISRWPIEDSSPEKGREEAASKG ::   ::   :   :   :
	0	209 HVIYEGKS-GHILSYDNIKNARECTRSPRTAHEISLKRSYESVEGNIKOGMSMRE

g	863	SSMITQSPYPSQSTSPVESSTTPSPGSPGTTLTSTSPSPSQSTTIGSTQGSTSPGISTTS	922
οy	1263	입	1322
q	923	EEMTSQGSTQTPGSTGSTVTQPSTVSDSTSSGS	955
οy	1323	PPIRAFEGAITKGRPYDGITTIKEMGRSIHEIPRQDILTQESRKTPEVVQSTRPIIEGSI	1382
g G	926	TVTVGSTEGSSSPIPSTSQNTNPSTSSGSSMSTQTPQSSQSTSP-VESST	1004
Š Š	1383	SQCTPIKFDNNSGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDV-KAG	1441
3 ,	500	19469661	/601
<u>ک</u> م	1442	ETVESHTSVVSGPSVLRSTLHEAPRAQLEPOITVDDTSARRTPVSYQNWSRGSPMNRR 	1501 1103
٥y	1502	TSDVT I PPNKSTNHERKSTLTPTQRES I PAKSPVPGVDPVVSHSPFDPHHRGSTAGEVYW	1561
g	1104	TSGATSSPGSSGTTLTSISPSPSQSSTIGSSGGSTSPVVSTTSGDMTSGGST	1155
ç q	1562	SHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGXPSQYQLYAMENTRQTILNDYITSQ::	1621
δ	1622	OMQVNLRPDVARGLSPREQPLGLPYPAT-RGIIDLTNMPPTILVPHPGGTSTPPMDRITY	1680
g	1199	: :   :   :   :   :   :   :	1251
οy	1681	IPGTQITFPPRPYNSASMSPGHPTHLAAAASAERERERERERERERERERIAAASSDLYLRP	1740
QQ	1252	LSSSSPVPSTSQSPNPSTSGSSTPTPNP	1279
οy	1741	GSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLD	1788
QQ	1280	SQSTSPVVSTTTGEMTSHGSTQTPSTIGSTVTQPSTVSGSNSSGSTVTIGSSE	1332
οy	1789	SIS	1830
qq	1333	ASTSGSSFKTSPSSISPVPTSSPIPSTTFASSTSGSTISDVSSVSTTSLAPLSSS	1387
<u>ئ</u> ج	1831	APOMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTS	1884
3 ,		E 614 F 561 QCF 561 SEGGSUNGSSE F 5Q 1851 F 1651 E551 EE551 EE551 SEGST QUI I	/ # # 1
ъ ф	1885	-SAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVIITRQIAS 	1943 1484
οy	1944	RYETPSDAIEVISPA	2001
qq	1485	STQPQMSTSQGSSAGSTVASSTASPAASSTAPSSTGTMSSTSGTVGSTI	1534
οy	2002	AENDPTRQYEGPLHHYRPQQESPSPQQQLPPSSQABGMGQ	2041
qq	1535	ESSTTASASSQTGSTVTMGSSSTSGVSTSSASSTQPQMST	1594
οy	2042	VPRTHRLITLADHICQIITQDFARNQVSSQTPQQP	2076
qq	1595	TSTVPSSTGTMGSTSSGTVGSTISESSTTASASSQTGSTVTMGSSSTSGVSTSSASSTQP	1654
οy	2077	PTSTEQNSPSALVSTPVRTKTSNRYSPESQAQSVHHQRPGSRVSPENL	2124
QQ	1655	QMSTSQGSSAGSTVASSTTGLVSTSTVPSSTGTMGSTSSGTVGSTISESSTAASASSQTG	1714
οy	2125	VDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVHEKQDSLLLLSQRGAEPAEQRNDARS:	2184
qq	1715	STVTMGSSSTSGVSTSSASSGQPQMSTSQGSSAGSTVVSST-ASPAASSTAPSS	1767
ογ	2185	PGSISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGGCDSDMAAAQPGTEIFNLPAV	2241
QQ	1768	TGTMSSTSSGTVGSTMSOSSTAASTTSHTGSTVTLGSSSTSSNOMSTSO-GSSVGSTVAS	1826

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C,Accession: B35098
R;Banerji, J.; Sands, J.; Strominger, J.L.; Spies, T.
Proc. Natl. Acad. Sci. U.S.A. 87, 2374-2378, 1990
A;Title: A gene pair from the human major histocompatibility complex encodes large pr A;Reference number: A35098; MUID:90192810
A;Accession: B35098
                                                                                                                                                                                                                                                                                                                                                                       - huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2142 - DBNN>
A;Cross-references: GB:M3509; NID:g179338; PIDN:AAA35585.1; PID:g179339; GB:M31293
A;Note: the authors translated the codon AGT for residue 97 as Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104;
                                                                                                                                                                                                                                                                                                                                                 B35098
MHC class III histocompatibility antigen HLA-B-associated protein 2 [imported]
C;Species: Homo sapiens (man)
C;Date: 10-Aug-1990 #sequence_revision 06-Nov-1992 #text_change 15-Sep-2000
2300
                                  1881
                                                                                                                                                                           1942 SSTAAST-----SQTGSTVTIGSTSGTNPSSPRSLSQITITP---SPS---QSTES 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | | : | : | : | | DRDSDEEGAEGHRDSQSASGEERPPEADGKKGNSPNSEPPTPRTAWAETSRPPETEPGP 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            555 DGTAEETE----EREQATPRGRKTANSQGRRKGRITRS--MTNEAAAASAAAAATE--- 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           406 PAPKPPLPPGDYPDRGGPPCKPPAPEDEDEAWRQRRKQSSSEISL--AVERAR----- 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MVGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRKPREERDVSQCESVASTVSAQEDE 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       713 DIEASNEEENPEDSEVEAVKPSEDSPENATSR---GNTEPAVELEPTTETAPSTSPSLAV 769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             503 QQIARPS--QEEKVEEKEEDKAEKTEKKEEEKKDEEEKD-----EKEDSKENTKEKDKI 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P--STKPAEDESVETQVN-----DSISAETAEQMDVDQQEHSAE--EGSVCDPPPAT--- 817
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                      2360 GDYHRQTPGWAWEDRPSSTGST----QFPYNPLTMRMLSSTPPTPIACAPSAVNQAAPH
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                                                                        VVTSGETRREEGDPSPHSGGVCKPKLISKSNSRKSKSPIPGQ-GYLGTERPSSVSSVHSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      606 -EPPPPLPP------PPEPISTEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.8%; Score 353; DB 2;
ilarity 20.4%; Pred. No. 3.4e-06;
Conservative 224; Mismatches 833
                                                                                                                                                                                                                                                    QONRIWEREPAP----LLSAQYETLS 2436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 439; Conserv
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2242
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qq	709	:      :	
δ	987	10	
g	761	APAMLRERGTPPVDPKLAWYGDVFTATPAEPRPLTSPLRQAADEDDKGMR-SETPPVPPP 819	
QY Db	1034	PPLIPSSKTTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQETPKPSVGSISLGLPRQ 1093    :	
٥y	1094	OESAKSATLPYIKQEEFSPRSQNSQPE-GLLVRAQHECVVRGTAGAIQEGS 1143	
QΩ	859		
ογ	1144	ISRMP	
qq	919	SRRGIPPEEPGAPPRRAGPIKKPPPPTKVEELPPKPLEQGDETPKPPKPD 968	
λ α	1204	AASKGHVIYEGKSGHILSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRES 1263    -  -  -  -  -  -  -  -  -  -  -  -  -	
2	1264	WITH GRANDER GOVERNMENT OF THE PROPERTY OF THE	
음	1006	GRGRGGQANSAVTESFEEMM- 104	
δý	1314	YPKQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHEIPRQDILTQESRKTPEVVQS 1373	
QO	1050	1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1	
δ	1374	TRPIIEGSISQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVERG 1433	
QQ	1067	:     : :       : :   AMPARHGARVQSMR-KSPSGAGSGAQKQAARPMRVIWLLQTRRLP 1110	
Qγ	1434	KYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMS 1493	
qq	1111		
ογ	1494	RGSPWMNRTSDVTIPPNKSTNHERKST-LIPTQRESIPAKSPVPGVDPVVSHSPFDP 1549	
qq	1155	PGPRRREAPPQVCPGWSPPAKSLAPKKPPTGPLPPSKEPLKEKL-IPGPLSP 1205	
δy	1550	LSPT	
QQ	1206	VARGGSNGGSNVGME-DGERPRRRHGRAQQQDKPPRFRLKQE 1248	
Qγ	1610	RQTILNDYITSQQMQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGG 1669	
qq	1249		
οy	1670	TSTPPMDRITYIPGTQITFPPRPXNSASMSPGHPTHLAAAASAERERERER 1720	
QQ	1271	PEEALTTVTVAPAPPRAAAKSPDLSNQNSDQANEEWETASESSDFTSERG 1321	
Qγ	1721	EKERERERIAAASSDLYLRPGSEQPGRPGSHG 1752	
q	1322	DKEAPPPVLLTPKAVGTPGGGGGAVPGISAMSRGDLSQRAKDLSKRSFSSQRPGMER 1379	
ογ	1753	YVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMPLPAGGPSISGG 1808	
QQ	1380	ONRRPGPGGKAGSSGSSGGGGGGGGGGGRTGPGRGDKRSWP 1419	
Qy	1809	LPASKYNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQ 1868	
qq	1420	SPKNRSRPPEERPPGLPLPPPPPSSSAVFRLDQVIHSNPAGIQQALAQ 1467	
οy	1869	KTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRGKTTIT 1928	
qq q	1468	LSSRQGSVIAPGGHPRHKPGPPQAPQGPSPRPPTRYEPQRNUSG 1511	
οy	1929	AANFIDVIITRQIASDKDARERGSQSSDSSSSLSSHRYETPSDAIEVISPASSPAPPQEK 1988	

DRKELPRE--OPLPPG--PIGTERSOR----TDRGTEPGPIRPSHR-PGP----PVQFGT 1749 2198 LENTSPM-----VKSKKQEIFRKLNSSGGDSDMAAAQPGTEIFN-LPAVTTSGSVSS 2249 ---LSSDPHFEEPGPMVRGVGG-----TPRDSAGV----SPFPPKRR 1546 1989 LQ-TYQPEVVKANQAENDPTRQYEGPLHHYRPQQESPSPQQQLPPSSQAEGMGQVPRTHR 2047 2048 LITLADHICQIITQDFARN--QVSSQTPQQPPTSTFQ------NSPSALV 2089 1588 TEALTPHIWNRLHTATSRKSYRPTSMEPWMEPLSPFEDVAGTEMSQSDSGVDLSGDSQVS 1647 --SQPMGVVPGTANTSVVTSG------ETRREEGDPSPHSGGVCKPKLISKSNSRK 2334 1919 CPSPLPDTSLLQVRQ-----DLPSPSDFYSTPLQPGGQSGFLPSGAPAQQMLLPMVDSQL 1973 ERPPRKPELL---QEESLPPPHSSGFL---GSKPEGPGPQAE------SRDTG ERSHVSSEPYEPISPPQVPVVHEKQDSLLLLSQRGAEPAEQRNDARSPGSISYLPSFFTK STPVRTKTSNRYSPESQAQSVHH---QRPGSRVSPENLV--DKSRGSRPGKSP----2335 SKSPIPGQGYLGTERPSSVSSVHSEGDYHRQ--TPGWAWEDRPSSTGSTQF-----2384 -----PYNPLTMRMLSSTPPTPIACAPSAVNQAAPHQQNRIWEREPAP 2426 1974 PVVNFGSLPPAPPAPPPAPLSLLPVGPALQPPSLAVRPPFAPATRVL---PSP 2022 R----GHSFADPASN---LGLEDIIRKALMGSFDDKVEDHGVVM----1547 2090 2138 1703 2250 1799 2287 1512 g 셤 ŏ g Ω 용 δ g ð 셤 ă ŏ 셤 ŏ 셤 à g δ

A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: EMBL: Z70043; NID: 91220275; PIDN: CAA93906.1; PID: 91220294; GSPDB: G
A; Experimental source: strain 972h-; cosmid c22E12
A; Experimental source: strain 972h-; cosmid c22E12
B; Deviin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, February 1996
A; Reference number: Z21750
A; Accession: T38530 hypothetical Myb family DNA-binding protein SPAC22E12.19 - fission yeast (Schizosacch Spacies: Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe C; Date: 20-oct.2000 #sequence\_revision 08-Dec-2000 #text\_change 08-Dec-2000 C; Accession: T38176; T38530 R; Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, March 1996 A; Reference number: Z21775 A; Accession: T38176

A;Molecule type: DNA A;Residues: 215-661 <DEV2> A;Cross-references: EMBL:269726; NID:91204194; PIDN:CAA93545.1; PID:91204195; GSPDB:G A;Experimental source: strain 972h-; cosmid c2E12 A;Gene: SPDB:SPAC22E12.19; SPDB:SPAC2E12.01 A;Map position: 1

Query Match 2.8%; Score 350; DB 2; Length 661; Best Local Similarity 21.8%; Pred. No. 1e-06; Matches 155; Conservative 122; Mismatches 298; Indels 136; Gaps

28;

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-----AERIRGEDEKS-----MLAKEHADKKIRLGVAKIPRLLTESERKMDEFVERPGS 198

RGAGLSATIARSEHEISEIIDGLSEQENNEKQMR-QLSVIPPMMFDAEQRRVKFINMNG-

LMEDPMKVYK - - - - DRQFMNVWTDHEKEIFKDKFIQHPKNFGLIASYLERKSVPDCVLYY

423 199 479 257 531 315

150

-----EKKDEEEKDEKEDSKENTKEKDKI--DGTAEETEEREQATPRGRKTANSQGRRK 582 583 GRITRSMINEAAAASAAAAATEEPPPPLPPPPEPISTEPVETSRWIEEEMEVAKKGLVE 642

YLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEKVEEKEEDKAEKTEKKEE------

-----VAVKFCTPCKNALTRWINDVNNKEETIMAELLNYEGOVGWTDDEKTKLV 453

643 HGRNWAAIAKMVGTKSEAQCKNFY----FNYKRRHNLDNLLQQHKQ----KT---

375

405 687 454 TLINSSPTLDWVSISEGMNRRPNECKMQYDAMNGVKTQPMIEEVDEDGNGQEEGGDALV 513

----SRKPREERDVSQCESVASTVSAQEDEDIEASNEEENPEDSEV

EAVKPSEDS-----PENATSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVET NTPTTSSAAARRSGLARNAKKPVRTPRAPRSAGGRRTGGAVTRAQAVP--KPVED----

514

783 QVNDSISAETAEQMDVDQQEHSAEEGS----VCDPPPATKADSVDVEVRVPENHASKVEGD 839

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C14B9.6 protein - Caenorhabditis elegans
C15Fecies: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Accession: 844758
R; Ravello, A.D.
Submitted to the EMEL Data Library, May 1993
A; Description: Sequence of the C. elegans cosmid C14B9.
A; Reference number: 844617
A; Accession: 844758
A; Status: preliminary
A; Wolecule type: DNA
A; Residues: 1-1018 < FAV>
A; Residues: 1-1018 < FAV>
A; Cross references: EMEL:L15188; NID:9289640; PID:9289645
C; Genetics:
A; Introns: 53/2; 74/3; 91/2; 120/2; 336/1; 360/2; 423/3; 535/2; 949/1
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                                                                                                                                                                                                                                                                                            417
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                                                                                                                                                                                                                                                                                                                      ---TEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAKMVGTKSEAQCKNFYFN---YKRRH 673
                                                                                                                                                                                                                                                                                                                                                                                                                              VEAVKPSEDSPENA----TSRGNTEPAVELEP-TTETAPSTSPSLAV----PSTKPAED 777
                                                                                                                                                                                                                                                                                                                                                                          NLDNLLQQH---KQKTSRKPREERD----VSQCESVASTVSAQEDEDIEASNEEENPEDSE 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QKICQRYDQLMEAWEKKVDRIENNPRRKAKESKTREYYEKQFPEIRKQREQQERFQRVGQ 364
267 NQPSDTKVYHENIKTNQVMRKKLILFFKRRNHARKQREQKICQRYDQLMEAWEKKVDRIE
                RLTEIDKTKNAKKSEPFIK-----RSTRKVMSNF-----TAGDIVRSEEFFLEILA
                                                                                                                     HQGHLPGWDEKEEALIFSLAQGMNPWKMPLTPRRASTGPRPRPTFQLTEIDSPNRRRASD
                                                                                                      GLSEQE---NNEKQMRQLSVIPPMMFDAEQRRVKFIN-MNGLMEDPMKVYKDRQFMNVWT
                                                                                                                                                                                                               NQQIARPSQE-EKVEEKEEDKAEKTEKKEEEKKDEEEKDEKEDSKENTKEKDKIDGTAEE
                                                                                                                                                                                                                                                                   TEEREQATPR-GRKTANSQGRRKGRITRSMTNEAAAAAAAAAATEEPPPPLPPPEPIS
                                                                                                                                                                                                                                                                                          371 VENVESANENVNNHNADEQMDEK---IKSLV-EGNSAYEIEKGAQE-----PDPMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ESVETQVNDSISAETAEQMDVDQQEHSAEEGSVCDPPPATKADSVDVEVRVPEN
                                                                                                                                                           DHEKEIFKDKFIQHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSHTTSDINAFPNSQSFPRASIHTLAALGEDIV------EROSKND 658
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Best Local S:
Matches 197,
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hypothetical protein ZK783.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: O-oct-1999 #sequence_revision 29-oct-1999 #text_change 29-oct-1999
C;Accession: T34513
R;Favello, A.; Vaudin, M.
submitted to the EMBL Data Library, August 1994
                                                                                                                                                                                                                                                                                                        SGYALYQRHI----KAMHESALLEEQRQRQEQIDLECRSSTSPCGTSKSPNREWEVLQPA 1010
                                                                                                                                                                                                                                                                                                                                                                                                                             1011 PHQLITNLPEGVRLPT-TRPTRPPPPLIPSSKTTVASEKPSFIMGGSISQGTPGTYLTSH 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1105 IKQEEFSPRSQNSQPE-----GLLV--RAQHEGVVRGTAGAIQ-EGSITRGTP--- 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NQASYTQETP------KPSVGSIS----LGLPRQQESAKSATLPY 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----LGEEIDEMEIEDNDEDASRGSRGKDSKAPSDRDGSPADMEGDSPEGQDQDADQD 620
                                                           840 NTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDVDGEPERQRMF 899
                                                                                                                                                                                PMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAA-----VIPPMVSCTPCNIPIGTPV 954
                                                                                                                                                                                                                                                                                                                                                                 SSHLIGSSSVGGSERELGGRGLVQQQQQQQQQQQAAAPPVTVSTAAAATAERLVNATSPS 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      621 QDQDQDVDEEEEEVIVRDIDSPVKTLL-----SPKILSGGHKPDFFP----V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1886 PDGFIGDGMICDDVDECNNAGMCDDENTKCENTIGSFNCVCLEGFKKVDEKCVVDEKKQP 1945
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                                                                                                                               -TRSPRTAHEISLKRSYES-----VEGNIK----QGMSMRESPVSAPLEGLICRALP 1278
                                                                                                                                                                                                                                                                                                                          CHSGFEGDGIKKCTNPLERSCEDVEKFCGRVDHVSCLSVRIYNGSLSSVCECEPGFRFEK 1711
                                                                                                                                                                                                                                                                                                                                                                                                     ----STHEIPRQD--ILTQESRKTPEVVQSTRPII 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSMAMCINFMGSCGCKCMAGYTGDGATCIKIEEEPKSDKTACTDEWSRLCELEKKQCTVD 1831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --EDVKAGETVRSRHTS------VVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRT 1484
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                                                                                       1475 ACFCPTGFRKADDGSCQDIDECTEHNSTCCGANAKCVNKPGTYSCECENGFLGDGYQCVP 1534
                                                                                                                                                                     1535 TTKKPCDSTQSSKSHCSESNMSCEVDTVDGSVECKECMGGYKKSGKVCEDINECVAEKAP 1594
                                                                                                                                                                                                                                                    1595 CSLNANCVNMNGTFSCSCKQGYRGDGFMCTDINECDERHPCHPHA---ECTNLEGSFKCE 1651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2108 SVTSTVPETSKSTVLSSEAPVTSTSPTEVHTSS--ETKPSLSASSTTGDTNSTT-PSTSS 2164
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          ---FEGAPPKKSCVDVDECATGDHNCHESARCQNYVGGY 1474
                                                                                                                                                                                                                                                                                             -----QGTPRATT---ESFEDGLKYPKQIKRES-PPIRAFEGAI------
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A;Description: The sequence of C. elegans cosmid ZK783.
A;Reference number: Z21536
A;Accession: T34513
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: DNA
A;Rolecule type: DNA
A;Rossidues: 1-3507
A;Cross-references: EMBL:U13646; PIDN:AAC24418.1; GSPDB:GN00021; CESP:ZK783.1
A;Experimental source: strain Bristol N2; clone ZK783
C;Genetics: A;Gene: CESP:ZK783.1
A;Map position: 3
A;Gene: CESP:ZK783.1
A;Map position: 3
A:Initrons: 14/1; 48/2; 84/1; 196/3; 303/1; 381/1; 586/1; 605/1; 1175/3; 1207/1; 1409/2;
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                                                                                                                                                                                                                                                                                                                Query Match 2.7%; Score 344.5; DB 2; Best Local Similarity 18.3%; Pred. No. 1.4e-05; Matches 432; Conservative 296; Mismatches 912;
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Db 671 LTPPSSVSSLSIPVSPLAASALNPTFTFPSHSLTQSGDSTEKNQRARKQTSAPAEPFSS 730  Qy 162 GQPCGDDQNASPSKLSKEELIQSMDRYDREIAKVEQQILK 201  Db 731 NSPALPPWFTPGSQTEKGRKKDTAPEELSKBRDADKSVERCKSREE-DREREKENKRESK 789  Qy 202 LKKKQQQLEEBAARPPEPEPRYSPPV	QY   282 NQVMRKKLILEFKRRNHARKQREQKICQRYDQLMEAWEKKVDRIENNPRRKAK 334   1   1   1   1   1   1   1   1   1	QY         435 QFMNVWTDHEKEIFRDKFIQHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYKALVRRN 494           Db         1051 RSRRGGCPGCPGCGVPEDCGICTNCLDKFKFGG	Db	702	QY 753	Qy   826 VRVPENHASKVEGDUTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCS- 884   1   1   1   1   1   1   1   1   1
QY 1996 VVKANQAENDPTROYEGPLHHYRPQOESPSPOQQLPPSSQAEGMGQVPRTHRLITLADHI 2055  Db 2489 STISSVLEEDLTKTTPSFIIEETTTASETSEPLTE-DSLIVSVRIHELTTSSENV 2542  QY 2056 COLITQDFARNQVSSQTPQOPPTSTFQNSPSALVSTPVRTSNRYSPESQAGS 2109  Db 2543 PK-ESESTTTSSESKRYSOEPAGILTSTVVVPTSSVBLITASEIEAITSNTPFKGRT 2599  QY 2110 VHHQRPGSRVSPENLVDKSRGSRPRSPRSSPSEPTSPPQVVVHEKQDSLLLLS 2169  Db 2600 PITTSPKSLVKSTTSPSTVTSSEPSESTKRTTVST-TVSTTTPTEETTTSSSLILIT 2654  QY 2170 ORGAEPAEQRNDARSPGSISYLPSFFTKLENTSPMYKSKKOEIFRKLNSSGGGDSD 2225	2655 AAPSKPTESTTESSEAPTTPAKTSETKPSNVSSTSRKSTENVETSTSQSGSLESS 2226 MAAAQPGTEIFNLPAVTTSGSVSSRGHSFADPASNLGLEDIIRKALMGSFDDKVED  2710 TMSSTSSEPETNAPAVTVSSEASSTLLEENSSTSSPTSSEASVKLSSLFPESITS 2282 HGVVMSQPMGVVPGTANTSVTSGETRREEGDPSPHSGGVCKPKLISKSNSRKSFSPIPG  1	UY 234.2 GGILGTERESSY-SSVHEEDYHRQTPGWWWEDRESTGSTOFPYRPLTMRALSSTPPT 2399  DD 2801LSTTVSPNVTASSIPSEEPILSSVTSSTPRVRLITGTPDD 2842  QY 2400 PIACAPSAVNQAAPHQONR 2418  DD 2843 LIVSVTVPSHGNR 2855  RESULT 38	All'1 protein +GTE form - mouse (fragment) C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Species: Of-oct-1994 #sequence_revision 07-oct-1994 #text_change 01-Dec-2000 C;Accession: A48205; B48206; R;Ma, Q.; Alder, H.; Nelson, K.K.; Chatterjee, D.; Gu, Y.; Nakamura, T.; Canaani, E.; Cr Proc. Natl. Acad. Sci. U.S.A. 90, 6350-6354, 1993 A;Title: Analysis of the murine All-1 gene reveals conserved domains with human ALL-1 an A;Reference number: A48205; MUID:93317679	A;Status: preliminary A;Molecule super mRNA A;Residues: 1.3869 <	C:Genetics: A;Gene: All-1 C;Keywords: alternative splicing; zinc finger C;Keywords: alternative splicing; zinc finger Query Match Best Local Similarity 19.0%; Pred. No. 1.8e-05; Matches 584; Conservative 381; Mismatches 1127; Indels 980; Gaps 140;	PNOGAFSTEQSRYPPHSVQYTFPNTRHQOEPAVPDYRSSHLEVSQASQLLQQQQ 61 :

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δλ	997	SKSPNREWEVLQPAPHQLITNLPEGVRLPTTRP 1029	
qq	1664	IROMERVFPWFSVKKSRFWEPNKVSNNSGMLPNAVLPPSLDHNYAQWQEREESSH 1718	
0y	1030	TRPPPPLIPSSKTTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQETPKPSVG 1084	
3 6	1085	-SISIGLPRODESAKSA-TLPYIKOEFFSPRSONSOPEGLUVRAOHEGVVRG 113	
qq	1776	:    :	
Qγ	1135	-TAGAIQEGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGIPTEALVKGSISRM 1190	
QQ	1836	LRCEFCQKPGATVGCCLTSCTSNYHFMCSRAKNCVFLDDKKVYCQRHRDLIKGEV 1890	
οy	1191	PIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIKNAREGTRSPRTAHEISLKRSYESV 1250	
а	1891	VPENG-FEVFRRVFVDFEG1916	
Οy	1251	EGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSI 129	
gg	1917	NGLEPENIHMMIGSMTIDCLGILNDLSDCEDKLFPIGYQCSRVYWSTTDARKRCVYTCKI 1976	
oy.	1297	MGGTPRATTESFEDGLKYPKQIKRESPPIRAFEGAITKG	
OD O	1977	MECRPPVVEPDINSTVEHDDNRTIAHSPSSFIDASCKDSQSTAAILSPPSPDRPHSQTSG 2036	
Qy 45	1336	KPYDGITTIKEMGRSIHEIPRQDILTQESRKTPEVVOSTRPIIEGSISQGTPI 1388	
3 8		COLLINATION TOWNS AND THE PROPERTY OF THE PROP	
<u> </u>	2087	RFDNNSGQSAI	
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g g	142b 2143	NIKVVERDYKAG	
οy	1471	LSPGIYDDT-	
QQ	2203	LVKGEKNRTSSSKSTDGSAHSTAYPGIPKLTPQVHNATPGELNISKIGSFAEPSTVPFSS 2262	
Οy	1526		
qq	2263	KOTVSYPQLHLRGGRSDRDQHMDPSQSVKPSPNEDGEIKTLKLPGMGHRPSILHEHIGSS 2322	
ΟŊ	1556	AGEVYWSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYA 1605	
qq	2323	SRDRRQKGKKSSKETCKEKHSSKSYLEPGQVTTGEEGNLKPEFADEVLTPGFLGQRP 2379	
δy	1606		
QQ	2380	CNNVSSEKIGDKVLPLSGVPKGQSTQVEGSSKELQAPRKCSVKVTPLKMEGENQ 2433	
οy	1645		
qq.	2434	SKNTQKESGPGSPAHIESVCPAEPVSASRSPGAGPGV-QPSPNNTLSQDPQSNNYQ 2488	
οy	1671	STPPMDRITYIPGTQITFPPRPYNSASMSPGHPTHLAAAAS1711	
qq	2489		
ΟŊ	1712	AERERERERERERERERIAAASSDLYLRPGSEQPGRPGSHGY 1753	
QQ	2544	IPFYSNSTGKKRGKRSAEGQVDGADDLSTSDEDDLYYYNFTRTVISSGGEERLASHNL 2601	
δλ	1754	VRSPSPSVRTQETMLQQRPSVFQGT-NGTSVITPLDPTAQLRIMPLPAGGPSISQGLPAS 1812	
, 6	2602	FILEEQCDLPKISQLDGVDGTESDTSVTATSRKSSQIPRRNGKENGTENLKID 2655	

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tpr protein - human
N;Alternate names: kinase-related transforming protein (tpr-met); protein with promot
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C; Date: 12-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-2000
C; Accession: S33124; S23740; S00928; G01185
R; Mitchell, P.J.; Cooper, C.S.
Oncogene 7, 2359-2333, 1992
A; Title: The human tpr gene encodes a protein of 2094 amino acids that has extensive A; Reference number: S33124; MUID:93064711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to the EMBL Data Library, October 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A) Status: preliminary; nucleic acid sequence not shown; translation not shown A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: mRM A; Molecule type: mRM A; Molecule the nucleotide sequence was submitted to the EMBL Data Library, Octobe R; Mitchell, P.J.; Cooper, C.S. Oncogene 7, 383-388, 1992 A; Title: Nucleotide sequence analysis of human tpr cDNA clones.
                               2656 RPEDAGEKEHVIKSAVGHKNEPKLDNCHSVSRVKAQGQDSLEAQLSSLESSRRVHTSTPS 2715
1813 RYNTAADALAALVDAAA--SAPQMD----VSKTKESKHEA----ARLEENLRSRSAAVS 1861
                                                                                                                                                                                                                                                       3265 ANQRLLGTPDIGSISHLLIKASH--QSLG--1QDQPVALPPSSGMFPQ------LGTS 3312
                                                                                                                                                                                                                  1910 PPKSRYEEELRTRGKTTITAANFIDVIITRQIASDKDARERGSQSSDSSSSLSSHRYETP 1969
                                                                                                                                                                                                                                                                                                                                                                                    2824 LELPSDLSVLTTRSPTVPSQNPSRLAVISDSGEKRVTITEKSVAS--SEGDPALLSPG-- 2879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2880 -----VDPAPEGHMTPDHFIQGHMD-----ADHISSPPCGSVEQGHGNSQDLT 2922
                                                                                                                                              2716 DKNLLDTYNAELLKSDSDNNNSDDC---GNILPSDIMDFVLKNTPSMQAL------GE 2764
                                                                                                                                                                                                                                                                                                                                                                                                                                             2015 HHYRPQQESPSPQQQLPPSSQAEGMGQVPRTHRLITLADHI----CQII-----TQDFA 2064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3043 SLFPPASKGLL--SVPHHQHLHSFPAAAQSSFPPN---ISSPPSGLLIGVQPPPDPQLLG 3097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3098 SEANQRIDLITIVA---TPSSGLKKRPISRLHTRKNKKLAPSSAPSNIAPSDVVSNMTLI 3154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3155 NFTPSQLSNHPSLLDLGSL-----NPSSHRTVPNIIKRSKSGIM--YFEQAPLLPPQ 3204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :| : | : | : 3205 SVGGTAATAAGSSTISQDTSHLTSGPVSALASGSSVLNVVSMQTTAAPTSSTSVPGHVTL 3264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2342 --QGYLGTERPSSVSSVHSEGDYHRQTPGWAWEDRPSS--TGSTQFPYNPLTMRMLSSTP 2397
                                                                                                         1862 EQQQLEQKTLEVEK-----RSVQCLYTSSAFPSG-----KPQPHSSVVYSEAGKDKGP
                                                                                                                                                                                                                                                                                                                                 -- EKLQTYQPEVVKANQAENDPTRQYEGPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2065 RNO-----VSSQTPQQ----PPTSTFQNSPS-----ALVSTPVRTKTSNR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- RPGSRVSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2983 NMQPLYVLQTLPNGVTQKIQLTSPVSSTPSVMETNTSVLGPMGSGLTLTTGLNPSLPPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2122 ENLVDKSRGSRPGKSPERSHVSSEPYEPIS--PPQVPVVHEKQDSLLLLSQRGAEP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2231 --PGTEIFNLPAVTTSGSVSSRGHSFADPASNLGLEDIIRKALMGSFDDKVEDHGVVMSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2289 PMGVVPGT-ANTSVVTSGETRREEGDPSPHSGGVCKPKLISKSNSR--KSKSPIPG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---AEQRNDARSPGSISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGGGDSDMAAAQ---
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3313 QTPSAAAMTAAS 3324
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Oy 508 PSQEEKVEEKEEDKAE	0.00   0.00	Db 1337ARNQHLVSQKDPDTEFYRLLSEKEVHTKRIQLTEEIGR 1377 QY 1378 IEGSISQCTPIKPDNNSQSAIKHNVKSLITGPSKLSRGMPPLEI-VPENIKVVERGK 1434 i:  :  :  :  :  :  :
A;Reference number: S23740; MUID:92195670 A;Accession: S23740 A:Status: preliminary A;Accession: S23740 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-725,'L' <miz> A;Cross references: EMBL:K63105; NID:g37257; PIDN:CAA44819.1; PID:g37258 B;King, Hw.S.; Tempest, P.R.; Merrifield, K.R.; Rance, A.J. A;Title: Tpr homologues activate met and raf. A;Title: Tpr homologues activate met and raf. A;Title: Tpr homologues activate met and raf. A;Title: Tpr homologues activate met and raf. A;Title: Tpr homologues activate met and raf. A;Title: Tpr homologues activate met and raf. A;Title: Tpr homologues activate met and raf. A;Nolecule type: mRNA A;Nolecule type: mRNA A;Residues: 1-31,'R', 33-142 <kin> A;Cross references: EMBL:Y00672; NID:g37255; PIDN:CAA68681.1; PID:g37256 B;Molecule type: DNA A;Residues: 144-228 <gre> A;Residues: 144-228 <gre> A;Cross references: EMBL:X94208; NID:g1296797; PIDN:CAA63904.1; PID:e221085; PID:g129679 C;Genetics: A;Cones GDB:TPR A;Cross references: GDB:128821; OMIM:189940 A;Map Position: 1q25-1q25 A;Introns: 177/3</gre></gre></kin></miz>	Query Match         2.7%; Score 342; DB 2; Length 2094;           Best Local Similarity 18.2%; Pred: No. 8.9e-06;           Matches 426; Conservative 350; Mismatches 871; Indels 696; Gaps 89;           QY 24 SVQYTFPNTHODERAVPDYRSSHLEVSQASQLLQQQQCQQLRRRPSELSEFHPGSD 80           1:1	474 KANKQSSVLERDNRRMEIQVKDLSQQIRVLLMELEEARGNHVIRDEEVSSADISSSSEVI 475VKFINMNGLMEDPMKVYKD-RQFMNVWTDHEKEIFKDKFIQHPKNFGLIASYLE

QY 503 QQIARPSQEEKVEEKEEDKAEKTEKKEEEKKDEEEKDEKEDSKENTKEKDKI 554 ::    :	OY 555 DGTAEETEEREQATPRGFKTANSQGRRKGRITRSMTNEAAAAAAAAAAATE 605	Db 346 DGRDSDEEGAEGHRDSQSASGEERPPEADGKKGNSPNSEPPTPKTAWAETSRPPETEPGP 405 Qy 606 -EPPPPLPP		OY 641 VEHGRNWAALAKMVGIKSEAQCKNFYENYKRRHNLDNLLQQHKQKISRKRREERDVSQCE 700 	QY 701 SVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSEDSPENATSRGNTEPAVELEPTT 757 :	758 ETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDVDQQEHSAEEG	Db 543 EKEPE-EPAQAPPAQSTPTPGVAAAPTLVSGGGSTSSTSSGSFEASPVEPQLPSKEGPEP 601  Qy 809 SVCDPPPATKADSVDVEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDL 860	Db 602 PEEVPPPTTPPVPKVEPKGDGIGPTRQPPSQGLGYPKYQKSLPPRFGRQQQEQ 654 Qy 861 VVAQQINAQRPEPQSDNDSSATCSADEDVDGEPERQRMFPMDSKPSLLNPTGSILVSSPL 920	::	QY 921 -KPNPLDLPQLQHRAAVIPPMYSCTPCNIPIGIPVSGYALYQRHIKAMHESALLEEQRQR 979 	QY 980 QEQIDLECRSSTSPCGTSK-SPNREWEVLQPAPHQLITNLPEG 1021 :	QY 1022 VRLPTTRPTRPPPPLIPSSKTTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQETPKP 1081	OY 1082 SVGSISLGLPRODESAKSATLPYIKQEEFSPRSONSQPE-GLLVRAQHEGV 1131  DD 864 LPWPPGSDEVAKIQTPPPKKEPPKEETAALTGPEAGRKLPASRSGAGPPPRRES 918	1132 VRGTAGAIQEGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGIPTBALVKGSISRMP	QY 1192 IEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIKNAREGTRSPRTAHEISLKRSYESVE 1251	QY         1252         GNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIMQGTP         1301           Db         1015        RGRCRGEYFARGRCRGRGRAGAN         1050	1302 RATTESFEDGLKYPKOIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHEIPRODILT	QY 1362 QESRKTPEVVQSTRPIIEGSISQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSRGMP 1418	QY 1419 PLEIVPENIKVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDD 1478
Db 1497 VENLOKTLSEKETEARNLOEOTVQLQSELSRLRQDLQDRTTQEEQLRQOITEKEEK 1552  Qy 1523 PTORESIPAKSPVPGVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMP 1573	1553	QY 1574 -FHRALDPAAAAYLEQRQLSPTPGYPSQYQLYAMENTRQTILNDYITSQQMQVNLRPDVA 1632	1633 RGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRITYIPGTQITFPPRP	OD 1003 SGEKGIAS-ISDFFTANIAFIFVVSIFSKVIAAAMAGNKSIFKA 1595  QY 1693 YNSASMSPGHPTHLAAAASAERERERERERERERIAAASSDLYLRPGSEQPG 1746	Db 1696 SIRPMYTPATVINFTTFTATVMPTQVESQEAMQSEGPVEHVPVFGS 1743 Qy 1747 RPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMPLP 1799	:	QY 1800 AGGPSISQGLPASRYNTAADALADA-AASAPQMDVSRTKESKHEAA 1847 : :         :  :       :  :      :      :      :      :      :    :      :	QY 1848 RLEBNLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVV 1899    :   :   : : : : : :	1900 YSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVIITRQIASDKD	OY 1947 ARERGSOSSDSSSLSS	Db 1964 DTGMGDEGEDSNEGTGSADGNDCYEADDAEGGDGTDPCTETEESMGGGEGCHHRAADSQNS 2023 Qy 1973 IEVISPASSPAPPQEKLQTYQPEVVKANQAENDPTROYEGFLHHYRPQQESPSPQQQLPP 2032	Db 2024 GEGNTGARESSFSGEVSREQQPSSASERQAPRAP-GSPRRPPHPLPPRLTIHAPPGELGP 2082 Qy 2033 SSQ 2035	80	clated protein	<pre>#sequence_revision 1/-Nov-1995 #text_change 15-Sep-2000 queleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, N-145, 1993</pre>	A:Title: Dense Alu clustering and a potential new member of the NFkappaB family within a A:Reference number: 836152; MUID:93272029 A:Status: preliminary. A.Status: preliminary.	Molecule type: DNA Residues: 1-1872 <iri> Cross-references: EMBL:215025 Note: in the authors' translation residues 32-34 are shown afte</iri>	Aynote: the authors translated the codon AAT for residue 1000 as His C;Genetics: 38/2; 97/2; 129/3; 154/1; 202/1; 252/3; 279/2; 327/1; 357/2; 429/3; 588/1; 65 C;Superfamily: collagen alpha 1(IV) chain	Query Match 2.7%; Score 340; DB 2; Length 1872; Best Local Similarity 20.3%; Pred. No. 9.2e-06; Matches 409; Conservative 209; Mismatches 757; Indels 636; Gaps 98;

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------PG----PEEAL----TTVTVAPAPRRAAAKSPDLSNQNSDQANEEW 1318
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                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGGGGGGGCGTGGGGCGCKSWPSPKNRSRPPEE-----RPPGLPLPPPPSSSAVF 1460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTNMPPTILVPHPGGTSTPPMDRITYIPGTQITFPPRPYNSASMSP------GHPTH 1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDK 1907
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1479 TSARRTPVSYQNTMSRGSPMMNRTSDVT---IPPNKSTNHERKST-LTPTQRESIPAKSP 1534
                                                                                                                                                                                                                                                                                                                                         1738 LRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMP 1797
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                                                                                                                                    PGYPSQYQLYAMENTRQTILNDYITSQQMQVNLRPDVARGLSPREQPLGLPYPATRGIID
                                                                                      1706 LAAAASAEREREREREREE
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                                   SLP-----EGAISPGPRREAPPQVCPGWSPPAKSLAPKKPPTGPLPPSKEPLKEKL-
                                                                 VPGVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPT
                                                                                                                                                                    1249 - DKPPRFRRLKQE-------RENAARG-SEGKPSLTLPASA----
                                                                                                                                                                                                                                                                                                                                                                                                            1798 LPAGGPSISQG------LPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAA
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RESULT 41
S13507
microtubule-associated protein MAP2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 13-Aug-1999
C;Accession: S13507
R;Marechal, D.; Delapierre, D.; Dresse, A.
Arch. Int. Physiol. Biochim. 96, 231-236, 1988
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A;Status: nucleic acid sequence not shown; translation not shown
A;Status: nucleic acid sequence not shown; translation not shown
A;Status: 1.1825 cMAR>
A;Residues: 1.1825 cMAR>
A;Cross-references: EMBL:X54100; NID:g56624; PIDN:CAA38034.1; PID:g56625
A;Cross-references: EMBL:X54100; NID:g56624; PIDN:CAA38034.1; PID:g56625
A;Cross-references: EMBL:X54100; NID:g56624; PIDN:CAA38034.1; PID:g56625
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1990
C;Superfamily: microtubule-associated protein MAP2b; MAP2/tau repeat
C;Seywords: microtubule binding; tandem repeat
C;Seywords: microtubule binding; tandem repeat
C;Seywords: microtubule binding; tandem repeat
C;Seywords: microtubule binding; tandem repeat
C;Seywords: microtubule binding; tandem repeat
C;Seywords: microtubule binding; tandem repeat
C;Seywords: microtubule binding; tandem repeat
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C;Seywords: microtubule binding; tandem repeat
C;Seywords: microtubule binding; tandem repeat
C;Seywords: microtubule binding; tandem repeat
C;Seywords: microtubule binding; tandem repeat
C;Seywords: microtubule binding; tandem r 94; SHNQASYTQETPKPSVGSISLGLPRQQESAKSATLPYIKQE-EFSPRSQNSQPEGLLVRA 1126 QHEGVV--RGTAGAIQ------EGSITRGTPTSKISVESIPSLRGSITQGTPALPQTG 1176 1312 LKYPKQIKRESPPIRAFEGAITKGKPYDGITTIKEMGR-SIHEIPRQDILTQESRKTPE- 1369 ---VVQSTRPIIEGSISQGTPIKFDNNSGQ----SAIKH-----NVKSLITGPSKLSRGM 1417 PPLEIVPENI -- KVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGI 1475 QRESIPAKSPVPGVDPVVSHSPFDPHHRG-STAGEVYWSHLPTQL-.DPAMPFHR--ALD 1579 QPAPHQLITNLPEGVRLPTTRPTRPPPLIPSSKTTVASEKPSFIMGGSISQGTPGTYLT 1067 -----SGHI-LSYDNIKNAR--EGTRS-------PRTAHEISLKRSYESVE 1251 --YDDTSARRTPVS-----YQNTMSRGSPMMNRTSDVTIPPNKSTNHERKSTLTPT 1524 PAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDY-----ITSQQMQVNL----R 1628 PDVARG-----LSPREQPLGLPYPATRGIIDLTN--MPPTILVPHPGGTSTPPMDRI 1678 ---FPPRPY--NSASMSPGHPTHLAAA-- 1709 EHAALVPQPDTSKTPQDKKDPQDMEGEKSPASPFAQTFGTNLEDIK-QITEPSITVPSIG 247 PKV------YGEKRDLHSKNKDDLTLSRSLGLGGRSAIEORSMSINLPMSCL 708 A;Title: Cloning and partial sequencing of a new rat brain specific cDNA. A;Reference number: S13507; MUID:89334524 A;Accession: S13507 ----QEKKETSTPSVQEPTLTETEPQ---TKLEETSKVSIEETVAKE---EESLKLKDD ------KMEPPEQOKLPSSFAEPLDKEETEFKMOSKPGED-----F LSAEPLAPKDQKDWFIEMPVESKKDEWGLAAPISPGPLTPMREKDVLEDIPRWEGKQFDS PMPSPFHSGSFTLPLDTVKDERVTEGSQPFAPVFFQSDDKMSLQDTSGSATSKESSKDEE GNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIMQGTPRATTESFEDG POKDKADKVADVPVSEATTVL-----GDVHSPAVEGFV--GENISGEEKGTTD----SQPSPPA------HEAGYSTLAQSYTSDHPSELPEEPSSPQERMFTID EKVISEPEAVSEKREIOGLFEEDIADK-----SKLEGAGSATVAEV--EMPFYEDKSGM 909 Length 1825; 119 OPAALPLAAE--ETVNLP-----PSPPPSPASEOTAALEEAS-----Indels IPTEALV - - - - KGSISRMPIEDSSPEKGREEAASKGHVI - - - - - -2.7%; Score 338; DB 2; ilarity 20.1%; Pred. No. 1.1e-05; Conservative 232; Mismatches 587 ---GTQIT----1 2.7%; Similarity 20.1%; TYIP----Matches 359; Query Match Best Local 9 1008 1068 1177 248 1252 1370 1418 1629 154 1127 189 308 368 463 514 995 1525 621 663 709 1679 q δ ŏ g q ŏ qq qq δ ò οy δy g ò 셤 g ò g ð q δ g οy g οy g δ

Db         756           Qy         1710           Db         816           Qy         1754           Db         1754           Db         1813           Qy         1818           Qy         1918           Db         1017           Qy         2099           Db         1135           Qy         2099           Qy         2183           Qy         2183           Qy         2204           Db         1413           Qy         2244           Db         1469           Qy         2279           Qy         2279           Qy         2279           Qy         2279           Qy         2311           Db         1529           Qy         2311           Db         1529           Qy         2311           Db         1529           Qy         2387           Qy         2387           Db         1529           Qy         2387           Db         1527

RESULT

149477 alpha-A-crystallin-binding protein I - mouse N;Alternate names: alpha-A-CRYBP1; DNA-binding protein PRDII-BF1 homolog C;Species: Mus musculus (house mouse) C;Date: 15-Mar-1996 #sequence\_revision 15-Mar-1996 #text\_change 20-Sep-1999

Ribrady, J.P.; Kantorow, M.; Sax, C.M.; Donovan, D.M.; Piatigorsky, J.
J. Biol. Chem. 270, 1221-1229, 1995
A; Title: Marine transcription factor alpha A-crystallin binding protein I. Complete s
A; Reference number: A55434; MUID:95138112
A; Reference number: A55434; MUID:95138112
A; Reference number: A55434; MUID:95138112
A; Reference number: A55434; MUID:95138112
A; Reference number: A55434; MUID:95138112
A; Reference number: A55434; MUID:95138112
A; Residues: 1-2688 CRES>
A; Residues: 1-2688 CRES>
A; Cross-references: GB:L36829; NID:9556285; PIDN:AAA98810.1; PID:9818008
A; Cross-references: GB:L36829; NID:9556285; PIDN:AAA98810.1; PID:9818008
A; Ribamara, T.; Donovan, D.M.; Hamada, K.; Sax, C.M.; Norman, B.; Flanagan, J.R.; Oza Mol. Cell. Biol. 10, 3700-3708, 1990
A; Title: Regulation of the mouse alphaA-crystallin gene: isolation of a CDNA encoding 94; ------TSPCGTSKSPNREWEVLQPAPHQLITNLPEGVRLPTTRPTR 1031 ----SYTQETPKPSV----QESISLGLPRQ----QESAK 1098 134 GTAGAIQEGSITRGTPTSKISVE--SIPSLRG---SITQGTPALPQTGIPTEALV---- 1183 313 TNLHTLESTKLEPIYNTAVTSTVGLT-SPSTRTQV--TPPHQQMDSVSPLSVSPASSTQS 369 | | | : | : | : | : | : | : | PPGPIYSSAH--VAS-----VVSQSVEQMCSLLLRDQKPKKQGKYICEYCNRACAKPSVL 422 423 LKHIRSHTGERPYPCVTCGFSFKTKSNLYKHKKSHAHTIKLGLVLQPEAGGLFLSQECPK 482 683 KQKTSRKPREERDVSQCESVASTVSAQE------DEDIEASNEEENPEDSEVEAVKP 733 734 SE-DSPENATSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAET 792 65 SPLRNPLQTKHKQNTE-----EPPFSVLPSASESHKKHNCVPAKQGRQFTKQNGETPGMT 119 AEQMDVDQQEHSAEEGSVCDPPPATKADSVDVEVRVPENHASKVEGDNTK-----ERDL 846 847 DRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDV---DGEPERQRMFPMDS 903 ----KPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTPVSGYAL 959 16 SCAIKTEKLRPNKTVRSPSKLKNSSLDAPN-----ATSPDLVVESPC-----PPCTSYPV 265 483 ALSVHSDIEDSGESDEEGLADGRQNNPCVKDLQPVQTMKTVSNPESLPKLIPSNSDHVVR 542 | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | Indels 762; Gaps 166 SSSSSK-----ARTDNSECSSPCCSTTPPSYTSTAFDVLLKAMEPELSTLSQKGS PPPPLIPSSKTTVASEKPSFIMGGSISQ-------GTPGTYLTSH-NQA--------PYIKQ-EEFSPRSQNSQPEGL--LVRAQHEGVVR A;Residues: 2024-2688 <NAK> A;Cross-references: GB:X68946; NID:g49859; PIDN:CAA48762.1; PID:g49860 Length 2688; A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 2024-2688 <NAK> A; Gene: alphaA-CRYBP1 A; Introns: 14/1; 32/1; 2011/3; 2056/2; 2115/1; 2149/1; 2315/3 C; Superfamily: HIV-EP2 enhancer-binding protein Query Match 2.7%; Score 336; DB 2; L. Best Local Similarity 18.6%; Pred. No. 2.1e-05; Matches 405; Conservative 267; Mismatches 742; 960 YORHIKAMHESALLEEQRORQEQIDLECRSS-----A;Reference number: A35677; MUID:90287161 A;Accession: A35677 Accession: I49477; A35677 SATL 266 991 1032 370 1099 793 1073 904 g ò Dp á Dp δ g δ g δ 셤 δý QQ δ g Qλ qq δ Dp δ

οy	1184	REEAASKGHVIYEGKSGHILSYDNIKNAREGTRSPRT	1242
QQ	603		639
8 6	1243	LKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIMQGTPR  :  :: :   :- :   1.1	1302
à	1303	ATTESFEDGLKYPKQIKRESPPIRAFEG	1362
QQ	674	:   : :	708
δý	1363	KHNVK-SL	1420
g	709		735
ογ	1421	EIVPENIKVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQL	1471
q	736	TKTLEERISKLISDNEALVDDKQLDSVKPRRTSLSRRGSIDSPKSY-	781
οy	1472	SPGIYDDTSARRTPVSYQNTMSRGSPMMNRTSDVTIPPRKSTNHERKSTLTPTQRESIPA	1531
g	782	FDL KPMGR	819
οy	1532	KSPVPGVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAMAAYLFQRQL	1591
q	820	LLSVPSLDCLPITRSNSMPTTGYSAIPANIIPPPPSLRG	858
οy	1592	SPTPGYPSQYQLYAMENTRQTILNDYITSQQMQVNLRPDVARGLSPREQPLGLPYPATR-	1650
g	859	SPDDKIGTLYDDVFVSGPNPSKHRPLVRQ	894
٥y	1651	-GIIDLINMPPTILVPHPGGTSTPPMDRITYIPGTQITFPPRPYNSASMSPGHPTHLAAA	1709
g	895	AAVEDSTASESHVPGSGQSVDESCQGCPSSSEAGPVQSKAA	935
οy	1710	ASAERE	1752
QQ	936	:   :   :   :   :   :     :   :     :	994
οy	1753	YVRSPSPSVRTQETMLQORPSVFQGTNGTSVITPLDPTA	1791
q	995	PAPGGAQPQVLHYRVAAPTAVWEQTPQIRKRRKMKSVGDEEDLQPHESGRSPESAD	1050
οχ	1792	QLRIMPLPAGGPSISQGLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEE	1851
q	1051	ALQLQPVPGAAPSPSKHTSATAADQAHRGVQLVARGPER	1089
οy	1852	NLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQP-HSSVVYS-	1901
g	1090		1149
οy	1902	-EAGKTILTAANFI	1933
qq	1150	QELGRIGMPGALKVIGMAPEEGHPPQDAMHQTALSHNLRGEPRESARKIPSERYVLGQPL	1209
οy	1934	DVIITRQIASDKDARERGSQSSDSSSSLSSHRYETPSDAIEVISPASSPAPPQE	1987
QQ	1210	RLVRQHNIQVPEILVTEEPDRDLEAQSHDEEKSEKFTWPQRS-ETLSKLPTE	1260
οχ	1988	KLQTYQPEVVKANQAENDPTRQYEGPLHHYRPQQESPSPQQQLPPSSQAEGMGQ	2041
qq	1261	KLPPKKKRLRLAEIEHSSTESSFESTLSRSLSRESSLSHASSFSASLDLEDISKVELAPK	1320
οy	2042	VPRTHRLITLADHICQIITQDFARNQVSSQTPQQPPTSTF	2081
QQ	1321	IDFPSKAEFLLIPLGSNTLSVPGSHREMRRAASEQISC-VPTLMEVSDF	1368
ογ	2082	ONSPSALVSTPVRTKTSNRXSPESQAQSVH	2111
a	1369	RSKSFDCGSIAPSHVVPALVESQPSYSPSAVGGTAHVPLLERRRGPLIRQISLNIASD	1426

Š A	ZIIZ -HORPGEKVSPERIVOKSKEGSRPGKSPEKSHVSSEPY ZI4/  I I : :   : :   : :   : :     : :
6ò	EPISPPOVPVVHEKODSLLLLSORGAEP-AEQRNDARSPGSISYLPSF 219
d d	TDTFPPQQLFGAHLLNKTNTSLSHQNTPLPLPVSAQGGKPDAAPTACVSSTGEGSFAPKY 154
οy	FTKLENTSPMVKSKKQEIFRKLNSSGGGDSDMAAAQPGTEIFNLPAVTTSGSVS 224
<del>Q</del>	1547 QLQCQAFTSDQGCSAPLRSSPNQVLPGQAGADPCPASEAPPA 1588
Oy Dp	2249 SRGHSFADPASNLGLEDIIRKALMGSFDDKVEDHGV 2284     : ::::    :     :     :       :         :
δλ	2285 VMSQPM GVVPGTANTSVVTSGETRREEGDPSPHSGGVCKPKL 2326
đ	:::  : : : :
Qy	2327 ISKSNSRKSKSPIPGQGYLGTERPSSVSSVHSEGDYHRQT 2366
<del>අ</del> .	1705 VSESSPŢVQKVSVGRLSPQQESSASSKRMLSPANSLDIAMEKHQKRAKDENGAVCST 1761
0у	PGWAWEDRPSSTGSTQFPYNPLTMRMLSSTPPTPIACAPSAVNQAAPHQONRIWERE
q <sub>Q</sub>	
ζ	24.24 PAPLISSON 24.39
qq	RPSTF
RESC T450 muci C; SE	RESULT 43 T45025 mucin WUC5B, tracheobronchial [imported] - human (fragment) C;Species: Homo sapiens (man) C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
, R , D , D	ccession: 143023 esseyn, J.L.; Guyonnet-Duperat, V.; Porchet, N.; Aubert, J.P.; Laine, A.
A;Ti	BAD2. CHEM. 274, 3105-3109, 1997 ILLLE: Human mucin gene MUC5B, the 10.7 kb large central exon encodes various alter eference number: 222899; MUID:97166151
A; AC A; St	ccession: T45025 tatus: preliminary; translated from GB/EMBL/DDBJ
A; Mc	olecule type: DNA saidues: 1-3570 <des></des>
A; Ge C; Ge A; Ge	ross-references: EMBL:272496; NID:gl834502; PIDN:CAA96577.1; PID:gl834503 xperimental source: placenta enetics: enetics:
S B B	<pre>Query Match 2.7%; Score 336; DB 2; Length 3570; Best Local Similarity 18.9%; Pred. No. 3e-05; Matches 410; Conservative 228; Mismatches 830; Indels 696; Gaps 91;</pre>
δy	567 ATPRGRKTANSQGRRKGRITRSMTNEAAAAAAAAAATEEPPPPLPPPEPISTEPVETS 626
QΩ	399 ATSRARPTGTASTASKEPLTTSLAPTLTSELSTSQAETSTPRTETTMSPLTNTTTSQGTT 458
Qy	627 RWIEEEMEVAKKGLVEHGRNWAAIA-KM 653
ΟQ	459 RCQPKCEWTEWFDVDFPTSGVASGDMETFENIRAAGGKMCWAPKSIECRAENYPEVSIDQ 518
Οy	654 VGTKSEAQCKNFYFNYRRHNLDNLLQQHKQKTSFKPR 691
Dp	519 VGQVLTCSLETGLTCKNEDQTGRFNMCFNYNVRVLCCDDYSHCPSTLATSSTATPSSTPG 578
Qy	692 EERDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSEDSPENATSRG 745
QQ .	579 ITWILTKPTTTATT-TASTGSTATASSTQATAGTPHVSTTATTPTVTSSKATPFSSPGTA 637

ò	746	NTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVET 782	
Q	638	TALPALRSTATTPTATSFTAIPSSSLGTTWTRLSQTTTPMATMSTAT	
8 8	783	QVNDSISAETAEQMDVDQQEHSAEEGSVCDPPPATKADSVDVEVRVPENHASKVEGDN 840   ::	
3 8	841	TKERDLDRASEKVEPRDEDLVVAQOINAQRPEPQSDNDSSATCSADEDVDGEPERQRMFP	
qq	731	TSPGRARTLP	
οy	901	MDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIG 951	
QQ	750	SIMA	
οy	952	-TPVSGYALYQRHIKAMHESALLEEQRQRQBQIDLE	
qq	793	ATP	
ΟŊ	1011		
QQ	802	PPSLTTTATILITATGSTTNPSSTPGTTPIPPVLTTTATTPAATSSTVTPSSALGTTHTPP 864	
ολ	1061	TPGTYLTSHNQASYTQETPKPSVGSISLGLPRQQESAKSA 1100	
qq	865	VPNTTATTHGRSLSPSSPHTVCTA	
0 y	1101	TLPYIKOEBESDRSQNSQNBGLLVRAQHEGVVRGTAGALQEGSITRGTPTSKISVESI	
9	943	STPALSSPHPSSKITESPP	
QY DP	1159	PSLRGSITQGTPALPQTGIPTEALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGH 1218 	
οy	1219	ILSYDNIKNAREGTRSPRTAHEISLKRSVESVEGNIKQGMSMRESPVSAPLE-GLICR 1275	
qq	1013		
δy	1276		
. qq	1064	:  : :   NREQVGKFKMCFNYEIRVFCCNYGHCPSTPATSSTATPSSTPGTTWILTELT 1115	
οχ	1301		
qq	1116		
δy	1343	TIKEMGRSIHEIPRODILTQESRKTPEVVQSTRPIIEGSISQG 1385	
qq	1176	ATTPTATSVTPIPSSSLGTTWTRLSQTTTPTATMSTATPSSTPETAHTSTVLTATTTG 1235	
δy	1386	TPIKFDNNSGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVKAGE 1442	
qq	1236		
οy	1443	TVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRT 150	
qq	1286	TPTTRGSTVTPSSIPGTTHTATVLTTTTTV-ATGSMATPSSSTQTSGTPPSLTT 1339	
δλ	1503	SDVTIPPNKSTNHERKSTLTPTQRESIPAKSPVPGVDPVVSHSPFDPHHRGSTAGEVY	
qq	1340	TATTITATGSTTNPSSTPGTRPIPPVLTTTATTPAATSSTVTPSS 1384	
οy	1563	HLPTQLDPAMPFHRA	
qq	1385	ALGITHIPPVPNTTATTHGRSLSPSSPHIVRIAWISAISGILGITHITEPS 1435	
οy	1623	MQVNLRPDVARGLSPREQP-LGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRITYI 1681	
g	r 1436		
Qy	1682	PGTQITFPPRPYNSASMSPGHPTHLAAAASAERERERERERERERERERIAAASSDLYLRPG 1741	

-----CAWSE-WLDYS 1531 1592 RNREQVGKEKMCENYEIRVFCCNYGHCPSTPATSSTATPSSTPGTTWILTEQTTAATTTA 1651 1823 ALVDAA-----ASAPQMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKR 1876 1652 TTGSTAIPSSTPGTAPPPKVLTSQATTPTA-----TSSKATSSSSPRTATTLPV--- 1700 1877 SVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVI 1936 1937 ITRQIASDKDARERGSQSSDSSSSLSSHRY-----ETPSDAIEVISPASSPAPP--- 1985 1811 TEPSTTATVTVPTGSTATASSTRATAGTLKVLTSTATTPTVISSRATPSSSPGTATALPA 1870 -----AEGMGQVPRTHRLITLADHICQIITQDFARNQVS-SQTPQQPPTSTFQNSP 2085 2086 SALVSTPVRTKTSNRYSPESQAQSVHHQR------PGSRVSP----ENL 2124 1925 -VLTTTATTTRTGSVATPSSTPGTAHTTKVPTTTTTGFTATPSSSPGTALTPPVWISTTT 1983 2125 VDKSRGS--RPGKSPERSHVSSEPYEPISPPQVPVVHEKQDSLLLLSQRGAEPAEQRNDA 2182 2183 RSPGSISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGGGDSDMAAAQPGTEIFNLPAVT 2242 2016 --TGSMA-TPSSSTQTSGTPPSLITTTATTI-----TATGSTTNPSSTFGTTPIP-PVLT 2065 2243 TSGSVSSRGHSFADPASNLGLEDIIRKALMGSFDDKVEDHGVVMSQPMGVVPGTANTSVV 2302 2066 TTATTPAATSSTVTPSSALGTTH----------TPPVPNTTAT 2098 2303 TSGETRREEGDPSPHSGGVCKPKLISKSNSRKSKSPIPGQGYLGTERPSSVSSVHSEGDY 2362 2363 HRQTPGWAWEDRPSSTGSTQFPYNPLTMRMLSSTPPTPIACAPSAVNQAAPHQQNRIWER 2422 1871 LRSTATTPTATSVTAIP-SSSLGTAWTRLSQTTTPTATMSTATPSSTPETVHTST---- 1924 1742 SEQPGRPG----SHGYVRSPSPSVRTQ----ETMLQQRPSVFQGTNGTSVITPLD---------PTAQLRIM----PLPAGGPSISQGLPAS-----RYNTAADALA 1701 -LISTATKSTATSFTPIPSSTLGTTGTSQNRPPHPMAT------MSTIHPSSTPETT 1984 TPTTRGSTVTPSSIPGTTHTAT---------VLTTTTTVA-----2099 THG----RSLPPSSPHT----VPTAWTSATS------GILGTTHITEPST----GTS 1986 QEKLQTYQPEVVKANQAENDPTRQYEGPLHHYRPQOESPSP-0000LPPSSO----| | | :::: | | | :::1 1484 SRTTATATPSKTRTSTLLPSSPTSAPITTVVTMGCEPQ-----2138 H--TPA-----ATTGTTQ---2423 EPAP 2426 2167 PPSP 2170 1789 2036 g οy g δλ 셤 δ g δ a δ QQ δ qq δý g ŏ g ŏ q ŏ g ò φ g ŏ g ŏ a

RESULT

C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 24-Mar-1999 #text\_change 21-Jul-2000
C; Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 21-Jul-2000
C; Accession: T03454
R; Prasad, R; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Ya
Oncogene 15, 549-560, 1997
A; Title: Structure and expression pattern of human ALR, a novel gene with strong homo A; Reference number: 214954; MUID:97388474

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA

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2121 PENLVDKSRGSRPGKSPERSHVSSEPYEPISP---PQVPVVHEKQDSLLLLS-QRGAEPA 2176
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A; Residues: 1-5262 <PRA>
A; Cross-references: EMBL:AF010403; NID:g2358284; PIDN:AAC51734.1; PID:g2358285
C; Genetics:
A; Gene: ALR
A; Map position: 12
C; Superfamily: human ALR protein
C; Keywords: alternative splicing
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                                                                                                                                                     1.6%; Score 335; DB 2; Length 5262;
Similarity 19.4%; Pred. No. 5.3e-05;
56; Conservative 267; Mismatches 882; Indels 786;
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δλ	1283	-HSD
qq	1212	FHCEWQNSYTHCGPCASLVTCPICHAPYVEEDLIQCRHCERWMHAGGESLFTEDDVDHA 1271.
Qy	1315	
Q	1272	PDEGFDCVSCQPYVVKPVAPVAPPELVPMKVKEPEPQYFRFEGVWLTETGMALLRN 1327
ý	1347	MGRS-IHEIPRQDILTQESRKTPEVVQSTRPIIEG 1380
qq	1328	LIMSPLHKRRQRRGRLGLPGEAGLEGSEPSDALGPDDKKDGDLDTDELLKGEGGVEHMEC 1387
δy	1381	SISQGTPIKFDNNSGQSAIKHNVKSLITGPSKLS 1414
g	1388	I
δý	1415	RGMPPLEIVPENIKRSTL 1463
qq	1448	GDGQPDEVIPADLPAEGAVEQSLAEGDEKKKQQRRGRKRSKLEGMFPAYLQEAFFGKELL 1507
οy	1464	HEAPKAQLSPGIXDDTSARRTPVSYQNTMS RGSPMMNRTSD-VTIPPNKSTNHERKST 1520
qq	1508	DLSRKALFAVGVGRPSFGLGTPKAKGDGGSBRKELPTSQKGDDGPDIADEESRGLEGKAD 1567
δ	1521	LIPTORESIPAKSPVPGVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDP 1580
qq	1568	PSDPEKPG-TPG
δ	1581	TPGYPSOYQLYAMEN-TROTILNDYITSOOMQVNLRPDVARGLSPRE   :  :  :  :  :
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ò	1640	OPLG
QQ	1630	QHLGCGTPGLEGSRTPLQRPFLQGGLPLGNLPSSSPMDSYPGLCQSPFLDSRERGGFFSP 1689
οy	1681	IPGTOITEPPRPY-NSASMSPGHPTHLAAAASBERERERER-EKERERERIAAASS 1734
qq	1690	TGSGGTTPSTPTTTEGEGDGLSYNQRSLQRWEKDEELGO
δy	1735	DLYLRPGSEQPGRPGSHGYVRSPSPSVRTQETM1767
g	1746	VLYANINFPNIKQDYPDWSSRCKQIMKLWRKVPAADKAPYLQKAKDNRAA 1795
οy	1768	LQQRPSVFQGTNGTSVITPLD-PTAQLRIMPLPAGGPSISQGLPA 1811
q	1796	HRINKVOKQAESQINKQTKVGDIARKTDRPALHLRIPPQPGALGSPPPAAAPTIFIGSPT 1855
δy	1812	SRYNTAADALAALVDAAASAPQMDVSKTKESKHEA-ARLEENLRSRSAAVSEQQQLEQKT 1870
qq	1856	TPAGLSTSADGFLKPPAGSVPGPDSPGELFLKLPPQVPAQAPSQDPFGLAPAYP 1909
. <b>О</b> Х	_	LEVEKRSVQCLYISSAFPSGKP-QPHSSVVYSEAGKDKGPPPKSRYEEE 1918
qq	1910	LEPREPTAPPTYPPYPSPTGAPAQPPMLGASSRPGAGQPGEFHTTPPGTPRHQPSTPDPF 1969
δy	1919	LRTRGKTTITAANFIDVIITRQIASDKDARERGSQSSDSSSSLSSHRYETPSDAIEVISP 1978
qq	1970	LKPRCPSLDNLAVPESPGVGGRASEPLLSPPPFGESRKALEVKKE 2015
οy	1979	ASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGPLHHYRPQ 2020
qq	2016	SPNIGFVDSPSSGTHLGGLELKTPDVFKAPLTPRASQVEPQSPGLGL
ογ	2021	OESPSPQQQLPPSSQABGMGQVPRTHRLTTLADHICQIITQDFARNQVS 2069
qq	2076	EPPPAQALAPSPPSHPDIFRPGSYTDPYAQPPLTPR
δλ	0	TSTFONS
a	2112	SS

Qy   759 TAPS-TSPSLAVP-STKPAEDES-VETQVNDSISAETAEQMDVDQQEHSAEGSVCDPPP   815	Db 547 - SAAQAKPALEKQMKASSRKGTPASATGASTSSHCKAGAV - TSSASLSSPALAKGTQRS 603  Qy 1096 SAKSATLEYIKQEEFSPRSQNSQBCLLUVRQHEGVYRGTAGAIQEGSITRGTPTSKISV 1155  Db 604 DVDS	1271 GLICRALPRGSPHSDLKERTVLSGSIMOGTPRATTESFEDGLKYPKQIKRESPPIRAFEG	QY         1436 EDVRAGETVRSHTSVVSGPSVLRSTLHEAPKAQLEFGIYDDTSARFTPVSYOTMARG 1495           Db         662 EGVQANTTKKASGTTAQSSSEBSEDGDEDLIPATQPSTYALFTSVTTPAALSRA 916           QY         1496 SPMMNRTSDVTIPPNKSTNHERKSTLTPTQRESIPAKSPVFGVDPVVSHSPFDPHHRGST 1555           Db         917 ASQPSKSEQSSRWFKGKKAKAAASAQTSSAVETLPMMPPCSAPIQPKA 964           QY         1556 AGEVYWSHLP-TQLDPAMP
	TYORAPYPGSLPLOOOQOOLWQQQQ	R; Paznekas, W.A.; Zhang, N.; Gridley, T.; Jabs, E.W. Biochem. Biophys. Res. Commun. 238, 1-6, 1997 A;Title: Mouse TCOF1 is expressed widely, has motifs conserved in nucleolar phosphoprote A;Attle: Mouse TCOF1 is expressed widely, has motifs conserved in nucleolar phosphoprote A;Attle: Mouse TCOF1 is expressed widely, has motifs conserved in nucleolar phosphoprote A;Accession: JC5630; MUID:97445113 A;Accession: JC5630 A;Ac	Query Match         2.6%; Score 334.5; DB 2; Length 1320;           Best Local Similarity 19.9%; Pred. No. 9.7e-06;         Matches 319; Conservative 197; Mismatches 610; Indels 481; Gaps 70;           Qy         503 QQIARPSQEEKVEEKEDEKAEEKKDEEKDEKEDSKENTKEKDRIDGTAEFTE 562

1757 PSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMPLPAGGPSISQGLPASRY 1814	1158 SVVKVLTELLEQERLKATEAIKESGKKSQKRKLSGDLEAGAP 1199	1815 NTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLE 1872	1200	1873 VEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPKSRYEEELRTRGKTTITA 1929	1230 LDKGSAGGKGKGSPGPGGAKEKPDGELLGIKLESGEQSDPKSKSKKKKSLKKK 1282	1930 ANFIDVIITRQIASDKDARERGSQSSDSSSLSSHRYETPSDA 1972	1283	
1757	1158	1815	1200	1873	1230	1930	1283	
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AAY70304
AAY72782
AAW11922
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AAB50363
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AAB50362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human HNRCR protein SEQ ID NO:20
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries

    protein search, using sw model

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5; 300 360 420 480 540 900 999 720 180 240 311 371 431 491 764 671 824 944 120 131 191 251 551 611 731 884 791 851 Gaps 36 36 71 QQQQLRRRPSLLSEFHPGSDRPQERRTSYEPFHPGPSPVDHDSLESKRPRLEQVSDSHFQ MSSSGYPPNQGAFSTEQSRYPPHSVQYTFPNTRHQQEFAVPDYRSSHLEVSQASQLLQQQ RVSAAVLPLVHPLPEGLRASADAKKDPAFGGKHEAPSSPISGQPCGDDQNASPSKLSKEE LIQSMDRVDREIAKVEQQILKLKKKQQQLEEEAAKPPEPEKPVSPPPVEQKHRSIVQIIY RVGQRGAGLSATIARSEHEISEIIDGLSEQENNEKQMRQLSVIPPMMFDAEQRRVKFINM NGLMEDPMKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNFGLIASYLERKSVPDCVLYYYL TKKNENYKALVRRNYGKRRGRNQQIARPSQEEKVEEKEEDKAEKTEKKEEEKKDEEEKDE PSLAVPSTKPAEDESVETQVNDSISAETAEQMDVDQQEHSAEEGSVCDPPPATKADSVDV EVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCS 129; nuclear Length 6; Indels of 21; homologue DB Score 11873.5; Pred. No. 0; 5; Mismatches human Ø represents 93.9%; 94.3%; Query Match Best Local Similarity 94.3 Matches 2316; Conservative sequence (HNRCR). ₹, 2343 The present coreceptor ( Sequence 37 121 37 181 72 241 132 301 192 361 252 421 312 481 372 541 432 601 492 661 552 721 612 765 672 825 732 882 792 2228 g Q Qy Dp g S g oy ob q b ç QQ g a g g g g ò ò οŽ ő ò ò ò ò ò οy ò

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      PSALVSTPVRTKTSNRYSPESQAQSVHHQRPGSRVSPENLVDKSRGSRPGKSPERSHVSS
                              DIIRKALMGSFDDKVEDHGVVMSQPMGVVPGTANTSVVTSGETRREEGDPSPHSGGVCKP
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91.2%; Score 11536.5; 91.0%; Pred. No. 0; 11ve 79; Mismatches

Query Match 91.2 Best Local Similarity 91.0 Matches 2245; Conservative

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                                         aesfedglkypkqikresppirafegaitkgkpydgittikemgrsiheiprqdiltqes
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Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; antiarthritic; immunosuppressant; cardiant; immunostimulant; carcopathic; antiarthritic; immunosuppressant; cardiant; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; antianteral; antibacterial; antifungal; antihemmatic; antidiabetic; antianaemic; gene therapy; cancer; prolliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
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οy	134	SQGTPIKFDNN-SGQSAIKHN 140
q	1419 vk	tqgtplkydtgasttgskkh
ογ	1403 VK	GPSVLRST 146
Q	1474 VI	ssggsi
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Retinoid X receptor interacting protein RIP13. Retinoid X receptor interacting protein; RXR; RIP;

27-SEP-1996

AAR99738;

95WO-US16311. 95US-0372652.

08-DEC-1995; 13-JAN-1995;

18-JUL-1996

W09621677-A1

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Moore D,

Choi H,

WPI; 1996-342241/34 N-PSDB; AAT31931.

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Retinoid X receptor (RXR) interacting protein (RIP) - useful to modulate or mediate RXR function, anti-RIP antibodies can be used determine RIP subcellular distribution patterns

Claim 2; Page 51-52; 90pp; English

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Mouse retinoid X receptor (RXR) interacting protein RIP13 (AAR99738) is a candidate transcriptional co-activator. It was identified using an in vivo interaction trap system for the isolation of proteins that physically interact with RXRs, esp. with the ligand binding domain of human RXR alpha. Recombinant RIP13 can be obtd. using a cDNA clone (AAT31931) obtd. from a mouse liver library. RIPs (see also AAR99735-37 and AAR99739) can be used to modulate or mediate RXR function, and may be used therapeutically or to raise antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                            1819 DALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSV 1878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RQIASDKDARERGSQSSDSSSSLSSHRYETPSDAIEVISPASSPAPPQEKLQTYQPEVVK 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQRNDARSPGSISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGGDSDMAAAQPGTEIF 2236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1879 QCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVIIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANQAENDPIRQYEGPLHHYRPQQESPSPQQQ--LPPSSQAEGMGQVPRIHRLITLADHIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QIITQDFARNQVSSQTPQQPPTSTFQNSPSALVSTPVRTKTSNRYSPESQAQSVHHQRPG
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                                                                                                                                                                                                                                                                                              619;
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                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                           22.8%; Score 2885.5; DB 17; Lengt
90.1%; Pred. No. 3.8e-150;
live 27; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                              Conservative
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Best Local Similarity
Matches 562; Conserv
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AAR99738 standard; Protein; 619

RESULT AAR99738 ID AAR9

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Sequence
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Matches
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                                                                                     New co-suppressor of steroid-thyroid hormone receptor activity - also methods for identifying compounds that relieve its suppressant
ing mediator for retinoic acid and thyrold hormone receptor; transcriptional co-repressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A novel receptor interacting factor (AAW18226) is designated SMRT,
                                   nlpavttsgavssrshsfadpasnlglediirkalmgsfddkvedhgvvmshpvgimpgs
                                                 ANTSVVTSGETRREEGDPSPHSGGVCKPKLISKSNSRKSKSPIPGQGYLGTERPSSVSSV
                                                                             HSEGDYHRQTPGWAWEDRPSSTGSTQFPYNPLTMRMLSSTPPTPIACAPSAVNQAAPHQQ
                                                                                                                                                                                                                                                                                                                                                         present in the original two-hybrid
                                                                                                                                                                                                                                                                                                            1061..1132
/label= glutamine-rich region
1201..1495
/label= C-terminal_region
                                                                                                                                                                                                                                                                          "proline-rich domain"
                                                                                                                                                                                                                                                             1..160
/label= N-terminal_region
                                                                                                                                                                                                                                                                                                                                                  "alternatively
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                                                                                                          NRIWEREPAPLLSAQYETLSDSDD 2440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 40-45; 71pp; English
                                                                                                                 Transcriptional co-repressor SMRT
                                                                                                                                                                                                                                                                                                       /label= SG_region
                                                                                                                                                          AAW18226 standard; Protein; 1495
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                                                                                                                                                                                                                  Silencing mediator
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                                                                                                                                                                        AAW18226;
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PCGTS--KSPNREWEVLQPAPH----QLITNLPEGVRLP-----TTRPTRPPPPLIPSSK 1041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1099 SATLPYIKQEEFSPRSQNSQPEGLLV-RAQHEGVVRGTA-GAIQEGSITRGTPTSKISVE 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSGHILSYDNIKNA----REGTRSPRTAHEISL-KRSYESVEGNIKQGMSMRESPVSAP 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSTRPIIEGSISQGTPIKFDNN-SGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVV 1430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1488 YONTMSRGSPWMNRTSDVTIP----PNKSTNHERKSTLTPTQRESIPAKSPVPGVDPVVS 1543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : ||: ||||:||||:||| | : ||:||| | : ||::: : : | 419 laprplkegsitggtplkydtgasttgskkhdvrsligspgrtfppvhpldvmad-aral 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 plissakhpsvlerqigaisqg----msvqlhvpysehakap-vgpvtmglplpmdpkk 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 lapfsgvkqeqlsprgqagppeslgvptaqeasvlrgtalgsvpggsitkgipstrvpsd 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.9%; Score 1879; DB 18.
llarity 35.8%; Pred. No. 1.5e-94;
Conservative 216; Mismatches 534.
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les 572; Conserv
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Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnezray; antipartic; antiparthinsonian; noctropic; neuroprotective; antioconvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiamatory; antivital; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; prollferative disorder; hypertension;
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                                                                                                                                                                                               1858 AAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKP----QPHSSVVYSEAGKDKGP--P 1910
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|||| :|:||||:||:||:||:||| | ::: :
thltkptttsssererdrdrerdrdrereksiltstttvehapiwrpgtegssgssgssg 820
                                                     ----PGRPGSHGYVRSPSP-SVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMPL
                                                                                     ggggsssrpashshahqhspisprtqda-lqqrpsvlhntgmkgiitavepskptvlrst
                                                                                                                                                             stsspv----rpaatfppathcplggtldgvyptlmepvllpk----eaprvarperpra
                                                                                                                                                                                                                               ----tghaflakpparsglepass---pskgseprplvp
                                                                                                                                                                                                                                                                 1911 PKSRYEEELRTRGKTTITAANFIDVIITRQIASDKDARERGSQSSDSS-----SSLSSH
                                                                                                                                                                                                                                                                                                    pvsghatiartpakn--laphhaspdppappasasdphrektgskpfsigelelrslgyh
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                                                                                                                                                                                                                                                                                                                                                                                                          HYRP---QQESPSPQQQLPPSSQAEGMGQVPRTHRLITLADHICQIITQDFARNQVSSQT
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; caquences have activities such as: cytostatic; hepatotropic; vulnerary; contingentic; antiparkinsonian; noctropic; neuroprotective; cateopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, confidential and nucleic acids may be used to treat cancers, graft vs host disease, cardiovacular disease, diabetes mellitus, graft vs host disease, cardiovacular disease, storage, systemic lupus hypothyroidism, cholesterol ester storage, 129; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; noctural haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance 158 SPIS------GQPCGDDQNASPSKLSKEELIQSMDRVDREI-AKVEQQILKLKKK 205 ----spk 793 Gaps 99 -VDHDSLESKRPRLEQVSDSHFQRVSAAVLPLVHPLPEGLRASADAKKDPAFGGKHEAPS 157 EVSQASQLLQQQQQQLR-----RRPSLLSEFHPGSDRPQERRTSYEPFHPGPSP--- 98 × neurodegenerative disorder; osteoarthritis; graft vs host disease; evqskkpipskpqlkqlqvlddqgperedvrknycslrdetperksgqekshsvnteeki Indels 814; Length 3266; peptides derived from open reading coagulation; to inhibit thrombosis; and as a contraceptive. disorders, <del>=</del> = = useful for treating e.g. cancers, proliferative disordeneurodegenerative disorders and cardiovascular disease Conservative 312; Mismatches 1034; Score 520; DB 21; Pred. No. 1.1e-19; Claim 11; Page 3700-3708; 5507pp; English 4.18; 31-MAR-1999; 99US-0127607. 02-APR-1999; 99US-0127636. 05-APR-1999; 99US-0127728. 30-MAR-2000; 2000US-0540763. 31-MAR-2000; 2000WO-US08621 thrombosis; contraceptive nucleic acids and Shimkets RA, Leach M; (CURA-) CURAGEN CORP WPI; 2000-602362/57 3266 AA; Similarity N-PSDB; AAC76700 WO200058473-A2. Homo sapiens 05-OCT-2000 Matches 545; Sequence Query Match Local Novel 49 697 ð g ò g ò

sppskkrmdhvdfdictkrernyrssrqi 848		sedsertggspsvrngsthededplgsprllsvkgspkvdekvlpysnltvreeslkinp 908 VDBNPKKaffranktffrctCDEVDF DIVNODCOMPKVUDDNIFmagnaby 207	agrfdvsfpnsiikr	KLILFFKRRNHARKQREQKICQRYDQLMEAWEKKVDRIENNPRRKAKESKTREYYEKQFP 347 :			NEKOMROLSVIPPMMFDAEORRVKFINMNGLMEDPMKVYKDROFMNVWTDHE 444		: :  : : qelfasrfihssifeqdskrlqhlerkeedsdfisgriygkqtsegan 1167	IAMPSQEEKVEEKEEDKAEKTEKKEEEKKDEEBKDEKEDSKENTKEKDKIDGTAEETEER 564	RKTANSGGRRKGRITRSMTNEAAAASAAAAAATEE 606	elktppsvgppsvtvvtlesapsalekttgdktveaplvteektvepatvseeakpasep 1286	613	apapveqleqvdlppgadpdkeaammpagveegssgdqppyldakpptpgasfsqaesnv 1346	KGLVEHGRNWAAIA 651	dpepdstgplskpagkseeanepkaekpdatadaepdangkaeaapesgppasedlevdp 1406	KMVGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRKPREERDV 696	pvaakdkkpnkskrsktpvqaaavsivekpvtrkseridreklkrsnsprgeagkllelk 1466	715	meaekitrtasknsaadlehpepslplsrtrrrnvrsvyatmgdhenrspvkepveqprv 1526	ASNEEENPEDSEVEAVKPSEDSPENATS 743	trkrlerelgeaaavpttprrgrppktrrradeeeeneakepaetlkppegwrsprsgkt 1586	RGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAE 791		TABLOMDVOQUEHSAEESSVCUPPFAIKAUSVOVEVRVENHASKVEGDNIKEK 844   :			PIGSILVS	r. · · · · · · · · · · · · · · · · · · ·	HRAAVIPPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEQRQRQEQID 984      : :                asetelaaaiqsiindisdepenfpapppypgesqtd 1843	
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1844 1qppostarentemerical		:	192	qq
184 14	1143	7 AKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVRGTAGAIQEG	109	δy
983 LECKNSTSPCGISKSFNKEWELLQPAFHQLITNLFEGVKLPTTRETRPPPPLIP 103	(7)	:	188	qq
985 LECKNSTSPCGISKSFNKEWEKLQPARHQLIINLFEGVKLPFTRKPTRPFPPLIP 103	1096	9 SSKTTVASEKPSFIMGGSISOGTPGTYLTSHNOASYTOETPKPSVGSISLGLPROOE	103	ô
	1038	<pre>5 LECRSSTSPCGTSKSPNREWEVLQPAPHQLITNLPEGVRLPTTRPTRPPPPLI 1</pre>	96 184	oy G

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Novel human prostate cancer marker gene termed as 07CG27 gene, useful for screening mutations in the gene in diagnosis of a predisposition to cancer - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides the protein and coding sequences of the human 07CG27 oncogene. This gene is found at the HPC1 region of chromosome 1. The sequences can be used in the diagnosis and identification of treatments for prostate cancer. The present sequence the 07CG27 protein.
1934 DVIITRQIASDKDARERGSQSSDSSSSLSSHRYETPSDAIEVISP----ASSP---- 1982
                                                                                                                                                    2873 nqlqglpltpp----vvvthgvqivhssgelfqeyrygdirtyhppaqltht-qfpaas 2926
                                                                                                                                                                                                                 svglpsrtktaaqgpppegeplqppqpvqstqpaqpappcppsql-----gqpgqppss 2980
                                                                                                                                                                                                                                                                                                        2186 GSISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGGGDSDMAAAQPGTEIFNLPAVTTSG 2245
                                                                                                                                                                                                                                                                                                                           2981 kmpqvsqeakgtqtgveqprlpagp-----anrppephtqvqraqaetgptsfpsp 3031
                                                                           2135 KSPERSHVSSEPYEPISPPQVPVVHEKQDSLLLLSQRGAEPAEQRNDAR-----SP
                           2772 sevlvmg-----seyrlhpytvprdvrimvhphvtavsegpraadgv
                                                                                                                        SQAEGMGQVPRTHRLITLADHICQII-----TQDFARNQVSSQTPQQPPTSTFQNSPSA
                                                                                                                                                                                   2088 LVSTPVRTKTSNR -----YSPESQAQSVHHQRPGSRVSPENLVDKSRGSRPG----
                                                           --APPQEKLQTYQP--EVVKANQAENDPTR----QYEGPLHHYRPQQESPSPQQQLPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; 07CG27 gene; chromosome 1; HPC1 region; prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rommens JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Simard J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 91-99; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MYRI-) MYRIAD GENETICS INC.
(HOSP-) HOSPITAL FOR SICK CHILDREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB35408 standard; Protein; 2819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0151049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene protein
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N-PSDB; AAF28060.
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AAB35408
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                                                                                                           260 ypplhgpm----rfpp-slsetnkglrgrgpppswaseperpsilsaselkeldkfdnl 313
                                                                                                                                               -----LQQQQQQLRRRPSLLSEFHPGSDRPQERRTSYEPFHPGPSPVDHDSLESKR 108
                                                                                                                                                                                                                      PRLEQVSDSHFQRVSAAVLPL---VHPLPEGLRASADAKKDPAF----GGKHEAPSSP-- 159
                                                                                                                                                                                                                                                         nenkketdevsntksssqipaqpsvakvpyg-----kgpsfngergtsshlppppkl 414
                                                                                                                                                                                                                                                                                                                     SDTKVYHENIKTNQVMRKKLILFFKRRNHARKQREQKICQRYDQLMEAWEKKVDRIENNP 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                speei----ekelekedege 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRKAKESKTREYYEKQFPEIRKQREQQERFQRVGQRGAGLSATIARSEHEISEIIDGLSE 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QENNEKQMRQLSVIPPMMFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHEKEIFK 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        510 QEEKVEEKEEDKAEKTEKKEEE---KKDEEEKDEKEDSKENTKEKDKIDGTAEETEEREQ 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           602 AATEEPPPPLPPPPEPISTEPVETS-----RWTEEEMEVAKKGLVEHGRNWAAIAKMVG 655
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                                                                       6 YPPNQGAFSTEQSRYPPHSVQYTFPNTRHQ---QEFAVPDYRSSHLEVSQASQL----- 56
                                                                                                                                                                                314 daeadegwagaqmevdyteqlnfsdddeggsnspkennse-----dggskasen
                                                                                                                                                                                                                                                                                               ISGQPCGDDQNASPSK----LSKEELIQSMDRVDREIAKVEQQILKLKKKQQQ----LEE
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 DB 22; Length 2819;
                                      Indels 1147;
                                    Mismatches 962;
                   Pred. No. 4.2e-19;
 Score 507.5;
                 Best Local Similarity 18.5%; Pr
Matches 557; Conservative 350;
4.0%;
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 Query Match
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à	995		42
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λ	1299	GTPRATTESFEDGLKYPKQIKRESPPIRAFEGAITKGKPYDG 1340	40
ą	1408	ppkferkfdparerprrgrptrpprqdkpprfrrlrereaasksnevvavptngtvnn 1465	65
à	1341	ITTIKEM-GRSIHEIPRQDILTQ1369	69
ą	1466	vaqepvntlgdisgnktpdlsnqnssdqaneewetasessdfnerrerdekknadlnaqt 1525	25
λ	1370	VVQSTRPIIEGSISQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSRGMPPLEI 1422	22
ð	1526	vvkvgenvlppkreiakrsfssgrpvdrgnrrgnngppksgrn-fsgprnerrsgpp 1581	81
λ	1423	VPENIKVVERGKYEDVKAGET1461	61
ą	1582	fddg	37
λ̈	1462	TLHEAPKAQLSPGIYDDTSARRTPVSYQ- 1489	89
ą	1638	l:    :   : : : :	97
à	1490	TIMSRGSPAMNR15D9	60
ą	1698	eerrkkeeqviqvwnkknanekgrsqtsklpprfakkqatgiqqaqssasvpplasaplp 1757	57
à	1510	NKSTNHERKSTLTPTQRESIPAKSPVPGVDPVVSHSPFDPHH 1551	51
ð	1758		12
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ą	1813	asasvsasvpastsaaaitsssapasapaptpilasvstpasvtilasasipilasalas 187	72
<b>≿</b>	1592	SPTPGYPSQYQLYAMENTRQTILNDYITSQQMQVNLRPDVARGLSPREQPLGLPYPA- 1648	48
ð	1873	tsaptpa-paasspaapvitaptipasaptasvplapasasapapaptpvsapnpap 1928	28
Σ	1649	TRGIIDLTNMPDTILVPHPGGTSTPPMDRITYIPGTQIT 1687	87
ā	1929	papaqtqaqthkpvqnplqttsgsskqpppsirlpsaqtpnqtdyvasqksiqtpqshqt 1988	88

ΟŊ	1688 F-	į
qq	686	:        :     :   :   :   :     :     :
č	722	170
3 1	3	
Q O	2046	esgleigtdtigigapasngnene 2069
δλ	1783 VI	VITPLDPTAQLRIMPLPAGGPSISQGLPASRYNTAADALAALVDAAASAPQMD 1835
Dp	2070 vv	pviseksadkipepkegrqkqpragpikaqkipd 2105
δλ	1836 VS	VSKTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQ 1893
QQ	2106 18	pvenkehkpgpigkerslknrkvkdagqvepeggek 2143
Qy	1894 PE	SSVVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVIITRQIASDKDARERGSQ 1953
qq	2144 ps	
Qγ	1954 SS	SSDSSSSLSSHRYETPSDAI 1990
qq	2185 ak	
Οy	1991	TYQPEVVKANQA-ENDP-TRQYEGPLHHYRPQQESPS 2025
qq	2240 svp	
Qy	2026	PQQQLPPSSQAEGMGQVPRTHRLITLADHICQIITQDFARNQVSSQ 2071
QQ	2298 fs	fssasmpqipvasvtptaslsgagtyttsslstkstttsdppnickvkpqqlq 2350
Qy	2072 TE	QOPPTSTFQNSPSALVSTPVRTKTSNRYSPESQAQSVHHQRPGSR 2118
qq	2351 ts	tsipsashfsqlscmpsliaqqqqnpqvyvsqsaaaqipafymdtshlfntghar 2406
οy		VSPENLVDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVHEKQDSL 2165 
qq	2407 19	ppsla-qqqqfqpglgqptsvqqipipiyaplqqqhqaqlslgagpa 2454
QY	2166	LLLSQRGAEPAEQRNDARSPGSISYLPSFFTK 2197
qq	2455 vs	vsqaqelfssslqpyrsqpafmqsslsqpsvvlsgtaihnfptvqhqelakaqsglafqq 2514
Qy	2198 LE	LENTSPMYKSKKQEIFRKLNSSGGGDSDMAAAQPG-TEI 2235
qa	2515 ts	tsntqpipilyehqlgqasglggsqlidthllqaranltqasnlysgqvqqpgqtnf 2571
Qy	w	₽.
q	2572 yn-	taqspsalqqvtvplpasqlslpnfgstgqplialpqtlqpplqhttpqaqa_2625
Οy	2281	DHGVVMSQPM-GVVP-GTANTSVVTSGETRREEGDPSPHSGGVCKPKLISKSNSRKS 2335
qq	2626 qs	lsrpaqvsqpfrglipagtqhsmiattgkmsemelkafgsgidikpg 2674
ΟŊ	2336 KS	HSEGDY
qa	2675 tp	tppiagrsttptsspfratstspnsgsskmnslvygkdfgsapatvrm 2722
QY	2396 TP	TPPTPIACAPSAVNQA 2411
qq	2723 tq	tqpfptqfapqakqra 2738
RESU AAY5	RESULT 8 AAY50976	
ΩX	AAY5097	6 standard; Protein; 3256 AA.
AC XX	AAY5097	9;
T X	10-MAR-2000	2000 (first entry)

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| | pepintpthtkgglkaslgkvgvkeellavgkftrtsgetththrepagdgks1rtfkes 1071
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                                                                                                                                                                                ----kdtargqnllqtqdhakapksekgkitkmpcqslq 1011
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   ---KOMROLSVIPPMMFDAEORRVKFI 418
                                   sg---rstefrnigklp--veskseetnteivecilkrggkatll-----ggrr---- 918
                                                                                                     --egemkeierpfetyke---nielkende--kmkamkrsrtwggkcapmsdltdlksl 970
                                                                                                                                                                                                                                                                                         ----KGRITRSMINEAAAAAAA 601
                                                                                                                                                                                                                                                                                                                                                                                                                                      653 MVGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRKPREE----RDVSQCESVASTVSA 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------RAAVIPPMVSCTPCNIP--IGTPVSGYALYQ-----RHIKAMH 968
                                                                       NMNGLM----EDPMKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNFGL----IASYLERKSV
                                                                                                                                                                                                                  ----SKENTKEEEKKDEEEKDEKED-----SKENTKEKDKIDGTAEET---E
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                                                                                                                                              PDCVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEKVEEKEEDKAEK - - - -
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   RGAGLSATIARSEHEISEIIDGLSEQENNE---
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                                                                                                                                                                                                                                                                                         563 EREQATPRGRKTANSQGRR--
                                                                                                                                                                              971 pdtelm---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel oligoribo- or oligodeoxyribonucleotide, characterized in that, it hybridizes to mank that encodes protein Ki-67 at a physiologically acceptable salt concentration. The oligoribo- or oligodeoxyribonucleotide which is complementary to Ki-67, a protein active at all stages of the cell cycle except G.0, is useful for therapy of illnesses with increased cell proliferation and particularly for treatment of tumors, autolmnume diseases, scar formation, inflammation, allergy, rheumatic diseases and defence against transplantation. This sequence represents the human cell cycle protein Ki-67 which is described in the method of the invention.
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Matches 516; Conservative 368;
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                                                             LLLLSQRGAEPAEQRNDARSPGSISYLPSFFTKLENTS-----PMVKSKKQEIFRKLNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nuclear thyroid hormone interacting proteins; TR; JL1; JL2;
transcriptional coactivator; treatment; diagnosis;
thyroid related disorders; modulation; thyroid hormone receptor;
nuclear hormone receptor; isolation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thyroid hormone receptor-interacting protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric Homo sapiens
Chimeric Bacterial sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1994-199808/24.
N-PSDB; AAQ63705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lee JW, Moore DD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-OCT-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                    2815
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                                                             2165
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Length 73;

Score 370; DB 15; Pred. No. 1.2e-13;

2.9%; S 100.0%;

ò 8

Matches

2291

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61

AAY40596;

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This sequence represents a human thyroid hormone receptor (TR-interacting protein) which is found to interact with a novel human Jil protein in an in vivo interaction trap assay. The Jil protein is potentially useful for the treatment of hyperthyroidism or thyroid disorders.
                                                                                                                                                                          Thyroid hormone receptor-interacting protein; TR-interacting protein; JL1; human; interaction trap assay; treatment; thyroid disorder; S243b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2231 PGTEIFNLPAVTTSGSVSSRGHSFADPASNLGLEDIIRKALMGSFDDKVEDHGVVMSQPM 2290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thyroid hormone receptor-interacting protein S243b partial sequence.
                                                                                                                                                                                                                                                                                                  1..73
/note= "Partial coding sequence, no start or stop
codons given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JL1 protein - that interacts with thyroid hormone receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.9%; Score 370; DB 20;
100.0%; Pred. No. 1.2e-13;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                          Human TR-interacting protein S243b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 28; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW85115 standard; Protein; 73 AA.
                                  AAW92403 standard; Protein; 73,AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-0222719.
92US-0969136.
95US-0470925.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.0
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2291 GVVPGTANTSVVT 2303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moore DD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAX01894
                                                                                                                                                                                                           hyperthyroidism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-APR-1994;
30-OCT-1992;
06-JUN-1995;
                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                       21-APR-1999
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                                                                     AAW92403;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lee JW,
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RESULT 11
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                  AAW92403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides a JL1 protein which specifically interacts with a thyroid hormone receptor in an in vivo trap assay. The Jl1 protein can be recombinantly produced by standard recombinant methodology. The JL1 protein is used in a trap assay for determining whether a test protein is capable of interacting with a nuclear hormone receptor protein and any also be used as a therapeutic peptide for treating thyroid disorders. Sequences AAY40572-596 represent partial amino acid sequences of thyroid hormone receptor (TR)-interacting proteins.
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                                  PGTEIFNLPAVTTSGSVSSRGHSFADPASNLGLEDIIRKALMGSFDDKVEDHGVVMSQPM 2290
Gaps
                                                  JL1 protein; thyroid hormone receptor; trap assay; therapeutic; nuclear hormone receptor protein; TR-interacting protein; human; thyroid disorder.
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                                                                                                                                                                                                                                                                                                                                 Partial amino acid sequence of TR-interacting protein S243b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Purified DNA comprising a sequence encoding a protein which specifically interacts with a thyroid hormone receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 73;
0; Indels
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100.0%; Pred. No. 1.2e-13;
tive 0; Mismatches 0;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 28; 68pp; English.
                                                                                                                                                                                                                             AAY40596 standard; protein; 73 AA.
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92US-0969136.
                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
Conservative
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                                                                                                     GVVPGTANTSVVT 2303
                                                                                                                                      gvvpgtantsvvt 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moore DD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Simil
Matches 73; C
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-OCT-1992;
                                                                                                                                                                                                                                                                                               03-DEC-1999
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73;
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Lee JW,

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Indels

Sequence

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Length 73;

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WPI; 1992-284685/34
           CANCER INST
                                                                                                                                                                                                                                2843 AA;
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Matches 418; Conserv
                                                               Kinzler
                                                                                                   N-PSDB; AAQ27234
                                                      Albertsen H,
                                                                                                                                                                                                                                Sequence
                   (ICIL)
(UYJO)
(UTAH)
                                                                                                                                                                                                                                                          Query Match
           (CANC-)
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                                                                                                                                                                                                                                      The present sequence represents thyroid hormone receptor-interacting protein 8243b. The protein was identified using the method of the invention. The method is used to determine if a test protein is capable of interacting with a nuclear hormone receptor protein in a ligand-dependent manner. The method is used especially to screen for proteins that interact with thyroid hormone receptors in a ligand-dependent or ligand-sensitive manner.
                                                                                                                                                                                                                                                                                                                                                                           2231 PGTEIFNLPAVTTSGSVSSRGHSFADPASNLGLEDIIRKALMGSFDDKVEDHGVVMSQPM 2290
                                                                                                                                                                                                                                                                                                                                                                                     neoplasm; cancer; oncogene; tumour; growth; detection; diagnosis; prognosis; treatment; sporadic colorectal carcinomas; ss.
                                                                                                                                                                                           Screening assay for nuclear hormone receptor modulators - using
                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                         Length 73;
                                                                                                                                                                                                                                                                                                                                                           Indels
Thyroid hormone receptor-interacting protein; S243b; nuclear hormone receptor protein; screen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APC gene product in familial adenomatous polyposis.
                                                                                                                                                                                                                                                                                                                                        Score 370; DB 20;
Pred. No. 1.2e-13;
0; Mismatches 0;
                                                                                                                                                                                                    cells containing reporter gene construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR26052 standard; Protein; 2843 AA.
                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                               100.0%; Pr
                                                                               94US-0222719
                                                                                                          92US-0969136
                                                                                                                                                                                                                                                                                                                                         2.98;
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91US-0741940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                            (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                     Disclosure; Fig 28; 69pp;
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              GVVPGTANTSVVT 2303
                                                                                                                                                                                                                                                                                                                                                                                                                                gvvpgtantsvvt 73
                                                                                                                                                               WPI; 1999-059040/05
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 73; Conserv
                                                                                                                                               Moore DD;
                                                                                                                                                                                                                                                                                                              Ź
                                                                                                                                                                         N-PSDB; AAV82605
                                                                                                                                                                                                                                                                                                             73
                                                                                                 04-APR-1994;
30-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JAN-1991;
08-AUG-1991;
                                            US5846711-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JAN-1993
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                                                              08-DEC-1998
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                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR26052
                                                                                                                                              Lee JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            13
                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                              2291
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98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1251 vssingetigtycvedtpicfsrcsslsslssaedeigcngttgeadsantlgiaeikgk 1310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene associated with tumorigenesis, found on chromosome 5q.
The sequence may be mutated by deletions insertions, inversions, or
point mutations of the gene. The APC gene is expressed in most normal
tissues as well suggesting that APC is a tumour suppressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     347 PEIRKQREQQE-RFQRVGQRGAGLSATIARSEH------EISEIIDGLSEQENNEK 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     396 QMRQLSVIPPMMFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHE--KEIFKDKFI 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------QKTSR 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             689 KPREE-----RDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSE--DSPEN 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              514 VEEKEEDKAEKTEKK - - EEEKKDEEEKDEKEDSKENTKEKDKIDGTAEETEEREGATPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R-----KTANSQGRRKGRITRSMTNEAAAAS------AAAAAATEEPPPPLPPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DQQEHSAEE----GSVC-----DPPPATKADSVDVEVR----VPEN-HASKVEGDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               841 TKE--RDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDVD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           454 QHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       615 PEPISTEPVET-----SRWT-----EEEMEVAKKGLVEHGRNWAAIAKM---
                                                                                                                                                                                                                                                                                                                            Detection of somatic and germ-line alterations of human APC gene - used to diagnose, treat and study familial adenomatosus polyposis and sporadic colorectal cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is encoded by the APC (Adenomatous Polyposis Coli)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              664;
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                                                                                                                         Hedge PJ;
Thliveris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.9%; Score 368; DB 13;
1larity 19.4%; Pred. No. 1.8e-11;
Conservative 281; Mismatches 797;
                                                                                                               Carlson ML, Groden JL,
Markham A, Nakamura Y,
Markham AF;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 47; 132pp; English.
IMPERIAL CHEM IND PLC. UNIV JOHNS HOPKINS. UNIV UTAH.
                                                                                                                                                        Joslyng, Kinzler KW, M
Vogelstein B, Whiterl,
                                                                                                                         Anand R,
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                      The present sequence is the human adenomatous Polyposis coli (APC) gene product, which was used in the development of a novel method of diagnosing or prognosing an APC gene associated neoplastic issue. The method comprises comparing APC gene coding sequences or mRNA in a tumour tissue, where a difference indicates an APC gene associated neoplastic tissue, where a difference indicates an APC gene associated neoplasia of the tumour tissue.

APC is a tumour repressor expressed in most normal tissues. APC mutations are found in familial adenomatous polyposis and sporadic colorectal cancer patients. The method enables mutations to be detected to provide an indication of predisposition to cancer.
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Best Local Similarity 19.4%; Pred. No. 1.8e-11;
Matches 418; Conservative 281; Mismatches 797; Indels
Example 1; Columns 33-52; 140pp; English.
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APC is a tumour repressor expressed in most normal tissues. APC mutations are found in familial adenomatous polyposis and sporadic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibodies to normal and mutant adenomatous polyposis coli proteins
            2553 khssslp--rvstwrrtgssssilsassessekaksedekhvnsisgtkqskenqvsakg
                                                                                                                           npr---sgrsptgntppvidsvsekanpnikdskdngakqnvgngsvpm--rtvglenrl
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                                                                                                        -----SQAEGMGQVPRTHRLITLADHI
                                                                                                                                                                  2056 CQIITQDFARNQVSSQTPQQPPT -- STFQNSPSALVST--- PVRTKTSNRYSPESQAQSV
                                                                                                                                                                                                                            2111 HHQRP----GŞRVSPENLVDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVH--EKQDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, adenomatous Polyposis coli, APC, diagnosis; prognosis; neoplastic tissue; tumour tissue; tumour repressor; mutation; sporadic colorectal cancer; detection.
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Nakamura Y,
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nzler K, Markham AF,
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(UYJO) UNIV JOHNS HOPKINS.
(UTAH ) UNIV UTAH.
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16-JAN-1991;
16-JAN-1991;
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                                                                                                                                                               797; Indels 664; Gaps
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colorectal cancer patients. The method enables mutations to be detected to provide an indication of predisposition to cancer.
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                                                                                                                        Length 2843;
                                                                                                                    Query Match 2.9%; Score 368; DB 19;
Best Local Similarity 19.4%; Pred. No. 1.8e-11;
Matches 418; Conservative 281; Mismatches 797;
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coli (ARC) gene, it encodes the tumour repressors described in AAR63507 and AAR63508. Determination of alterations in APC or its expression products, can be used for the diagnosis and prognosis of cancer e.g. colorectal, lung and breast tumours; and for determining predisposistion to certain cancers such as familial adenomatous polyposis (FAP) and canners such as familial adenomatous polyposis (FAP) and canners such as familial adenomatous polyposis (FAP) and canners as syndrome. The wild type APC gene (or a part of it) can be used the tapeutically to restore gene function, while primers and probes detect mutations. Also APC proteins or analogues can be administered to compensate for a defective gene, and epithelial cells, or transgenic animals carrying a mutated APC allele are useful for detecting therapeutic agents able to suppress tumorigenesis.
                                                 2723 tsfiqvd-----pfsssss 2768
                                                                                                                                             CQIITQDFARNQVSSQTPQQPPT--STFQNSPSALVST---PVRTKTSNRYSPESQAQSV 2110
                                                                                                              2111 HHQRP----GSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEPISPQVPVVH--EKQDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 familial adenomatous polyposis; cancer diagnosis and prognosis; tumorigenesis suppression.
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Nakamura Y, Thliveris
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Pred. No. 1.9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repressor
                                                                                                                                                                                                                                                                                                                   AAR63507 standard; Protein; 2860 AA
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91GB-0000974.
91GB-0000975.
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Vogelstein B, White RL;
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418; Conservative 281; Mismatches 797; Indels 664; G	PEIRKOREQOE-RFORVGORGAGLSATIARSEHEISEIIDGLSEQENNEK	QMRQLSVIPPEMMFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHEKEIFKDKFI 	OHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEK	VEEKEEDKAEKTEKKEEEKKDEEEKDEKEDSKENTKEKDKIDGTAEETEEREQATPRG ::  :	RKTANSQGRKGRITRSMTNEAAASAAAAAATEEPPPPLPPP 	PEPISTEPVETSRWTBEEMEVAKKGLVEHGRNWAAIAKM	VGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSR    :	KPREERDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSEDSPEN	A-TSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDV	DQQEHSAEEGSVCDPPPATKADSVDVEVRVPEN-HASKVEGDN	TKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDVD	GEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVI 	PPMVSCTPCNIPIGTPVSGYAL	SALLEEGRORQEQIDLECRSSTSPCGTSKSPNREWEVL	QPAPHQLITNLPEGVRLPTTRPTRPPPLI	SSKTTVASEKPSFIMGGSISQGTPGTYLJTSHNQASYTQETP	FPSYGSISLGLPRQQESAKSATLPYIKQEEFSPRSQNSQPEGLUVRAQHEGVVRGTAGAI           :	QEGSITRGTPTSKISVESIPSLRGSITQCTPALPQTGIPTEALVK
Matches	347	396 1058	454	514	572 1208	615 1268	654 1328	689	741	799	841	891 1599	938	970	1008	1039 1828	1080	1140 1931
M	oy G	Oy Db	δγ	O.Y	VQ Q	5 G	Qy Db	Oy Dp	δγ	Oy Db	Qy	oy Ob	O.Y	Oy Dp	Qy Db	op Oy	Oy Ob	Oy Dp

δλ	1186	SISRM1219
qq	1985	slsslsdidgennnkenepiketeppdsggepskpgasgyapksfhvedtpvcfsrnssl 2044
Qy Dp	1220	LSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPL 1269     :
δ	1270	SPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYPKQIKRESPPIRAFE 132
qq	2105	sehglspdsenfdwkalqegansivsslhqaaaaaclsrqassdsdsilslk 2156
δy	1330	GAITKGKPYDGITTIKEMGRSIHEIPRQDILTQESRKTPEVVQSTRPIIEGSISQGTPIK 1389
qq	2157	:    :   Sgislgspfpgekstletkk 2197
λ̈́o	1390	FDNNS-GQSAIKHNVKSLITGPSKLSRGM-PPLEIVPENIKVVERGKYEDVKAGET 1443
QQ	2198	ieseskgikggkkvykslitgkvrsnseisggmkqplqanmpsisrg 2244
ογ	1444	VRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTS 1503
Dp	2245	rtminipgvrnsssstspvskkgp 2268
ογ	1504	DVIIPPNKSTNHERKSTLTPT-QRESIPAK-SPVPGVDPVVSHSPFDPHHRGSTAGEVYW 1561
QQ	2269	
δŏ	1562	SHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITSQ 1621
QQ	2323	dstpaqqplsr 2336
ò	1622	OMQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRI 1678
QQ	2337	piqspqrnsispgrngisppnklsqlprt-sspstastkssgsgkm 2381
δŏ	1679	TYIPGTQITFPPRPYNSASMSPGHPTHLAAAASAEREREREREKERER 1726
QQ	2382	sytspgrqmsqqnltkqtglsknassiprsesaskglnqmnngngankkvel 2433
δy	1727	ERIAAASSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITP 1786
qq	2434	srmsstkssgsesdrserpvlvrqstfikeaps 2466
δ	1787	LDPTAQLRIMPLPAGGPSISQGLPASRXNTAADALAALVDAAASAPQMDVSKTKESKHEA 1846
qq	2467	ptlr-rkieesasfesispssrpasptrsqaqtpvlspslpdmsls-thssvqag 2519
οy	1847	A RLEENLKSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVYYSEAG 1904
q	2520	gwrklppnlsptieyndgrpakrhdiarshsespsrlpinrsgtwkrehs 2569
Óλ	1905	KDKGPPPKSRYEEELRIRGKITIITAANFIDVIITRQIASDKDARERGSQSSD 1956
QQ	2570	
δ	1957	ANO
qq	2628	twrkikenefsptnstsgtvssgatngaesktliygmapavsktedvwvriedcpin 2684
ΟŊ	2016	HYRPQQESPSPQQQLPPSQAEGMGQVPRTHRLITLADHI 2055
g	2685	or   .
δy	2056	CQIITQDFARNQVSSQTPQQPPTSTFQNSPSALVSTPVRTKTSNRYSPESQAQSV 2110
qq	2740	tsfiqvdpfsssss 2785
οy	2111	NDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVHEKQDS 216
a G	2786	khsspsgtvaarvtpfnynpsprkssadstsarpsgip-tpvnnntkkrds 2835

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1191 qkqsfsfsksssgqssktehmssssentstpssnakrqnqlhpssaqsrsgqpqkaatck 1250
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                                                                                                           Adenomatous polyposis coli protein gene;
familial adenomatous polyposis; colorectal tumor; adenoma.
                                                                                                                                                                                                                                                                                                                               Antibodies to adenomatous polyposis coli protein - detecting mutations in the APC gene for predicting pre-disposition to cancer, partic. colon cancer
                                                                                                                                                                                                                                                                             Vogelstein B;
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2.9%; Score 366; DB 15
Best Local Similarity 19.4%; Pred. No. 2.4e-11
Matches 418; Conservative 280; Mismatches 79
                                                                                       Adenomatous polyposis coli protein (APC)
                     AAR58634 standard; Protein; 2843 AA
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VGTKSE--
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APC gene; Adenomatous Polyposis Coll gene; human; chromosome 5q21; familial adenomatous polyposis; FAP locus; Gardner's syndrome; GS; sporadic tumnour; adenoma; carcinoma; cancer; lung; breast; colon; rectum; bladder; liver; sarcoma; stomach; prostate; leukaemia; lymphoma; tumnour suppressor; anti-APC antibody; detection; diagnosis; prognosis; genetic predisposition; drug screening; DP2.5; splice variant.
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                                                               SHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITSO
                                                                                                                            1622 QMQVNLRPDVA---RGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRI
                                                                                                                                                            pigspgrnsispgrngisppnk-----lsqlprt-sspstastkssgsgkm
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                   ---dstpsrpaqqpl-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry
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The invention relates to a novel method for detecting Adenomatous Polyposis Coli (APC) protein in a sample. The method involves contacting the sample with antibodies which specifically binds to the contacting the sample with antibodies which specifically binds to the protein, and detecting an APC-antibody complex. Mutations in the APC gene play a role in tumorigenesis, indicating that it is a tumour suppressor gene. It is located on chromosome 5q21, which corresponds to thousands of adenomatous polyposis) locus. FAP is an autosomal dominant inherited disease in which affected individuals develop hundreds to thousands of adenomatous polyps in the colon and rectum, some of which progress to malignancy. The FAP locus is often found to be deleted in sporadic (i.e., non-familial) adenomas and carcinomas, and chromosome 5q deletions have also been observed in tumours of the lung, breast, colon, rectum, bladder, liver, sarcomas, stomach, and prostate, and in leukaemias and lymphomas. Although the FAP locus contains several other genes such as FER, TB1, TB2, and MCC, it is thought that mutations in the APC gene play a key role in the development of FAP and sporadic tumours. The method is useful for detecting APC protein and its mutations in foreatl tissue, placental tissue, amnibiotic fluid, blood, serum or a tumour sample. The method is useful for diagnosing or prognosing neoplastic tissue, for detecting a genetic predisposition to cancer, for detecting germline and somatic alteration of wild-type APC genes, and for testing therapeutic agents for the ability to suppress tumours. The present sequence represents a 2742 amino acid splice our cancer, and the human APC protein. This variant is less abundant than the contains the contains.
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Thliveris A, Nakamura Y, Vogelstein B;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting Adenomatous Polyposis Coli (APC) protein in a sample for diagnosing cancers, involves contacting the sample with antibodies specifically bind to APC protein and detecting the complex formed -
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                                    16-JAN-1991;
16-JAN-1991;
16-JAN-1991;
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12-AUG-1994;
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-LSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPLE 1270			ć
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PSVGSISLGLPRQQESAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVRGTAGAIQ 1140	PSVGSISLGLPROOESAKSATLP	1081 F	ò
kqnlknnskdfndklpnnedrvrgsfafdsphhytpiegtpycfsrnd 1759	kkqnlknnskdfndklpnnedrv	1711 k	qq
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::	::   :    asssapnkngldgkkkpts	1654 a	qq
PPLIPS 1039	OPAPHOLITNLPEGVRLPTTRPTRPPPPLI	1008	δ
	:::   rstdeagggktssvtipelddnk	1594 I	QQ
-LEEQROROEQIDLECRSSTSPCGTSKSPNREWEVL 1007	ALLEEOR	971 #	οy
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rorhikamhes 970	PMVSCTPCNIPIGTPVSGYAL-	939 -	ò
	:  :   :     amptkssrkakkpaqtasklpppvar	1481 a	QQ
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:  ddsddddielleeclis 1480	:::  : pkesnengekeaektidsekdll	1441 p	g
-RDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDVD 890	TKERDLDRASEKVEPRDEDLV	841 I	ò
		1385 d	QQ
-DPPPATKADSVDVEVRVPEN-HASKVEGDN 840	DOQEHSAEEGSVC	799	ογ
		1329 t	qq
ATSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDV 798	A TSRGNTEPAVELEPTTETAP	741 A	ογ
		1270 s	g
-RDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSEDSPEN 740	KPREERDVSQCESVAST	689 K	δý
vefssgakspsks	:  :  igtrsaedpvsevpavsqhprtk	1210	qq
-AQCKNFYFNYKRRHNLDNLLQOHKOKTSR 688	VGTKSEAQCKNFY	654 \	ò
:    :   sslssaedelgcnqttqeadsantlqiaeikek 1209	:  ::  vssinqetiqtycvedtpicfsrcssl	1150 v	qq
SRWTEEEMEVAKKGLVEHGRNWAAIAKM 653	PEPISTEPVET	615 F	ογ
:	: qkqsfsfsksssgqssktehmss	1090	Q
AAAASAAAAAATEEPPPPLPPP 614	RKTANSQGRRKGRITRSMTNEAAAAS	572 1	δ
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g G	2040	gislgspfpgekstletkki 20	2080
δ	1391	NNS-GQSAIKHNVKSLITGPSKLSRGM-PPLEIVPENIKVVERGKYEDVKAGETV 1	444
QQ	2081	::	2126
ογ	1445	EAPKAQLSPGIYDDISARRIPVSYQNIMSRGSPMMNRISD	1504
qq	2127	ringyipgvringssstspvskkgpp 21	151
Qy	1505	VIIPPNKSTNHERKSTLTPT-QRESIPAK-SPVPGVDPVVSHSPFDPHHRGSTAGEVYWS 1:	1562
Qy	1563	DYITSQQ	1622
qq	2205	:	2219
Qy	1623	PLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRIT	1679
qq	2220	sppnklsqlprt-sspstastkssgsgkms 2	264
Qy	1680	3HPTHLAAAASAEREREREKERERE	1727
q	2265	ytspgrqmsqqnltkqtglsknassiprsesaskglnqmnngngankkvels 23	2316
Οy	1728	LYLRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPL	1787
q	2317	rmsstkssgsesdrserpvlvrqstfikeaps 2	2348
Qy	78		1847
Q	2349	-ptlr-rkleesasfeslspssrpasptrsqaqtpvlspslpdmsls-thssvqagg 24	2402
δλ	1848	SAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGK 1	905
đ	2403	wrklppnlsptieyndgrpakrhdiarshsespsrlpinrsgtwkrehsk 24	452
ζ	1906	DKGPPPKSRYEEELRTRGKTTITAANFIDVIITRQIASDKDARERGSQSSDS 19	957
qq	2453	silsassessekaksedekhvnsisgtkqskenqvsakgt 2	510
Oy	1958		2016
qq	2511	wrkikenefspinstsgivssgaingaeskiliygmapavsktedvwvriedcpinn 25	2567
ογ	2017		2056
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Οy	2057		2114
q	2623	C)	677
Qy	2115	RVSPENLVDKSRGSRPGKSPERSHVSSEPYEPISPPOVPVVH	
qq	2678	:  :   arvtpfnynpsprkssadstsarpsq1p-tpvnnntkkrds 2717	
RESUL	SULT 19		
AAR ID	AAR63508	508 standard; Protein; 2842 AA.	
X X	AAR63508	508;	
<b>5</b> 5 5	23-MA	23-MAY-1995 (first entry)	
S E S	Adenc	Adenomatous polyposis coli tumour repressor.	
KW	Adenc famil	Adenomatous polyposis col1; tumour repressor; Gardner's syndrome; familial adenomatous polyposis; cancer diagnosis and prognosis;	
X X	TUMOT	igenesis suppression.	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                And AARONGO. Determination of activations at an extraction products, can be used for the diagnosis and prognosis of cancer e.g. colorectal, lung and breast tumours; and for determining predisposistion to certain cancers such as familial adenomatous polyposis (FAP) and Gardner's syndrome. The wild type APC gene (or a part of it) can be used therapeutically to restore gene function, while primers and probes derived from the CDNA (AAQ72333-400 and AAQ72541-568) can be used to compensate for a defective gene, and epithelial cells, or transgenic animals carrying a mutated APC allele are useful for detecting therapeutic agents able to suppress tumorigenesis.
                                                                                                                                                                                                                                                                                                                                                                                                            AAQ72297 is a cDNA isolated from the human adenomatous polyposis coli (APC) gene, it encodes the tumour repressors described in AAR63507 and AAR63508. Determination of alterations in APC or its expression
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1087 kfqphfg-----qqecvspy----rsrgangsetnrvgsnhginqnvsgslcqe-
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                                                                                                                                                                                                                                       Hedge PJ;
, Thliveris A;
                                                                                                                                                                                                                                                                                                                                New human adenomatous polyposis coli DNA encoding tumour repressor - and derived primers and probes for diagnosis, prognosis and treatment of cancer
                                                                                                                                                                                                                                        Groden J, H
Nakamura Y,
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nzler K, Markham AF,
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(ICIL ) IMPERIAL CHEM IND.
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(UTAH ) UNIV UTAH.
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B, White RL;
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 Homo sapiens
                                                                              08-AUG-1991;
                          US5352775-A.
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                                                                                                                                                                                                                                                                      Adenomatous polyposis coli protein - useful in the treatment of cancers associated with mutation(s) on human chromosome 5q21
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llarity 19.0%; Pred. No. 2.7e-11;
Conservative 288; Mismatches 807;
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Nakamura Y,
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               16-JAN-1991;
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                                              30 YIPGTQITFPPRPYNSASMSPGHPTHLAAAASAERERERERE------KERERE 1727
                                                                                                                                             28 RIAAASSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPL 1787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           milial adenomatous polyposis coli; APC; tumour suppressor; therapy; romosome 5q21; tumourigenesis; retinoblastoma; colorectal tumour; P; Gardner's Syndrome; GS; predisposition.
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slyn G, Kinzler K, Markham AF, Nakamura Y, Thliveris A;
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Vogelstein B, White RL;

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WPI: 1998-427100/36.

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Adenomatous polyposis coli protein - useful in the treatment of PT cancers associated with mutation(s) on human chromosome 5q21

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Disclosure; Column 63-78; 102pp; English.

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This sequence represents a human familial adenomatous polyposis coli (APC) protein isolated from 87 cDNA clones. The gene for the protein isolated from 87 cDNA clones. The gene for the protein isolated thome on the sequence of the protein isolated the protein isolated from 87 cDNA clones. The gene for the protein isolated to human chromosome 5q21 and is also referred to as adenomatous cc polyposis coli gene. It is a tumour suppressor gene, and mutations in this gene have been associated with tumourigenesis in reflinoblastoma and cc colorectal tumours, and especially familial adenomatous polyposis (RAP) cc and Gardner's Syndrome (CS). The protein can be used in therapy to cc replace lack of native functional protein and the nucleic acids can be cc used as probes and primers in detection of the cancers and predisposition XX

Sequence 2843 AA;

Sequence 2843 AA;

94; 1251 vssingetigtycvedtpicfsrcsslsslssaedeigcngttgeadsantlgiaeikek 1310 1311 igtrsaedpvsevpavsqhprtkssrlggsslssesarhkavefssgakspsksgagtpk 1370 1371 sppehyvqetplmfsrctsv-ssldsfesrsiassvqsepcsgmvsgiispsdlpdspgq 1429 396 QMRQLSVIPPMMFDAEQRRVKFINMNGLMEDPMKVYKDRQFWNVWTDHE--KEIFKDKFI 453 689 KPREE-----RDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSE--DSPEN 740 347 PEIRKOREQOE-RFORVGORGAGLSATIARSEH------EISEIIDGLSEQENNEK 395 891 ---GEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLD----LP----QLQHRAAVIP 938 :|| | | || ::: :| 1088 kfqphfg-----qqecvspy----rsrgangsetnrvgsnhginqnvsgslcqe-615 PEPISTEPVET-----WAAIAKM 454 QHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEK 514 VEEKEEDKAEKTEKK -- EEEKKDEEEKDEKEDSKENTKEKDKIDGTAEETEEREQATPRG tmppsrsktppp---ppqtaqtkrevpknkaptaekresgpkqaavnaavg-rvqvlpda || : : :|| : :|| pkesnenqekeaektidsekdll------ddsd------dddieileeciis 572 R-----KTANSQGRRKGRITRSMTNEAAAAS------AAAAAATEEPPPPLPPP 741 A--TSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDV DQQEHSAEE----GSVC-----DPPPATKADSVDVEVR----VPEN-HASKVEGDN dtllhfatestpdgfscssslsalsldepfigk----dvelrimppvgendngneteseg TKE---RDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDVD-----807; Indels 648; Length 2843; 654 VGTKSE-----AQCKNFYFNYKRRHNLDNLLQQHK----7. Match 2.9%; Score 365; DB 19; Local Similarity 19.0%; Pred. No. 2.7e-11; les 409; Conservative 288; Mismatches 807; Query Match Best Loca Matches 1430 799 1486 841 a ð ò 셤 6 g ò g P 4 8 ö q 셤 ò ð à q ő g ò

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APC gene; Adenomatous Polyposis Coll gene; human; chromosome 5q21; familial adenomatous polyposis; FAP locus; Gardner's syndrome; GS; sporadic tumnour; adenoma; carcinoma; cancer; lung; breast; colon; rectum; bladder; liver; sarcoma; stomach; prostate; leukaemia; lymphoma; tumour suppressor; anti-APC antibody; detection; diagnosis; prognosis; genetic predisposition; drug screening; DP2.5; splice variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting Adenomatous Polyposis Coli (APC) protein in a sample for diagnosing cancers, involves contacting the sample with antibodies that
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-ptlr-rkleesasfes1s---pssrpasptrsqaqtpv1sps1pdms1s-thssvqagg 2503
                           --RLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGK 1905
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                                             SSSLSSHRYE-TPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGPLHH
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Thliveris A, Nakamura Y, Vogelstein B;
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N-PSDB; AAA93449.
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08-AUG-1991;
12-AUG-1994;
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Polyposis Coli (APC) protein in a sample. The method involves
contacting the sample with antibodies which specifically binds to the
2843 amino acid form of the human APC protein, or to a mutant APC
2843 amino acid form of the human APC protein, or to a mutant APC
protein, and detecting an APC-antibody complex. Mutations in the APC
gene play a role in tumorigenesis, indicating that it is a tumour
cappears of gene. It is located on chromosome 5421, which corresponds to
the FAP (familial adenomatous polyposis) locus. FAP is an autosomal
dominant inherited disease in which affected individuals develop
thundreds to thousands of adenomatous polypos in the colon and rectum,
some of which progress to malignancy. The FAP locus is often found to
be deleted in sporadic (i.e., non-familial) adenomas and carcinomas, and
chromosome 5 deletions have also been observed in tumours of the lung,
chromosome 5 deletions have also been observed in tumours of the lung,
and in leukaemias and lymphomas. Although the FAP locus contains
and in leukaemias and lymphomas. Although the FAP locus contains
chromosome for the genes such as FER, TBI, TB2, and MCC, it is thought that
mutations in the APC gene play a key role in the development of FAP and
sporadic tumours. The method is useful for detecting APC protein and its
mutant forms in forest lissue, placental tissue, aminotic fluid, blood,
comment forms in the APC and more approach to a such as the method is useful form served.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     serum or a tumour sample. The method is useful for diagnosing or prognosing neoplastic tissue, for detecting a genetic predisposition to cancer, for detecting germline and somatic alteration of wild-type APC genes, and for testing therapeutic agents for the ability to suppress tumours. The present sequence represents a 2843 amino acid splice variant of the human APC protein. This variant is more abundant than the 2742 amino acid variant (AAB23012).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | ::: | : :: | | : :| gkqsfsfskssggpqkaatck 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                981 psiesyseddeskfcsyggypadlahkihsanhmddndgeldtpinyslkysdeglnsgr 1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1251 vssingetigtycvedtpicfsrcsslsslssaedeigcngttgeadsantlgiaeikek 1310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    347 PEIRKQREQQE-RFQRVGQRGAGLSATIARSEH------EISEIIDGLSEQENNEK 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             396 QMRQLSVIPPMMFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHE--KEIFKDKFI 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----qqecvspy---rsrgangsetnrvgsnhginqnvsqslcqe-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 514 VEEKEEDKAEKTEKK--EEEKKDEEEKDEKEDSKENTKEKDKIDGTAEETEEREQATPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R-----ATANSGGRRKGRITRSMINEAAAAS------AAAAAAIEEPPPPLPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     615 PEPISTEPVET-----WAAIAKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 654 VGTKSE------QCKNFYFNYKRRHNLDNLLQQHK------QKTSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KPREE-----RDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSE--DSPEN
specifically bind to APC protein and detecting the complex formed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        454 QHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEK
                                                                                                        invention relates to a novel method for detecting Adenomatous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative 288; Mismatches 807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.9%; Score 365; DB 21;
19.0%; Pred. No. 2.7e-11;
                                                     Claim 1; Fig 3A-C; 125pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 409; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .088 kfqphfg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1191
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qq

1430 tmppsrsktppp---ppgtagtkrevpknkaptaekresgpkgaavnaavg-rvgvlpda 1485

741 A--TSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDV

94;

9 9	799	DQQEHSAEEGSVCDPPPATKADSVDVEVRVPEN-HASKVEGDN 840 	
ογ	841	TKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDVD 890	
д	1542	pkesnenqekeaektidsekdllddsddddieileeciis 1581	
දු දි	891	GEPERQRMEPMDSKPSLLNPTGSILVSSPLKPNPLDDPOLQHRAAVIP 938	
ð	939	A TEACHT A TATE OF THE TANK AND	
QQ	1635		
οy	971	AL	
qq	1695		
ò	1008	OPAPHQLITNLPEGVRLPTTRPTRPPPLI	
qq	1755	asssapnkngldgkkkptspvkpipgnteyrtrvrknadsknnlnaervfsdnkds 1811	
٥y	1040	SKTTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQETPK 1080	
qq	1812	kgnlknnskdfndklpnnedrvrgsfafdsphhytpiegtpycfsrnd 1860	
ογ	1081	PSVGSISLGLPRQQESAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVRGTAGAIQ 1140	
qq	1861		
ογ	1141	EGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGIPTEALVKGS 1186	
q	1915	kapinrgapkpilakgstfpgsskdipdrgaatdeklanfaientpvcfshnss 1968	
ογ	1187	ISRM1219	
g	1969	lssisdidgennnkenepiketeppdsggepskpqasgyapksfhvedtpvcfsrnssis 2028	
δ.	1220		
අ	2029	slsidseddilqecissampkkkkpsrikgdnekhspromggilgeditldikdigrpds 2088	
ογ	1271	GLICRALPRGSPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYPKQIKRESPPIRAFEG 1330	
q	2089	ehglspdsenfdwkaiqegansivsslhqaaaaaclsrqassdsdsilslks 2140	
ογ	1331	AITKGKPYDGITTIKEMGRSIHEIPRODILTQESRKTPRVVQSTRPIIEGSISQGTPIKF 1390  :    :    -    -    -    -  -  -  -  -  -  -	
g	2141	gislgspfhltpdqeekpftsnkgprilkpgekstletkki 2181	
δ	1391	DNNS-GQSAIKHNVKSLITGPSKLSRGM-PPLEIVPENIKVVERGKYEDVKAGETV 1444	
යු	2182	eseskgikggkkvykslitgkvrsnseisgqmkqplqanmpsisrg 2227	
'n	1445	RSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTSD 1504	
g	2228	rtmihipgvrnsssstspvskkgpp 2252	
ογ	1505		
q	2253	iktpaskspseggtattsprgakpsvkselspvarqtsgiggsskapsrsgsr 2305	
οχ	1563	HLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITSQQ 1622	
g	2306	srp 2320	
λά	1623	MQVNLRPDVARGLSPREQPLGLFYPATRGIIDLTNWPPTILVPHPGGTSTPPMDRIT 1679	
අ	2321	19spgrnsispgrngisppnk1sqlprt-sspstastkssgsgkms 2365	_

DPTAQLRIMPLPAGGPSISQGLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAA 1847 --RLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGK 1905 1958 SSSLSSHRYE-TPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGPLHH 2016 2554 hssslp--rvstwrrtgssssilsassessekaksedekhvnsisgtkgskengvsakgt 2611 2017 YRPQQESPSPQQQLPP----SQAEGMGQVPRTHRLITLADHIC 2056 2669 pr---sgrsptgntppvidsvsekanpnikdskdngakqnvgngsvpm--rtvglenrln 2723 1680 YIPGTQITFPPRPYNSASMSPGHPTHLAAAASAERERERERE------KERERE 1727 2366 y-----tspgrqmsqqnlt--kqtglsknassiprsesaskglnqmnngngankkvels 2417 1728 RIAAASSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPL 1787 1906 DKGPPPKSRYEEELRTRGKTTITAAN------FIDVIITRQIASDKDARERGSQSSDS 1957 2057 QIITQDFARNQVSSQTP-QQPPTSTFQNSPSALVS-TPVRTKTSNRYSPESQAQSVHHQR 2114 Tcf; beta-catenin; human; drug; familial adenomatous polyposis; FAP; cancer; adenomatous polyposis coli; APC; neoplastic. 2115 PGSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVH--EKQDS 2164 Intron-free DNA encoding Tcf-4 protein - useful for, e.g. identifying drugs for treating FAP patients, or patients with increased risk of developing cancer Barker N, Clevers H, Kinzler KW, Korinek V, Morin PJ; Sparks AB, Vogelstein B; Disclosure; Page 32-37; 58pp; English AAW76821 standard; Protein; 2973 AA 98WO-US05506 97US-0821355. (UYUT-) RIJKSUNIV UTRECHT. (UYJO) UNIV JOHNS HOPKINS. 25-JAN-1999 (first entry) WPI; 1998-531569/45. Human APC protein. Homo sapiens. WO9841631-A2. 20-MAR-1998; 20-MAR-1997; 24-SEP-1998. AAW76821; 23 2418 1788 1848 RESULT 2
AAW76821
ID AAW7 a δý g δy Ω ò g δλ g g ò 셤 g δ δ οy 쉱

This sequence represents a human APC protein which is used in a method of identifying candidate drugs for use in familial adenomatous polyposis (C fAP) patients, or patients with increased risk of developing cancer. The protein can also be used to determine the presence or absence in a cell of wild type adenomatous polyposis coll (APC) gene or a downstream protein in the APC transcription regulatory pathway. This method involves introducing a Tcf-responsive reporter gene into the cell, and measuring cranscription of the reporter gene where a cell which supports active transcription of the reporter gene where a cell which supports active transcription of the reporter gene does not have wild type APC or a downstream protein of the APC transcription regulatory pathway. The converted of being neoplastic and for treating a patient with colorectal cancer or other cancer associated with FAPC, comprising administering to the patient a polypeptide comprising a portion of the APC sequence, comprising the beta-catenin binding site.

981 psiesyseddeskfcsygqypadlahkihsanhmddndgeldtpinyslkysdeglnsgr 1040 1191 qkqsfsfsksssgqssktehmssssentstpssnakrqnqlhpssaqsrsgqpqkaatck 1250 1251 vssingetigtycvedtpicfsrcsslsslssaedeigcngttgeadsantlgiaeikek 1310 1371 sppehyvgetplmfsrctsv-ssldsfesrsiassvgsepcsgmvsgiispsdlpdspgg 1429 amptkssrkakkpaqtasklpppvar----kpsqlpvykllpsqnrlqpqkhvsftp 1634 396 OMROLSVIPPMMFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHE--KEIFKDKFI 453 654 VGTKSE------AQCKNFYFNYKRRHNLDNLLQQHK-------QKTSR 688 741 A--TSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDV 798 : :|| | | || ::: :| 1088 kfqphfg-----qqecvspy----rsrgangsetnrvgsnhginqnvsgslcge-PEPISTEPVET-----WAAIAKM 689 KPREE-----RDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSE--DSPEN DQQEHSAEE----GSVC------DPPPATKADSVDVEVR----VPEN-HASKVEGDN 514 VEEKEEDKAEKTEKK -- EEEKKDEEEKDEKEDSKENTKEKDKIDGTAEETEEREQATPRG R-----KTANSQGRRKGRITRSMTNEAAAAS------AAAAAATEEPPPPLPPP ---GEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLD----LP----QLQHRAAVIP 454 QHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEK tmppsrsktppp---ppqtaqtkrevpknkaptaekresgpkqaavnaavg-rvqvlpda TKE--RDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDVD----pkesnengekeaektidsekdll-----ddsd-----dddieileeciis Query Match 2.9%; Score 365; DB 19; Length 2973; Best Local Similarity 19.0%; Pred. No. 2.9e-11; Matches 409; Conservative 288; Mismatches 807; Indels 648; 347 PEIRKOREQOE-RFORVGORGAGLSATIARSEH--------PMVSC---TPCNIPIGTPVSGYAL-799 1430 1486 841 939 q 셤 å 셤 δ δŻ δy ŏ

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QQ	Db 1635 gddmprvycvegtpinfstatslsdltiesppnelaag	gegvrggagsgefekrdtipteg 16	694
δ	971 AL	SPCGTSKSPNREWEVL 10	007
QQ	1695 rstdeagggktssvtipelddnkaeegdilaeci	::           ::: nsampkgkshkpfrvkkimdqvqqas 175	754
δ	1008 OPAPHOLIT	s 10	039
οp	Db 1755 asssapnkngldgkkkkptspvkpipgnteyrtrvrknadsknnlnaervfsdnkd	rknadsknnlnaervfsdnkds 181	811
ογ	1040	GTYLTSHNQASYTQETPK	1080
qq	Db 1812 kkqnlknnskdfndklpnnedrvrgsfafdsphhytplegtp	ycfsrnd 1	860
δλ	1081 PSVGSISLGLPRQQESAKSATL	11	140
QQ	Db 1861 -slssldfddddddlsrekaelrkakenkeseakvtshte	ıteİtsnqqsanktqaia 19	914
οy	1141 EGSITRGTPTSKISVESIPSLRGSITQGTPALPQT	GIPTEALVKGS 110	186
qq	Db 1915 kqpinrgqpkpilqkqstfpqsskdipdrgaatdeklqnfai	entpvcfshnss 1	968
δy	QY 1187 ISRMPIEDSSPEKGREEAASKGHVIYEGKSGHI	YEGKSGHI	219
οg	1969 lsslsdidgennnkenepik	yapksfhvedtpvcfsrnssls 202	028
δ	Qy 1220 -LSYDNIKNAREGTRSPRTAHEISLKRSYE	SVEGNIKQGMSMRESPVSAPLE 1	270
qq	Db 2029 slsidseddllqecissampkkkkpsrlkgdnekhsprnmggi	nmggilgedltldlkdiqrpds 208	880
δ	QY 1271 GLICRALPRGSPHSDLKERTVLSGSIMOGTPRATTESFEDGLKYPKQIKRESPPIRAFEG	13	330
qq	Db 2089 ehglspdsenfdwkaiqegansivsslhqaaaaac	:   : : lsrqassdsdsilslks 21	140
ΟŸ	1331 AITKGKPYDGITTIKEMGRSIHEI	STRPILEGSISQGTPIKF 13	390
QQ	Db 2141 gislgspfhltpdqeekpftsnkgprilk	rilkpgekstletkki 218	181
οy	1391 DNNS-GQSAIKHNVKSLITGPS	KLSRGM-PPLEIVPENIKVVERGKYEDVKAGETV 144	444
qq	2182 eseskgikggkkvykslitgkvrsnseisggmkgpl	anmpsisrg 222	227
δλ	1445 RSRHTSVVSSGPSVLR	SD 1	504
QQ	Db 2228ipgvipgv	rnssstspvskkgpp 229	252
ολ·	1505 VIIPPNKSTNHERKSTLTPT-QRESIPAK-	SPVPGVDPVVSHSPFDPHHRGSTAGEVYWS 156	562
qq	Db 2253 lktpaskspseggtattsprgakpsvkselspvargtsgiggsskapsrsgsr	qiggsskapsrsgsr 230	305
οy	OY 1563 HLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITSQQ	Н	622
QQ	2306dstpsr	paqqplsrp 23;	320
οy	Qy 1623 MQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPPT	ILVPHPGGTSTPPMDRIT 1	619
QQ	2321 iqspgrnsispgrngisppnk	prt-sspstastkssgsgkms 23	365
δy	QY 1680 YIPGTQITFPPRPYNSASMSPGHPTHLAAAASAERERERE	TERERE 17	127
q	2366 ytspgrqmsqqnltkqtglsknassi	r prsesaskglngmnngngankkvels 241	117
οy	1728 RIAAASSDLYLRPGSEQPGRPGSHGYVRSPSP	FOGTNGTSVITPL 17	187
qq	Db 2418 rmsstkssgsesdrserpvlvrqs	tfikeaps24	149
ογ	1788 DPTAQLRIMPLPAGGPSISQGL	KTKESKHEAA 1 	347
Q	<pre>Db 2450 -ptlr-rkleesasfeslspssrpasptrsqaqtpvlspslpdmsls</pre>	-thssvqagg 2	503
٥	Ov 1848 RLEENLRSRSAAVSEOODLEOKTLEVEKRSVOCLYT	SSAFPSGKPOPHSSVVYSEAGK 190	305

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associated with APC or beta-catenin mutations. Human Tcf-4E protein expressed in colorectal epithelium transactivates transcription when associated with beta-catenin. Adenomatous polyposis coli (APC) regulates this transcriptional activation, at least in part by binding to beta-catenin. Determining wild-type APC protein for diagnosing cancer comprises introducing a Tcf responsive reporter gene having upstream sequences of c-MTC into a cell and measuring transcription of the reporter gene. The candidate drug identified is useful for treating familial adenomatous polyposis patients with APC or beta-catenin mutations and patients with increased risk of developing cancers such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Tcf-4E protein; transcription factor; beta-catenin; Adenomatous polyposis coli; APC; transcriptional activation; Tcf responsive reporter gene; APC transcription regulatory pathway; familial adenomatous polyposis; FAP; cancer; colorectal; thyroid; brain; medulloblastoma; breast; head; neck; desmoid tumour; osteoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Determining wild-type adenomatous polyposis coli protein for diagnosing cancer comprises introducing a Tcf responsive reporter gene having upstream sequences of c-MTC into a cell -
                                                                                                                                         2612 wrkikenefsptnstsqtvssgatngaesktliyqmapavsk---tedvwvriedcpinn 2668
2504 wrklppnl---sptieyndgrpakrhdiar----shsespsrlpinrsgtwkrehsk 2553
                                      1906 DKGPPPKSRYEEELRTRGKTTITAAN------FIDVIITRQIASDKDARERGSQSSDS 1957
                                                                                                                                                                                                                                  2669 pr---sgrsptgntppvidsvsekanpnikdskdngakqnvgngsvpm--rtvglenrln 2723
                                                                                                                                                                                                                                                                       2057 QIITQDFARNQVSSQTP-QQPPTSTFQNSPSALVS-TPVRTKTSNRYSPESQAQSVHHQR 2114
                                                          2554 hssslp--rvstwrrtgssssilsassessekaksedekhvnsisgtkgskengvsakgt
                                                                                                                 SSSLSSHRYE-TPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGPLHH
                                                                                                                                                                                                -----SSQAEGMGQVPRTHRLITLADHIC
                                                                                                                                                                                                                                                                                                           2724 sfiqvdapdqkgteikpgqnnpvpvsetnessivertpfsssssskhsspsgtva----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein used in cancer diagnosis associated with APC/beta-catenin
                                                                                                                                                                                                                                                                                                                                                                          present sequence is a protein involved in cancer diagnosis
                                                                                                                                                                                                                                                                                                                                                  2115 PGSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVH--EKQDS 2164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 58-65; 70pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYJO ) UNIV JOHNS HOPKINS SCHOOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY70304 standard; Protein; 2973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kinzler KW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US18774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0136605
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Best Local Similarity 19.0%; Pred. No. 2.9e-11
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The invention relates to human Tcf-4 proteins and their corresponding CDNA molecules which encodes transcriptional activation factors of human Tcf/Lef family. Human Tcf-4 binds to beta-catenin and activates transcription in colorectal epithelial cells. Moreover it has been found that adenomatous polyposis coli (APC) regulates this transcriptional activation, by binding to beta-catenin. The invention also provides a recombinant adenovirus, Ad-Mini-Me le., APC Minus its aminor and carboxyl terminal Ends which expresses a fusion protein, green fluorescent protein (GFP)/CAPC containing GFP fused to the central third of APC which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contains its beta-catenin binding domain useful for inducing apoptosis or treating colorectal cancer. These fusion proteins are useful for treating colorectal cancer, and other cancers associated with cancer, e.g. colorectal cancer, and other cancers associated with Familial Adenomatous Polyposis (FAP) or patients with increased risk of developing cancer. Human Tof-4 cDNA provides an excellent system for screening agents for their ability to promote delivery, integration, hybridization, expression, replication or integration in cells or in an animal. It also provides methods for diagnosis cancer in a sample
                                                                                                                                                                                                                                                                                                                                                                                        Human; Tcf-4 protein; transcriptional activation factor; beta-catenin; apoptosis; colorectal cancer; Familial Adenomatous Polyposis; FAP; APC; adenomatous polyposis coli; recombinant adenovirus; Ad-Mini-Me; therapy; GFP; green fluorescent protein; GFP/cAPC fusion protein; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present sequence is a transcriptional activation protein related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New fusion protein comprising an enzyme covalently linked to a portion of the adenomatous polyposis coli comprising its beta-catenin binding domain useful for inducing apoptosis or treating colorectal cancer -
2057 QIITQDFARNQVSSQTP-QQPPTSTFQNSPSALVS-TPVRTKTSNRYSPESQAQSVHHQR 2114
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                                        2724 sfiqvdapdqkgteikpgqnnpvpvsetnessivertpfsssssskhsspsgtva---
                                                                                                                                                                                                                                                                                                                                                      Transcriptional activation protein #1 related to the invention.
                                                                                                        2115 PGSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVH--EKQDS 2164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 74-81; 83pp; English.
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                                                                                                                                                                                                                            AAY72782 standard; Protein; 2973
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Vogelstein B, He T;
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Query Match Best Local Similarity

648; Gaps 94;	DENNEK 395    : : 1   1	FKDKFI 453    : 	PROPER 513 :  slcqe-1132	2ATPRG 571   tdlpss 1190	PPLPPP 614 kaatck 1250	WAALAKM 653     :  qiaeikek 1310	-OKTSR 688 : : gaqtpk 1370	-DSPEN 740  11  pdspgg 1429	AEQMDV 798   qvlpda 1485	KVEGDN 840 :   : eteseq 1541	eeciis 1581	RAAVIP 938 :   hvsftp 1634	KAMHES 970   Lipteg 1694	1007 gyggas 1754	PS 1039   1   sdnkds 1811	TQETPK 1080	IAGAIQ 1140 	GS 1186 
409; Conservative 288; Mismatches 807; Indels	7 PEIRKOREQQE-RFQRVGQRGAGLSATIARSEHEISEIIDGLSEQENNER	6 OMRQLSVIPPMAFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHEKEIFKDKFI   : : :	4 QHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEK :			PEPISTEPVETSRWTEEEMEVAKKGLVEHGRN  :   :   :   : : : : : : : : : : : :	VGTKSEAQCKNFYFNYKRRHNLDNLLQQHK	9 KPREERDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSEDSPEN	1 ATSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDV	9 DQQEHSAEEGSVCDPPPATKADSVDVEVRVPEN-HASKVEGDN	1 TKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDVD	1GEPERQRMFPMDSKPSLINPTGSILVSSPLKPNPLDLPQLOHRAANIP	9PMVSCTPCNIPIGTPVSGYALYQRHIKAMHES	1 AL	8QPAPHQLITNLPEGVRLPTTRPTRPPPPLI	0 SKTTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQETPK	1 PSVGSISLGLPRQQESAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVRGTAGAIQ 	1 EGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGIPTEALVKGS
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oy D	1187	ISRMPIEDSSPEKGREEAASKGHVIYEGKSGHI	1219
Qy	1220	LSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPLE	1270
qq	2029	 qrpds	2088
oy	1271	GLICRALPRGSPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYPKQIKRESPPIRAFEG 1	1330
qq	2089	vsslhqaaaaaclsrqassdsdsilslks	2140
δ	1331	STRPIIEGSISQGTPIKF	1390
qq	2141	lgspfpgekstletkki	2181
δy	1391	VPENIKVVERGKYEDVKAGETV	1444
qq	2182		2227
ογ	1445	APKAQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTSD	1504
qq	2228		2252
οy	1505	HERKSTLTPT-ORESIPAK-SPVPGVDPVVSHSPFDPHHRGSTAGEVYWS	1562
qq	2253	arqtsqiggsskapsrsgsr	2305
δ	1563	HLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLXAMENTRQTILNDYITSQQ 1	1622
qa	2306	srp	2320
οy	1623	MQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRIT 1	1679
QQ	2321	 pnklsglprt-sspstastkssgsykms	2365
Qy	1680	GHPTHLAAAASAEREREREKERERE	1727
Ωp	2366	gramsqanltkqtglsknassiprsesaskglnamnngngankkvels	2417
Qy	1728	T.RPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPL	1787
οp	2418	esdrserpvlvrqstfikeapsrserpvlvrqstfikeaps	2449
Qy	1788	*LPAGGPSISQGLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAA	1847
q	2450		2503
ογ	1848	SSRAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGK	1905
qΩ	2504	wrklppn1sptieyndgrpakrhdiarshsespsrlpinrsgtwkrehsk 2	2553
ΟŅ	1906	SDKDARERGSQSSDS	1957
q	2554	ssekaksedekhvnsisgtkqskenqvsakgt	2611
δy	1958		2016
qq	2612		2668
οy	2017		2056
qq	2669	pmrtvglenrin	2723
οy	2057	TKTSNRYSPESQAQSVHHQR	2114
qq	2724		2778
ΟŊ	2115	PGSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVHEKQDS 2164	
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                                                                                                                                                                                                                                                                                                                                         This sequence represents the wild type human adenomatous polyposis coli (APC) protein. This sequence, and the APC peptide fragments represented by AAWI1923 wil1929 can be used in the method of the invention. The method of the invention is for the detection of abnormal APC, using antibodies directed against this sequence, or one of the partial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1088 kfqphfg-----qqecvspy---rsrgangsetnrvgsnhginqnvsqslcqe- 1132
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                                                                                                           Adenomatous polyposis coli; APC; human; antibody; mutant detection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.9%; Score 364; DB 16; Length 2843;
llarity 19.0%; Pred. No. 3.1e-11;
Conservative 290; Mismatches 803; Indels 652
                    standard; protein; 2843 AA.
                                                                                     Adenomatous polyposis coli protein.
                                                                                                                                                                                                                                                                                                                     Claim 1; Page 7-13; 13pp; Japanese.
                                                                                                                                                                                                                                            (SANK-) SANKO JUNYAKU CO LTD
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1695 rstdeagggktssvtipelddnkaeegdilaecinsampkgkshkpfrvkkimdgvggas 1754
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1542 pkesnengekeaektidsekd11------ddsd------dddieileeciis 1581
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689 KPREE-----RDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSE--DSPEN
                                                                                                                                                                                                                                                                                                                799 DQQEHSAEE----GSVC------DPPPATKADSVDVEVR----VPEN-HASKVEGDN
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                                                                                                                                                            741 A--TSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDV
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OY 1623 MOVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRIT		_
1680		SAX
1000	KERERE 1727	
2366		
QY 1728 RIAAASSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPL	INGTSVITPL 1787	
1788		
Oy 1848 RLEBNLRSRSAAVSEQOQLEOKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGK	SSVVYSEAGK 1905	
Db 2504 wrklppnlsptieyndgrpakrhdiarshsespsrlpinrsgtwkrehsk	 sgtwkrehsk 2553	Qy
Qy 1906 DKGPPPKSRYEEELRTKGKTTITAANFIDVIITRQIASDKDARERGSQSSDS	KERGSQSSDS 1957	අ <u>ත්</u>
Db 2554 hssslprvstwrrtgssssilsassessekaksedekhvnsisgtkgskengvsakgt	:  cenqvsakgt 2611	Oy Oy
OY 1958 SSSLSSHRYE-TPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQAENDFTRQYEGPLHH	гротесрин 2016	aa —
Db 2612 wrkikenefsptnstsgtvssgatngaesktliyqmapavsktedvwvriedcpinn	:  ::: /riedcpinn 2668	О
Qy 2017 YRPQQESPSPQQQLPPSQAEGMGQVPRTHRLITLADHIC	RLITLADHIC 2056	<b>q</b> a
Db 2669 prsgrsptgntppvidsvsekanpnikdskdngakgnvgngsvpmrtvglenrln	tvglenrln 2723	Qy
OY 2057 QIITQDFARNOVSSQTP-QOPPTSTFQNSPSALVS-TPVRTKTSNRYSPESQAQSVHHQR	SQAQSVHHQR 2114 :	<b>q</b> a
Db 2724 sfiqvdapdqkgteikpgqnnpvpvsetnessivertpfsssssskhssp	sgtva 2778	Oy
Qy 2115 PGSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVHEKQDS 2164	QDS 2164	<b>a</b> a —
<pre>Db 2779arvtpfnynpsprkssadsys-arpsqiptpvnnntkkrds</pre>	rds 2818	٥٥ 
7. T. T. T. T. T. T. T. T. T. T. T. T. T.		da
75745: AA)		
XX AC AAY57453;		<b>q</b> a 
XX DT 22-FEB-2000 (first entry)		
XX DE Human transcriptional regulatory factor SEQ ID NO:10.		ති 
XX Human: transcriptional regulatory factor: TCoA1; BLAST detection KW bromo-domain; cell proliferation; cancer.	detection;	od ——
XX OS Homo sapiens.		δ
XX PN W09957143-A1.		qa
XX PD 11-NOV-1999.		- o
XX PF 30-APR-1999; 99WO-JP02340.		- 
XX PR 30-APR-1998; 98JP-0137631.		δ
XX CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC. XX		- QC
AA PI Jones MH;		О
AA DEI; 2000-052940/04.		ਰੂਹ 

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The present sequence represents a human transcriptional regulatory factor containing a bromo domain. The factor interacts with proteins involved in the chromatin-mediated transcription regulatory mechanism. It binds to hSNF2H, hSNF2L and NCOA-62/Skip. It can be used for screening compounds binding to it and acting as agonists or antagonists, which are potentially useful for the treatment and prevention of cancer and other cell proliferation disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 865; Gaps 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 SPVDHDSLESKRPRLEQVSDSHFQRVSAAVLPLVHPLPEGLRASADAKKDPAFGGKHEAP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 SSPISGQPCG-------DDQNASPSKL----SKEELIQSMDRVDREIA 193
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                                                                                                                                                                                                                                                                                                                                                                                                          DB 21; Length 2781;
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.8%; Score 356.5; DB 21; Best Local Similarity 17.6%; Pred. No. 7.7e-11; Matches 449; Conservative 354; Mismatches 889;
                                                                                                            Claim 1; Page 139-151; 154pp; Japanese
                                                                                                                                                                                                                                                                                                                                          2781 AA;
                                                               TCOAl encoding it
N-PSDB; AAZ39033.
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kteshvnoqessqrdvunvsegfhlrtsykktksskldgllerrikgftleekgrlekiLEPTTETAPSTSPSLAVPSTRABEDESVETQVNDSISAETAEQMDVDQQEH ::: :: :		LOPAPHQLITNLPEGVRLPTTRPTRPPPPLIPSSKTTVASEKPFFI	dsltttggtlvtsmtvskeystrdkvklmkf-srpkktrsgtalpsyrkfvtkstkks HILSYDNIKN-AREGTRSPRTAHEISLKRSYESVEGNIK fvlpnddlklarkggirevpyfnynakpaldiwpypsprptfgitwryrlqtvkslag fvlpnddlklarkggirevpyfnynakpaldiwpypsprptfgitwryrlqtvkslag GMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIMOGTPRATTESFEDGIKYP i
724 884 753 944 804 1001	1060 874 1120 920 1180 977	1007 1289 1053 1349 1100 1406 1134 1146	1524 1218 1582 1257 1642 1317 1682 1375 1732 1732 1732 1732
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1912 v-----kaii----rt
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                          -----ipsstgtsqqtftsfqprtatvtirpntsgsggttsnsq 1911
                                                                                                                                                                                                                      1782 SVITPL----DPTAQLRIMP-----LPAGGPSISQ-GLPASRYNTAADALAALVDAAAS 1830
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                                                                                                                                                                                                                                                                                               1887 FPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRG--KTTITAANFIDVIITRQIASD 1944
                                                                                                           1662 ILVPHPGGTSTPPMDRITYIPGTQITFPPRPYNSASMSPGHPTHLAAAASAERERERER 1721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; SRCAP; Snf2 related CBP activator protein; antiviral; CREB; cAMP regulatory element; CREB binding protein; CBP; AfPase; transcription activation; DBAD box RNA dependent helicase; adenoviral DBP protein; beta-actin; nuclear receptor; viral infection.
                                                                                                                                                                                 1603 LYAMENTRQTILINDXITSQQMQVNLRPDVARGLSPREQ-PLGLPYPATRGIIDLTINMPPT : : | : | : | : | | : | | | | |
                                                                                                                                                                 1722 KERERERIAAASSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGT
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                                                                                                                            2179 RNDARSPGSISYLPSFFTKLENTSPMVKSKKQEIFRK 2215
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Gaps 128; 522 613 ppsavtgrnkqpwhpdeddeeftaneeeaedeedtlaaeeqle---gevdhamelsela 386 296 RNHA----RKOREQKICQRYDQLMEA--WE-KKVDRIENNPRRKAKESKTREYYEKQFPE 348 349 IRKQREQQERFQRVGQRGAGLSATIARSEHEISEIIDGLSEQENNEKQMRQLSVIPPMMF 408 409 DAEQRRVKFINMNGLMEDPMKVYKD-RQFMNVWTDHEKEI-FKDKFIQHPKNFGLIASYL 466 EKTEKKEEEKKDEE-----EKDEKEDSKENTKEKDKIDGTAEETEEREQATPRGRKTAN 576 651 KWVGTKSEAQCKNFYFNYKRRHNLDNLLQQH-----KQKTSRKPREERDV----SQCE-- 700 r------egelsmeellqqyagayapgsgssedededevdanssdcepe 429 759 ERKSVPDCVLYY-YLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEKVEEKE---EDKA ----TNEAAAASAAAAATEEPPPPL--PP 614 PPEPIS-------TEPVETSRWTEEEMEVAKKGLVEHGRNWAAIA -SVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSEDSPENATSRGNTEPAVELEPTTET Query Match 2.8%; Score 349.5; DB 22; Length 3118; Best Local Similarity 18.5%; Pred. No. 2.1e-10; Matches 497; Conservative 329; Mismatches 914; Indels 945; lsadfaqerrwkr----gvarkvvrm----virhheegrqkeerarr-467 171 331 652 96 135 523 387 701

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Qy	760	APSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDVDQQEHSAEEGSVCDPPPAT 817	7
QQ	485	sqsqadeeeedddfgveyllardeeqseadagsgpp-tpgpttlg 528	80
QY	818	-KADSVDVENHASKVEG 838	æ
QΩ	529		80
οy	839	DNTKERDLDR	7
qq	589	ilademgigktiqtisllahlacekgnwgphliivptsvmlnwemelkrwcpsfkiltyy 648	80
οy	863	-AQQINAQRPEPQSDNDSSATCSADEDVDGEPERQRMFPMDSK 904	4
q	649		æ
OY	905	PSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTPVS 955	2
q	709		2
δy	926	SALLEEQ	0
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ογ	991	993	e
qq	826	ttketlatghfmsvinilmqlrkvcnhpnlfdprpvtspfitpgicfstaslvlratdvh 885	2
ō	994	1002	02
qq	886	plgridmgrfdliglegrvsryeadtflprhrlsrrvllevatapdppprpkpvkmkvnr 945	Z.
ογ	1003	EWEVLOPAPHQLITULPEGVRLPTTRPTRPPP-PLIPSSKTTVASEKPSFIMGGS 1056	26
QΩ	946	egrtvvvnnpraplgpv-'-pvrp	6
QY	1057	SIS	12
qα	066	plipasrppgpvl1pplgpnsgslpgv 103	34
οy	1113	.VRAQHEGVVRGTAGAIQEGSITRGTPTSKISVESIPSLRGSIT- 116	99
q	1035	pgsssllkpltv 108	82
ογ	1167	OTGIPTEALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSG 121	17
QQ	1083	ppgytfppaaatttstttatatttavpaptpapgriilspdmqarlpsgevvsig 1137	37
Qγ	1218	HILSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRAL 1277	11
q	1138	1117	75
Qy	1278	133	30
đ	1176	v 122	28
Qy	1331	r 137	74
qq	1229	Inprptltpgrlptptlgtarapmptptlvrpllklvhs-pspevsasapgaapltissp 1287	87
Qy	1375	RPIIEGSISQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVE 1431	31
đ	1288	: :	36
οy	1432	148	83
q	1337	pasapltipisapltvsasgpalltsvtpplapvvpaapgppslq 1381	81
, 0,	1490	TNHERKSTLTPTQRESI-PAKSPVPGVDPVVS 154	43
q	1382	-psgaspaasaltlglataps1sssqtpghp1llaptsshvpglnstvapacs 1433	33

Οy	y 1544HSPFD	PHHRGSTAGEVYWSHLPTQLDP-AMPFHRALD 157	62
БЪ	1434		98:
oy og	1580	PAAAAYLEQRQ-LSPIPGYPSQYQLYAMENTRQTILNDYITSQQMQVNLRPDV 1631  :	131
ζŎ	1632		181
අ .	1547	tqtmlpapvpsplpspastqtlalapalaptlggsspsqtlslgtgnpqgpfptqtlslt 1606	90
o	1682	PGTQLTFPPRPYNSASMSPGHPTHLAAAASAERERERERERERERERTAAASSDLYL 1738   : :	38
oy Og	1739	RPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLD-PTAQLRIMP 1797	97
ο <sub>γ</sub>	1798	ALAALVDAAASAPQMDVSKTKESKHEAARLEEN	152
අ (	1682		1737
දු දු	1853	LKSKSAAVSEQQQLEQKTLEVEKKSVQCLYTSSAFPSGKPQPHSSVYYSEAGKDKGPPPK 19: 	1912 1768
οy	1913		150
qq	1769	spfyldsleekrkrgrserlerifglseahgalapvygtevldfctlpgpvaspigprsp 1828	128
oy Op	1951	G	191
ογ	1992	YQPEVVKANQAENDPTRQYEGPLHHYRPQQESPSPQQQLPPSSQAE 2037	137
qq	1889	rqaafqeqlaselwprarplhrivcnmrtqfpdlrliqydcgklqtlavllrqlkae 194	145
Qy Dp	2038 GMGQ       1946 g	VPRTHRLITLADHICQIITQDFARNQVSSQTPQQPPTSTFQNSFAL 2088	88
οy	2089		.19
qq	1999	fcfilstrsggvgvnltgadtvvfydsdwnptmdaqaqdrchrigqtrdvhiyrlisert 205	158
oy D	2120	SPENLVDKSRGSR	51
δy	2152	PPQVPVVHEKQDSLLLLSQRGAEPAEQRNDARSPGSISYLPSFFTKLENTSPWVKSKKQE 2211	111
QQ	2116	:         : : : : : : : : : : : : : : :	.62
οy	2212 IF-	RKINSSGGGDSDMAAAQPGTEIFNLPAVTTSGSVSSRGHSFADPASNLGLEDI 2266	99
g	2163 gfp	gfpagegeeagrpgaedeemsraeqeiaalveqltpieryamkfleasleev 2214	14
δy	Y 2267 IRKALMGSFD	DKVEDHGVVMSQPMGVVPGTAN-TSVVTSGETRREEGDPSP 2316	16
QQ	2215	sreelkqaeeqveaarkdldqakeevfrlpqeeeegpgagdesscgtgggthr 2267	29
oy Og	2317	HSGGVCKPKLISKSNSRKSKSPIPGQGYLGTERPSSVSSVHSEGDYHRQTPG-2368	68 02
δλ	2369	WAWEDRPSSTGSTQFPYNPLTMRMLSSTPPTFIACAPSAVNQAAP 2413	
qq	2303	:   ::  sahqtrstttpprcsparervprpaprprptp-asapaaipalvp 2346	

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Indels 877; Gaps 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 SPVDHDSLESKRPRLEQVSDSHFQRVSAAVLPLVHPLPEGLRASADAKKDPAFGGKHEAP 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 SSPISGQPCG------DDQNASPSKL---SKEELIQSMDRVDRE-- 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275 YHENIKTNQVMRKKLILFFKRRNHARKQREQKICQRYDQLMEAWEKKVDRIENNPRRKAK 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcriptional regulatory factor containing a bromo domain and gene TCOAl encoding it.
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                                                                                                                                                                  Human; transcriptional regulatory factor; TCOA1; BLAST detection;
bromo-domain; cell proliferation; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.7%; Score 341.5; DB 21; Length 2907; Best Local Similarity 17.6%; Pred. No. 5.4e-10; Matches 447; Conservative 331; Mismatches 878; Indels 877;
                                                                                                                                 Human transcriptional regulatory factor SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                  (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
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                               AAY57452 standard; Protein; 2907 AA.
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à 6	391 EP	ENNEKQMRQLSVIPPMMFDAEQRRVKFINNNGLMEDPMKVYKDRQFMN 4:	438
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ą	; 720 sfa]	: sfalnkhqhredhdkrrhlahkfcltpagefkwngsvhgskvltistlrltitqlennip 7	977
ά	488 KALY	KALVRRNYGKRRGRNQQIARPSQE 5:	511
ą	780 ssf1	refalalailecavkpvvmlpiwreflghtrlhrm	839
à	512 EKVE	EKVEEKEEDKAEKTEKKEEEKKDEEEKDEKEDSKENTKEKDKIDGTAEFTEEREQATPRG 5: :   :	571
ą	840 tsi		867
λ	572 RKT	RKTANSQGRRKGRITRSMTNEAAAASAAAAATEEPPPPLPPPPEPISTEPVETSKWTE- 6:	630
g	898	wvkytfpvkhqvwkqk 8	883
23	631 - EE	TKSEAQCKNFYFNYKRRHNLD-	929
q	884 gee		931
λχ	677 NLLK		717
q	932 nmde		991
ά	718 NEE		751
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λ	752 E	PSTKPAEDESVETOVNDSIS	789
q	1052 err	errikqftleekqrlekikleggikgigktstnssknlsespvitkakegcqsdsmr l	1108
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λά	836	æ	356
q	1169 qns.	gnsiend-leekvsdlasrggeptksktkgndffiddsklasaddigtlicknkkplige 1	1227
λά	857 DEDI	QQINAQRPE-PQSDNDSSATCSADEDVDGEPERQRMFPMD	902
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q	1288 ssee	sseedmivgnsnesiseqfrtreqdvevleplkcelvsgestgncedrlpvkgteang 1	1345
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ά	1007	VRLPTRPPPP	1034
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ζ	1035 PLI	PGTYLTSHNQASYTQETPKPSVGSISLGLPRQ-	1093
අ	:: 1457 vime	c	1513
λ	1094	QESAKSATLPYIKQEBFSPRSQNSQPEG 1.	1121
ą	1514 svnc	:     :   svnqvedmeietsevkkvtsspitseeesnlsndfidenglpinknenvngeskrktvit l	1573

o da	1122	LLVRAQHEGVVRGTAGAIQEGSITRGTPTSKISVESIPSLRGSI 1165   : :       : :       : :         : :
δλ	1166	EDSSPEKGREE 120
qq	1632	tttggtlvtsmtvskeystrdkvklmkfsrp
Qy Dp	1204	AASKGHVIYEGKSGHILSYDNIKN-AREGTRSPRTA 1238   :     :
δ	1239	HEISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIMQ 1298
qq	1750	fgitwryrlqtvkslagvslmlrllwaslrwddmaakvppgg1791
Qy Dp	1299	GTPRATTESFEDGLKYPKOIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHEIPR 1356   :
ΟŊ	1357	QDILTQESRKTPEVVQSTRPIIEGSISQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSRG 1416
qq	1840	etptpqrkglrssalrpkrpetpkq
δò	1417	146
9	18/4	1
e S	1467	PKAQLSFGIYDDTSARRTFVSYQNTMSRGSPMMNRTSDVTIPPNKSTRHERKSTLTPTQR 1526
è	1527	SPENDHHRGSTAGEV
g g	86	
οy	1585	a
ф	2020	vtirpntsgsggttsnsqvitgpqirpgmtvirtplqqstlg 2061
δy	64	YPATRGIIDLTNMPPTILVPHPGGTSTPPMDRITYIPGTQITFPPRPYNSASMSPGHP :     :     :     :     :     :
a a	2062	kaiirtpvmvqpgapqqvmtqiirgqpvstavsapntvsstpg 2104
οy	1704	VRT 176
eg G	2105	
δy	1764	
a a	2134	ltmaqltqltqghggnqgltvviqggqqttgqlqlipqgvtvlpgpgqqlmqaampng 2191
δy	1813	RYNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQ-KTL 1871
g	2192	tvqrflftplattattasttttvsttaagtgeqrqsklspqmqvhqdktl 2242
٥y	1872	EVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRGKTT 1926
đ	2243	ppagsssvgpakaqpqtaqpsarpqpqtqpqspaqpevqtqpevqtq 2289
ΟŊ	1927	ITAANFIDVIITRQIASDKDARERGSQSSDSSSSLSSHRYETPSDAIEVISPASSPAPPQ 1986
g	2290	shvpseaqpthaqsskpqvaaq
οy	1987	EKLQIYQP-EVVKANQAENDPIRQYEGPLHHYRPQQESPSPQQQLPPSSQAEGMGQ 2041
qq	2336	irpstpsqlspgqqsqvqtttsqpipiqphtslqipsqgqpqsqpq
οy	2042	VPRTHRLITLADHICQIITQDFARNQVSSQTPQQPPTSTFQNSPSALVSTPVRT 2095
-qa	2396	tlnqvsvsspsrpqlqiqqpqpqviavpqlqqqqvqvls 2433
Οy	2096	KTSNRYSPESQAQ 2108

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------CGTSKSP-----NREWEVLOPAPHO----LITNLPE 1020
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                                                     eeeddeetieveeqqegndaeaqrreiell-----rregelpleellrslppqll 147
                                                                                                                          egpsspsqtpsshdsdtrdgpeegaeeeppqvleikpppsavtqrnkqpwhpdeddeeft 207
                                                                                                                                                                   -----TEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAKMVGTKSEAQCKNFYFNYKRRHN 674
                                                                                                                                                                                                                                              LDNLLQQH-----KQKTSRKPREERDV----SQCE---SVASTVSAQEDEDIEASNEEEN 722
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                     EKEDSKENTKEKDKIDGTAEETEEREQATPRGRKTANSQGRRKG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               binding protein (GBP) activator protein (SRCAP) polypeptide. It has a pulpage activity and is capable of activating transcription. SRCAP polypeptides are useful for activating transcription in a cell, for enhancing CREB (CAMP requiatory element) binding protein (GBP) mediated activation of transcription in a cell, for treating a patient having a disease involving a function such as insufficient transcription of a gene, e.g. a gene mediated by CBP co-activation, DEAD box RNA dependent helicase, adenoviral DBP protein, beta-actin or a nuclear receptor affected by SRCAP protein. Compounds that modulate SRCAP function, such as antibodies, antisense molecules, polynuclectides or ribozymes, are useful for treating diseases mediated by SRCAP-activated transcription, for example, infection by adenovirus, hepatitis C virus, human immunodeficiency virus type-1, Epstein Barr virus, cytomegalovirus or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present sequence is an Snf2 related CREB (cAMP regulatory element)
                                                                                                                                                                                                                                                       Human; SRCAP; Snf2 related CBP activator protein; antiviral; CREB; cAMP regulatory element; CREB binding protein; CBP; ATPase; transcription activation; DEAD box RNA dependent helicase; adenoviral DBP protein; beta-actin; nuclear receptor; viral infection.
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CREB binding protein,
affecting viral infection
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18.6%; Pred. No. 2.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Snf2 related cAMP regulatory element (CREB) activator protein, capable of co-activating useful for modulating transcription and for
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                                                                                                       AAB50363 standard; protein; 2972
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25-MAY-2000; 2000US-0579181.
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Matches 472;
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                                                                                                                                                                                                                                                      This protein sequence is as the sequence given in AAR23962 except that Ala at position 2460 is replaced by Val.

This protein specifically binds to the enhancer of the alpha-fetoprotein gene. The DNA encoding this protein may be useful for the prodn. of biologically active proteins by inscrting the DNA into an expression vector and co-transfecting animal cells with another expression vector in which a gene for the biologically active protein is placed under the control of alpha-fetoprotein gene enhancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --RRTSYEPFHPGPSPVDH-DSLESKRPRLEQVSDSH--------- 118
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                                                                                                                                                                                              DNA encoding protein binding to alpha-fetoprotein gene enhancer useful for prodn. of biological active protein
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.6%; Score 327; DB 13; Length 2783; Best Local Similarity 17.8%; Pred. No. 3.2e-09; Matches 514; Conservative 343; Mismatches 1014; Indels 1016;
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                                                                                                                                    Yasuda
                                                                                                                                   Tamaoki T,
                                                                                                            (SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                                                                                                                                                                                                Claim 3-4; Page 7; 24pp; English.
                                                            91EP-0310334
                                                                                   90JP-0301412
                                                                                                                                    Morinaga T,
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N-PSDB; AAQ24829.
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                                                            07-NOV-1991;
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                                   27-MAY-1992
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1302 RATTESFEDGLKYPKQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHEIPPROD 1358  1817rsrhwheakragynltlsamlldcdgglqmkgdifdg-tsfshlppsssdgggvplsp 1873  1359 ILTQESRKTPEVVQSTRPI-IEGSISQGTPIKFDNNSGQSAIKHNVKSLI 1407  1874 V-sktmelsprtllspssikvegledfespsmssvnlnfdqtkldnddcssvntaitdtt 1932  1408 TGPSKLSRGMPPLEIVPENIKVVERGKYEDVKAGETVRSRHTSVVSGGPSVLRSTLHEAP 1467  1933 tgd	1526 RESIPAK-SPVPGVDPVVSHSPFDPHHRGSTAGEVYWSHL	1639 EOPLGLPYPATRGIIDLTNUMPPTILVPHPGGTSTPPMDRITYIPGTOIT 1687	1803 PSISQGLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAVSE 1862	201 QESPSPQQLPPSSQAEGMGQVPRTHRLITLADHIGQIITQDFARNQYGGSLQGVQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ
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n reading frame; ORFX; detection; cytostatic; hepatotropic; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; sant; osteopathic; antiparkinsonian; nootropic; neuroprotective; sant; osteopathic; antiarthritic; immunosuppressant; cardiant; ulant; thrombolytic; coagulant; vasotropic; antidiabetic; e; dermatological; immunosuppressive; antinflammatory; c; gene therapy; cancer; proliferative disorder; hypertension; erative disorder; osteoarthritis; graft vs host disease; antial and disease; diabetes mellitus; hypothroidism; SCID; AIDS; il ester storage; systemic lupus erythematosus; infection; blined immunodeficiency; malaria; autoimmune disorder; asthma; plastic annemia; nocturnal haemoglobinuria; burn; wound; e; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC77606 encode the proteins given in AAB40237 to AAB43397, nt the human ORFX open reading frames 1 to 3161. The ORFX excitation is excitationally as extractionally vulnerary; antiparkinsonian, nootropic; neuroprotective; anticonvalsant; antiarthritic; immunosuppressant; nt; cardiant; thrombolytic; coagulant; vasotropic;
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------rtitraarnakehps11 2652
                                                                                             VKLISKSNS--RKSKSPIPGQGYLGTERPSSVSSVHSEGDYHRQTPGWAW-E 2372
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antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX-associated disorder. The proteins are needed to express OREX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypethyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, nocturnal hemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive. antidiabetic; hypotensive; dermatological; immunosuppressive; 

2971 AA; Sequence Query Match 2.6%; Score 327; DB 21; Length 2971; Best Local Similarity 18.4%; Pred. No. 3.4e-09; Matches 465; Conservative 307; Mismatches 879; Indels 878; Gaps 117; 432 KD-RQFMNVWTDHEKEI-FKDKFIQHPKNFGLIASYLERKSVPDCVLYY-YLTKKNENYK 488 |:|| :| ::::| |:|| eeeddeetieveeggegndaeagrreiell------rregelpleellrslppg11 147 619 | | : ||::| | |:| : | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : LDNLLQQH-----KQKTSRKPREERDV----SQCE---SVASTVSAQEDEDIEASNEEEN 722 PEDSEVEAVKPSEDSPENATSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVET 782 ----sqsqadee 346 990 489 ALVRRNYGKRRGRNQQIARPSQEEKVEEKE---EDKAEKTEKKEEEKKDEE-----EKD 539 ----TEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAKMVGTKSEAQCKNFYFNYKRRHN 674 247 meellqqyagayapgsgssedededevdanssdcepegpveaeeppqedsssgsdsvedr 306 347 eedddfgveyllardeeqseadagsgpp-tpgpttlgpkkeitdiaaaaeslgpkgytla 405 -----ENHASKVEGDNTKERDLDR------AS 850 406 ttqvktpiplllrgglreyqhigldwlvtmyekklngilademglgktigtisllahlac 465 466 ekgnwgphliivptsvmlnwemelkrwcpsfkiltyygaqkerklkrggwtkpnafhvci 525 526 tsyklvlqdhqafrrknwrylildeaqniknfksqrwqsllnfnsqrrllltgtplqnsl 585 -----AQQINAQRPEPQSDNDSSATCS 884 885 AD----ED-----VDGEPERQRMFPMDSKPSLLNPTGS---ILVSSPLKPNP 924 48 dll-----sqslnqpltsskagsspclgsssaassppppasrlddedgdfqpqed 97 3 kdvrqf---wsnvekvvqfkqq-----srleekrkkaldlhldfivgqtekys 47 148 egpsspsqtpsshdsdtrdgpeegaeeeppqvleikpppsavtgrnkqpwhpdeddeeft 540 EKEDSKENTKEKDKIDGTAEETEEREQATPRGRKTANSQGRRKG-----RITRSM---------TNEAAAAAAAATEEPPPPL--PPPPEPIS------783 QVNDSISAETAEQMDVDQQEHSAEEGSVCDPPPAT---KADSVDV-------925 LDLPQLQHRAAVIPPMVSCTPCNI-----PIGTPVSGYALYQRH-IKAMHE-----307 sedeedehseeeetsgssaseesesesedag---------SALLEEQRORQEQIDLECRSS------851 EKVEPRDEDLVV-----825 --EVRVP-----= 675 86 290 620 723 qq δ g QΥ g δ g ò QQ g δ g q g ö 셤 δy ò ò δ g ò à

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ογ	7	SSISLGLPRQDESAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVRGT 1
qq	867	rllpplqpnsgslpqvlpspl
à i	1136	GAIQEGSITRGTPTSKISVESIPSLRGSITOGTPALPQTGIPTEALVKG 11
QQ	900	pptptlslkptppapvrlspapppgpssllkpltvppgytfppaaatttstttata 9
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QY	1241	SMRESPVSAPLEGLICRALPR
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ΟŸ	1296	IMQGTPRATTESFEDGL-KYPKQIKRESPPIRAFEGAITKGKP 1337
qq	1053	vrqaprdgltpvpplapaprppssglpavlnprptltpgrlptptlgtara
δy	1338	YDGITTIKEMGRSIHEIPRODILTQESRKTPEVVQSTRPIIEGSISQGTPIKFDNNS 1394
QQ	1106	mptptlvrp1lklvhs-pspevsasapgaapltissplhvpsslpgpasspmpip 1159
οy	1395	INVKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVKAGETVR-SRHTSVV
qq	1160	nssplaspvsstvsvplssslpisvpttlpapasapltipisapltvsa 1208
Qy	1454	SGPSVLRS-TLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSPMN 1500
qq	1209	sgpalltsvtpplapvvpaapgppslapsgaspsasaltlglatapslsssgtpghplll 1268
Οy	1501	RISDVIIPPNKSTNHERKS-TLIPTQRESIPAKSPVPGVDPVVSHSPFDPHHRGSTA 1556
đ	1269	pvlvpasalaspfps
οy	1557	GEVYWSHLPTQLDP-AMPFHRALDPAAAAYLFQRQ-LSPTPGYPSQYQLYAME 1607
qq	1321	sqalatplapmaapqtailapspapplaplpvlapspgaapvlassqtpvpvmaps 1376
Οy	1608	TROTILNDY
đ	1377	stpgtslasaspvpaptpvlapsstgtmlpapvpsplpspastgtlalapalaptlggss 1436
0y	1667	GGTSTP
qq	1437	
Qy	1715	EREREREKERERERIAAASSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSV 1774
qq	1495	
Qy	1775	FQGTNGTSVITPLD-PTAQLRIMPLPAGGPSISQGLPASRYNTAADALAALVDAA 1828
qa	1517	
δλ	1829	ASAPQMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFP 1888
qq	1572	

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This protein specifically binds to the enhancer of the alpha-
fetoprotein gene. The DNA encoding this protein may be useful for
the prodn. of biologically active proteins by inserting the DNA into
an expression vector and co-transfecting animal cells with another
expression vector in which a gene for the biologically active protein
is placed under the control of alpha-fetoprotein gene enhancer and
promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         391 avpd-rdgnsnleeagk--gpetsedlgknilpsastegsgdlkpspadpgsvredsgfi 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding protein binding to alpha-fetoprotein gene enhancer useful for prodn. of biological active protein
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Best Local Similarity 17.8%; Pred. No. 3.6e-09;
Matches 514; Conservative 343; Mismatches 1014;
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                                                                                                                                                                                                                                                                                                2133 ----PGKSPERSHVSSEPYEPISPPQVPVVHEKQDSLLLLSQRGAEPAEQRNDARSPGS
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/label= homeodomain
1727..1786
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/note= "homeodomain'
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Gaps

S S	119	-FORVSAAVLPL	
Qy		DDQNASPSK17	
qq	295	: :    :     additiveedkeeesdledkgsptgsdsgs-vqedsgsepkralpfrkgpnftmekfl 625	
ΟŅ		MDRVD	
qq	626	dpsrpykctvckesftgknillvhynsvshihklkralqesatgqpeptsspdn 679	
οy	226	PPVEQKHRSIVQIIYDENRKAEEAHKIFEGLGPKVELPLXNQ-PS 270	
q	680	akleaasgssngtgnsssislssst	
οy	271	DTKVYHENIKTNQVMRKKLILFFKRRNHARKQREQKICQRYDQLMEAWEKKVDRIE-NNP 329	
qq	740 ]	pvstsgsntfttsnpssagiapssnllsgvptesvgmpplgnp 782	
οy	330	RRKAKESKTREYYEKQFPEIRKQREQQERFQRVGQRGAGLSATIARSEHEISEII 384	
рр	783	anrkkladmiasrqqqqqqqqqqqqqqqqqqq	
οy	385 1	FDAEQRRVKFINMNGLMEDPM	
Dp	839	aaliqsqlfnptllphf	
ΟŊ	439	VWTDHEKEIFKDKFIQHPKNFGLIASYLERKSVPDCVLYYYLFKKNENYK 488	
ф	885 ]	jis i i i i i i i i i i i i i i i i i i	
οy	489	ALVRRNYGKRRGRNQQIARPSQEEKVEEKEEBDKAEKTEKKEEEKKDEEEKDEKEDSKENT 548	
οp	945	shsallqpsqhpekknklvikek	
οy	549	KEKDKIDGTAEETEEREQATPRGRKTANSQG579	
Dp	066	: :	
οy	280	RRKGRITRSMINEADAASAAA 600	
ф	1050	kqkvqkkngktdqgenleklecdscgklfsnililkshqehvhqnyfpfkqlerfakqyr 1109	
Οy	601	LPPPP	
qq	1110	dhydklyplrpgtpepppppppppppppppppppppppppppppppppp	
δy	622	ETSRW	
qq	1170		
οy	673 1	ASTVSAQEDEDIEASNEEENPEDSEVE	
Dp	1220	ptllqqqnkrprtritddqlrvlrqyfdinnsps	
ΟŊ	732 1	S.	
qq	1270		
οy	774	A.	
qq	1319		
ΟŊ	823	-DVEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQIN 867	
д	1377	qnarqkarknyenggegkdgerreltndryirtsnlnyqckkcslvfqrifdlikhqk 1434	
οy		AQRPEPQSDNDSSATCSADEDVDGEPERQRMFPWDSKPSLLNPTGSILVSSPLKPNPLDL 927	
qq	1435	klcykdedeegqddsqnedsmdam-eiltptss 1466	

ΟŊ	928	PQLQHRAAVIPPMVSCTPCNIPIG
qq	1467	sastp
ογ	988	
ф	1505	fnskteagdekpklaeapsaqpnqtqekqgqpkpelqqqeqpeqktntpqqklpqlvslp 1564
Qy	1026	TTRPTRPPPLIPSSKTTVASEKPSFIMGGSISQGTPGTYLTSHNQ-ASYTQETPKPS :   :         : : :   :   :   :   :   :
qq	1565	slpqpppqapppqcplpqsspspqlshlplkplhtstpqqlanlppqlipyqcdqckla 1624
δŏ	1083	VGSISLGLPRQQESAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEG
DP	1625	
Qy	1138	AIQEGSITR-GTPTSKISVESIPSLRGSITQGTPALPQTGIPTEALVKGSISR
qq	1681	-
Qy	1197	PEKGREEAASKGHVIYEGKSGHILSYDNIKNAREGTRE
QQ	1718	gtggeepgrdkr1rttitpeqleilygkylldsnptrkmldhlahevglkkr 1769
δλ	1247	
qq	1770	vvqvwfqntrarerkgqfravgpaqahrrcpfcralfkaktaleahi 1816
δλ	1302	×
q	1817	rsrhwheakragynltlsamlldcdgglqmkgdifdg-tsfshlppsssdgggyplsp 1873
δy	1359	PEVVQSTRPI-IEGSISQGTPIKFD
qq	1874	v-sktmelsprtllspssikvegiedfespsmssvnlnfdqtkldnddcss
δy	1408	TGPSKLSRGMPPLEIVPENIKVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAP 1467
qq	1933	tgdltkaa 1965
δλ	1468	KAQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTSDVTIPPNKSTNHERKSTLTPT
qq	1966	mmamseyedrissglvspapsfyskeydnegtvdyse 2002
δy	1526	RESIPAK-SPVPGVDPVVSHSPFDPHHRGSTAGEVYWSHL-
qq	2003	tssladpcspspgasgsagksgdsgdrpgqkrfrtqmtnlqlkvlkscfndyrtptmlec 2062
Οy	1569	DPAMPFHRALDPAAAAYLEQRQLSPTPGYPSQYQI
đ	2063	evlgndigipkrvvqvwfqnarakekksklsmakhfginqtsyegpktectlcgikysar 2122
δy	1612	TILNDYITSQQGLSP
qq	2123	: i:
δy	1639	EQPLGLPYPATRGIIDLTNMPPTILVPHFGGTSTPPMDRITYIPGTQIT 1687
qq	2183	qqgmfdntplqalnlpta
οy	1688	FPPRPYNSASMSPGHPTHLAAAASAERERERERERERERERIAAASSDLYLRPGS 1742
q	2231	tspkpnlmglpsttvpspglpts 2253
οy	1743	EQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMPLPAGG 1802
qq	2254	glpnkpss-aslssptpagatmamgpgqppgqqqqqqqqqqqqqqqppppaag 2303
δλ	1803	PSISQGLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAVSE 1862
qq	2304	ppptpqlplqqqqqrkdkdsekv kekekahkg 2335
οy	1863	QQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRTR 1922

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                                                                                                                                                                                                              1979 ASSPAPP-----QEKLQTYQPEVVKANQAENDPT-----RQYEGPLHHYRPQ 2020
                                                                                                                                                                                                                                                                                         2653 phsacfpdpstastsgsaahsndspppp----saaapssasp-----hasrkswpqvv 2701
                                                                                                                                                                                                                                                                                                           2373 DRPSSTGSTQFPYNPLTMRMLSSTPPTPIACAPSAVNQAAPHQQNRIWEREPAPLLSAQY 2432
                                   2404 yyapqipgalqsgylqpmygmeglfpyspalsqalmglspgsllqqyqqyqqslqeaiqq
                        1923 GKTTITAANFIDVIITRQIASDKDARE--RGSQSSDSSSSLSSH--RYETPSDAIEVISP
                                                                                            2021 QESPSPQQQLPPSSQAEGMGQVPRTHRLITLADHICQIITQDFARNQVSSQTPQQPPTST
                                                                                                              ----asqtpvpp----
                                                                                                                                                2484 --gaps----pdkdpakespkpeegkntprevspllpklpe-----epeae
                                                                                                                                                                 2141 HVSSEP-YEPISPPQV--PVVHEKQDSLLLLSQRGAEPAEQRNDARSPGSISYLPS--FF
                                                                                                                                                                                                   2196 TKLENTSPMVKSKKQEIFRKLNSSGGDSDMAAAQPGTEIFNLPAVTTSGSVSSRGHSFA
                                                                                                                                                                                                                                     2256 DPASNIGLEDIIRKALMGSFDDKVEDHGVVMSQPMGVVPGTANTSVVTSGETRREEGDPS
                                                                                                                                                                                                                                                      2614 cesalcgee----alsghlesalhkh------rtitraarnakehpsll
                                                                                                                                                                                                                                                                        2316 PHSGGVCKPKLISKSNS--RKSKSPIPGQGYLGTERPSSVSSVHSEGDYHRQTPGWAW-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSeCKS; tumour suppressor gene; rat; protein kinase C; mitosis; cancer; malignancy; cell proliferation; Alzheimer's disease;
       ----kgeplpvpk----kekgeap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="nuclear localisation signal"
757..760
/note="nuclear localisation signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "nuclear localisation signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "glycine-rich region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat tumour suppressor protein SSeCKS.
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                                                                                                                                                                                                                                                                                                                                                              2741 seesdtd 2747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                           AAW31347;
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 klpqkngqlssvngvaeggdvhvqeenqegqeeevvdedvgqresedvr---ekdrvee 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 maanstaveditkdgqeetseiiegipasennveemvqpa----esqandvgf---- 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----fvgfkftv 167
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                                                                                                  /note= "proposed protein kinase C phosphorylation
    site"
                                                                                                                                                                                                 /note= "proposed protein kinase C phosphorylation
    site"
                                                                                                                                                                                                                                                                                            /note= "proposed protein kinase C phosphorylation site"
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/note= "proposed protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour suppressor gene SSeCKS – used as a mitotic regulator, and inhibitor of malignant phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.6%; Score 325; DB 18; Length 1596; Best Local Similarity 17.8%; Pred. No. 2e-09; Matches 348; Conservative 285; Mismatches 682; Indels 642;
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1399..1421
/note= "zinc finger"
279..307
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96US-0635121.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAV02302
                                                                   Modified-site
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S G	y 482 KKNENYKALVRRNYGKRRGRNQQIARPSQEEKVEEKEDKAEKTE   ::   :	TE 526    
λ Q	527	.NG 583 264
ķa i	584 RITRSMTNEAAAAAAAAAAAAAAEPPPPLPPPPEPISTEFVETSRWTEEEMEVA	
g 2	265	-kkffth 290 FFBDVSO 698
5 B		
£ 8	699 CESVASTVSAQ-EDE-DIEASNEEENPEDSEVEAVKPSEDSPEN :	EN 740   
λ	741	
ą	409 qggggeaeggvvvegtges1ppeklaepqevpqeaepaeelmksremcvsg	sg 459
λ	801 QEHSAEEGSVCDPPPATKADSV : :	-D 845
<del>8</del>	460	sg 510
ž 8	9 846 LDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCSADED	888 kap 570
λ	889	
ą	571 leapqdgeaeegt	: ke 619
ž d	935	PC 994 661
λά	995 GTSKSPNREWEVLQPAPHQLIINLPEGVRLPITRPTRPP 	
<del>Q</del>	662 -tsvs	eg 689
ž q	# 1055 GSISQGTPCTYLTSHNQASYTQETPRPSVGSISLGLPRQQESAKSATLFYIKQEEFSP	sp 1112   ep 733
λ	1113 RSQNSQPEGLLVRAQHEGVVRGTAGAIQEGSITRG	
a	734 agslsegegvstwesfkrlv	ik 791
¥ 9	1170 PALPQTGIPTEALVKGSISRMPIEDSSPEKCREEAASKGHVIYEGKSGHILSYDNIK :	1226 ek 842
λ <del>(</del>	7 1227 -NAREGTRSPRTAHEISLKRSYESVEGNIKOGMSMRESPVS	VS 1266  : vt 899
}		
<u>ن</u> ۾	7 1267 APLEGLICRALPRGSPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYPKQIKRESPPIR 1	IR 1326 : vd 949
%	7 1327 AFEGAITKGKPYDGITTIKEMGRSIHEIPRQDILTQESRKTPEVVQSTRPIIEGSISQ   1:   :   :   :   :   :   :   :   :   :	SQ 1384 es 1006
À	1385	
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Gravin; kinase anchoring protein; type II regulatory subunit; PKA; PKC; cAMP-dependent protein kinase; protein kinase C; autoimmune disease; Myasthenia gravis; nicotinic acetylcholine receptor. 1468 KAQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTSDVTI--PPNKSTNHERKSTLTPTQ 1525 1526 RESIPAKSPVPGVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAAY 1585 1179 eeaataqkeepstlp--nnvpaqeeh-geepgr-----dvleptqqeltaaavpv 1225 1586 LFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITSQQMQVNLRPDVARGLSPREQPLGLP 1645 1226 laktev----gqegev------dwldgekvk------eeqevfv- 1253 1646 YPATRGIIDLINMPPTILVPHPGGTSTPPMDRITYIPGTQITFPPRPYNSASMSPGHPTH 1705 1826 DAAASAPQMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSS 1885 -----LRSTLHEAP 1467 1706 LAAAASAERERERERERERERERIAAASSDLYLRPGSEOPGRPGSHGYVRSPSPSVRTOE 1765 1766 TMLQQRPSVFQGTNGTSVITPLDPTAQLRIMPLPAGGPSISQGLPASRYNTAADALAALV 1825 1968 TPSDAIEVISP-----T 2007 ------vtydsevmgvagcqekeste 1284 1388 -----tvvisetgespecvgdhllpaekss----atgghwtlqhaedtvplgp 1431 1928 -TAANFIDVIIT--------RQIASDKDARERGSQSSDSSSSLSSHRYE 1967 1492 aepeilelesksnkivlnvigtavdgfartetapethaydsgtgvpacrldsrepnrcwt 1551 1886 AFPSGKPQPHSSVVYSEAGKDKG------PPPKSRYEEELRTRGKTTI------2008 RQYEGPLHHYRPQQESPSPQQQLPPSSQAEGMGQVPR 2044 ---PSV---AAW53863 standard; peptide; 1780 AA. 1435 YEDVKAGETVRSRHTSVVSSG---96US-0769309. 96US-0769309. 13-JUL-1998 (first entry) Human gravin polypeptide. Homo sapiens 19-DEC-1996; 19-DEC-1996; US5741890-A. 21-APR-1998 AAW53863; RESULT 35 1254 AAW53863 g g g q a q g q δ g ογ δ δŽ ΟY q δy δλ à δ g

This sequence corresponds to the human gravin polypeptide, and represents a polypeptide of the invention. The polypeptides are fragments capable of binding to type II regulatory subunit of cAMP-dependent protein kinase (PKA). Gravin is a kinase anchoring protein that binds to type II regulatory subunits of PKA and protein kinase C (PKC). Gravin is also an antigen of the autoimmune disease Myasthenia gravis (MG), where a patient develops antibodies against their own nicotinic acetylcholine receptors. The polypeptides are useful for providing analogues of gravin in the study of the modulation (e.g. blocking, inhibiting and stimulating) of interactions between gravin and kinase. The peptides are involved in the modulation of gravin-kinase interactions. New polypeptide fragments of protein kinase binding protein gravin are useful for the study of modulation of action between gravin and Example 1; Column 19-32; 32pp; English. (UYOR-) UNIV OREGON HEALTH SCI. Nauert JB, 1998-260552/23 protein kinase(s) N-PSDB; AAV23545 Klauck TM, 

1780 AA; Sequence

82; 957 YALYQRHIKAMHESALLEEQRQRQEQIDLECRSSTSPCGTSKSPNREWEVLQPAPHQLIT 1016 200 vkkdegegaagagdhqdpslgageaaskesepkqstekpeetlkreqshaeisppaesgq 259 989 746 781 823 GKRRGRNQQIARPSQEEKV-----EEKEEDKAEKTEKKEEEKKDEEEKDEKEDSKENT 548 143 rniegipssesnleeltgpt---esgandigfkkvfkfvgfkftvkkdktekpdtvgllt 199 erteeqkteveetagsvpaeelvgmdaepqeaepakelvklketcvsgedptggadlspd 484 824 VEV--RVPENHASKVEGDNTKER-------DLDRASEKVEP-----RDEDLV 861 :| : || |:|| :::|| ekvlskppegvvsevemlssgermkvggsplkklftstglkklsgkkgkrgggdeesg 544 -----VDGEPERQ 896 ||| :|: 545 ehtqvpadspdsgeegkgessassspeepeeltclekglaevqqdgeaeegatsdgekkre 604 RMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTPVSG 956 Gaps |:: | | | |||||: : || :|: || | | :| :| || gqkgalngqgalnsqeeeevivtevgqrdsedvserdsdkematksavvhditddgqeen ----GRITR SMINEAAAASAA-------PAAAIEEPPPPLPPPPEPISTE------PVETSR 628 WTEE-EMEVAKKGLVEHGRNWAAIAKMVGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKT 260 aveeckeegeekqekepsksaesptspvtsetgstfkkff-----tggwagwrkkts 687 SRKPREERDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSEDSPENATSRGN -----TQVND---SISAETAEQMDVDQQEH------SAEEGSVCDPPPATKAD-SVD 747 TEP-----AVELEPTTETAPSTSPSLAVPSTKPAE--DESVE-------Length 1780; 2.6%; Score 323.5; DB 19; 18.6%; Pred. No. 2.7e-09; tive 273; Mismatches 741; KEKDKIDGTAEETEEREQATPRGRKTANSQGRRK-862 VAQQINAQRPEPQSDNDSSATCSADED----: i | :: | gvtpwasfkkmvtp------Conservative Local Similarity nes 361; Conserv Query Match Best Local S: Matches 361 496 83 549 588 782 425 897 g g g 8 g g ò 셤 ò 8 8 õ à à ò q ò ò

qq	619	::::    :: ::    :: :::       : :   :        :   :       :       :       :
Qγ	1017	NLPEGVRLPTTRPTRPPPPLIPSSTTTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQ 1076
qq	668	
λō	1077	ISLGLPRODESAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVRGTA
Q D	700	eggpkamggdhqkade-agkdketgtdgilagsqehdpgqgss 741
Q D	1137	GAIQEGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGIPTEALVKGSISRMPIEDSS 1196
Qy	1197	AASKGHVIYEGKSGHILSYDNIKNAREGTRSPRTAHEISLKRSYE
qq	793	
ΟŸ	1255	KQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIMQGTPRAT 1304
g	832	
Qy	1305	TESFEDGLKYPKQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHE 1353
qa	892	aaavadgtraatiieerspswisasvtepleqveaeaallteevlereviaeeepptvte 951
Οy	1354	-IPRQDILTQESRKTPEVVQSTRPIIEGSISQGTPIKFDNNSGQSAIKHN 1402
qq	952	pipenreargdtvvseaeltpeavtaaetagplgseegteasaaeettemvs 1003
QY	1403	-VKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVKA-GETVRSRHTSVVSSGP- 1456
qq	1004	avsgltdspdtteeatpygeveggvpd-ieegerrtgevlgavaekvkeesglpgtggpe 1062
φy	1457	SVLRSTLHEAPKAQL-SPGIXDDTSARRTPVSYQNTMSRGSP-MMNRT 1502
q	1063	dvlqpvqraeaerpeeqaeasglkketdvvlkvdaqeaktepftqgkvvgqttpesfeka 1122
Qy	1503	SDVTIPPNKSTNHERKSTLTPTQRESIPAKSPVFGVDPVVSHSPFDPHHRGSTAGEVY 1560
р	1123	pqvtesiesselvttcqaetlagvksqemvmeqaippdsvetptdsetdgstpvadf 1179
οy	1561	WSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQT 1612
q	1180	dapgttqkdeiveiheenevhlvpvrgteaeavpaqkerppapsf-vfqeetkeqs 1235
Qy	1613	ILNDXITSQQMQVNLRPDVARGLSPREQPLGLP-YPATRGIIDLTNMPP 1660
අ	1236	
Qγ	.1661	TILVPHPGGTSTPPMDRITYIPGTQITFPPRPYNSASMSPGHPTHLAAAASA 1712
qq	1291	tvsrekvtevalkgegteeaeckkddalelgshaksppspveremvvgv 1339
Qy	1713	ERER-EREPGRERERERIAAASSDLYLRPGSEQPGRPGSHGYVRSP 1757
QΩ	1340	erekteaepthvneeklehetavtvsee
Qy	1758	SPSVRTQETMPQQRPSVFQGTNGTSVITPLDPTAQLRIMPLPAGGPSISQ 1807
ф	1395	ppclggeeavctkigygsseasfiltaaaeeekvlgetaniletgetlepagahlvle 1452
Qγ	1808	GLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAAR 1848
q	1453	eksseknedfaahpgedavptgpdcgakstpvivsattkkglssdlegekttslkwksde 1512
. Qy	1849	LEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSG 1890
đ	1513	velori i i i i i i i i i i i i i i i i i i
Qy	1891	KPQPHSSVVYSEAGKDKGPPPKSRYEE-ELRTRGKTTITAANFIDVIITRQIASDKDARE 1949 :   : :: :    :     :     :

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The present sequence is the protein sequence of human gravin. Gravin is an A-Kinase anchoring protein (ARAP) which is involved in the localisation of cAMP dependent protein kinase A (PRA) via interactions between the RII binding region and the PRA regulatory subunit RII. Gravin is also an antigen found in myasthenia gravis sufferers, and it is thought that antibodies to it may be useful in modulating the binding of PKA, and thus ald in the treatment of the disease. The gravin coding sequence was isolated by first screening a human umbilical vein endothelial cell cDNA library with serum from a myasthenia gravis patient, and then searching a human heart cDNA library for sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polynucleotides useful for detecting gravin in patients suffering from Myasthenia gravis encodes cAMP-dependent protein kinase-binding polypeptide and protein kinase.C-binding polypeptide of gravin
1612
                            2009
                                                         1653
                                                                                                                   1698
                                                                                                                                                                    RGSQSSDSSSSLSSHRYETPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQ
                                                     --keesestavggah----sdiskdmseas----ektmtveve---gstvnd--gg
                                                                                                                                               ----DFARNQVSS------QTPQQPPTSTFQNSPS-----ALVSTPVRTKTS
                                                                                    2010 YEGPLHHYRPQQESPSPQQQLPPSSQAEGMG--QVPRTHRLITLADHICQIITQ-----
                                                                                                                  le----evvlpseeegggagtksvpeddghallaeriekslvepkedek
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; gravin; PKA RII binding site; myasthenia gravis;
kinase anchoring protein; cAMP dependent protein kinase.
elqtqahvikads-qdagqetekegeepqasaqdetpitsa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1526...1582
/note= "PKA RII binding site"
1537...1563
/note- "PKA anchoring site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "PKC binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Column 35-45; 34pp; English.
                                                                                                                                                                                                                                                                                                                 AAB15380 standard; Protein; 1780 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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/note= "P
1526..158
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N-PSDB; AAA74903.
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Binding-site
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1573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1017 NLPEGVRLPTTRPTRPPPPLIPSSKTTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQ 1076
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                                                                                                                                                                                                                                                                                                                                                                            496 GKRRGRNQQIARPSQEEKV-----EEKEEDKAEKTEKKEEEKKDEEEKDEKEDSKENT 548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 vkkdegegaagagdhgdpslgageaaskesepkqstekpeetlkregshaeisppaesgq 259
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                                                                                                                                                                                                                                                                                                          Gaps
resembling the isolated sequence. This was done because the first sequence obtained was shown to be shorter than the full length cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 aveeckeegeekqekepsksaesptspvtsetgstfkkff-----tggwagwrkkts
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                                                                                                                                                                                                                           DB 21; Length 1780;
                                                                                                                                                                                                                                                               Best Local Similarity 18.6%; Pred. No. 2.7e-09;
Matches 361; Conservative 273; Mismatches 741; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   747 TEP-----AVELEPTTETAPSTSPSLAVPSTKPAE--DESVE---
                                                                                                                                                                                                                       Score 323.5; DB 2 Pred. No. 2.7e-09;
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                                                                                                                                                                                                                           2.6%;
                                                                                                         1780 AA;
                                                                                                                 Sequence
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Chromatin aggregation induction; human; Acinus; AIDS; herpes; diabetes; Alzheimer's disease; Parkinson's disease; cardiac infarction; brain infarction; adenovirus infection; viral hepatitis.

Human Acinus L protein sequence.

(first entry)

12-FEB-2001

AAY85657;

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Tsujimoto

Eguchi Y,

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Sahara

WPI; 2000-665130/64

N-PSDB; AAC61196

07-APR-2000; 2000WO-JP02254

WO200061743-A1

19-OCT-2000

Homo sapiens

99JP-0103317

09-APR-1999;

(SHIO ) SHIONOGI & CO

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2061
 ----PIRAF--EGAITKGKPYDGITTIKEMGRSIHE 1353
                                                                                                 952 plpenreargdtvvseaeltpeavtaa-----etagplgseegteasaaeettemvs 1003
                                                                                                                                                                    1004 avsqltdspdtteeatpvqeveggvpd-ieeqerrtqevlqavaekvkeesglpgtggpe 1062
                                                                                                                                                                                                      1457 SVLRSTLH---EAPKAQL-SPGIYDDT-----SARRTPVSYQNTMSRGSP-MMNRT 1502
                                                                                                                                                                                                                                                                                                                                               1561 WSHLPTQLDPAMPFHRA----LDPA----AAAYLFQRQLSPTPGYPSQYQLYAMENTRQT 1612
                                                                                                                                                                                                                                                                                                                                                                                                                  1613 ILNDYITSQQMQVNLRPDVARGLSPR------EQPLGLP-YPATRGIIDLTNMPP 1660
                                                                                                                                                                                                                                                                                                                                                                                                                                         1661 TILVPHPGGTSTPPMDRITYI----PGTQITFPPR----PYNSASMSPGHPTHLAAAASA 1712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERER-ERE----REKERERERIAAASSDLYLRPGSEQ------PGRPGSHGYVRSP 1757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1758 SPSVRTQETM-----LQQRPSVFQGTNGTSVITPLDPTAQLRIMPL-----PAGGPSISQ 1807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1395 ppclgqeeavctkiqvgsseasftltaaaeeekvlgeta--niletgetlepagahlvle 1452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1808 GLPASRYNTAA-----DALAALVDAAASAPQMDVS-------KTKESKHEAAR 1848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1453 eksseknedfaahpgedavptgpdcgakstpvivsattkkglssdlegekttslkwksde 1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1891 KPQPHSSVVYSEAGKDKGPPPKSRYEE-ELRTRGKTTITAANFIDVIITRQIASDKDARE 1949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1950 RGSQSSDSSSSLSSHRYETPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQ 2009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2062 ----DFARNQVSS-----QTPQQPPTSTFQNSPS------ALVSTPVRTKTS 2098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1699 gddyddpengnsaladtdasggltkespdt----ngpkgkekedagevelgegkyhsesd 1754
                                                                                                                                                                                                                               pqvtesiesselvttcqaetlagvksqemvmeqaip---pdsvetptdsetdgstpvadf
                                                                                                                                                                                                                                                                                                                                                                       1180 dapgttqkdeiveiheenevhlvpvrgteaeavpaqkerppa---pssf-vfqeetkeqs
                                892 aaavadgtraatiieerspswisasvtepleqveaeaallteevlereviaeeepptvte
                                                                  -IP-----RQDILTQESRKTPEVVQSTRPIIEGSISQGTPIKFDNNSGQSAIKHN-----
                                                                                                                                                                                                                                                                           1503 SDVT--IPPNKSTNHERKSTLTPTQRESIPAKSPVPGVDPVVSHSPFDPHHRGSTAGEVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----tvsrekvtevalkgegteeaeckkddalelgshaksppspveremvvgv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1849 LEENLRSRSAAVS---EQQQLEQKTLEVEKRS-------VQCLYTSSAFPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2010 YEGPLHHYRPQQESPSPQQQLPPSSQAEGMG--QVPRTHRLITLADHICQIITQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1654 le-----evvlpseeegggagtksvpeddghallaeriekslvepkedek
                                                                                                                                     1403 -VKSLITGPSKLSRGMPPLEI---VPENIKVVERGKYEDVKA-GETVRSRHTSVVSSGP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2099 NRYSPESQAQSVHHQRPGSR 2118
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1755 kaitpqaqeelqkqeresak 1774
TESFEDGLKYPKQIKRESP
1305
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This invention relates to a polypeptide which induces chromatin agregation. The polypeptide is a fragment of the human Acinus protein. Included in the invention is a nucleotide sequence encoding the polypeptide, antisense oligonucleotides, antibodies recognising the polypeptide, uncleotide sequence, and sense or antisense containing the polypeptide sequence, and sense or antisense oligonucleotides. Also included in the invention is a method for screening compounds for their activity as chromatin aggregation in the coll nucleus without inducing DNA fragmentation. The polypeptide can be used in the investigation and treatment of diseases in which apoptosis is implicated, including AIDS, Alzheimer's diseases, Parkinson's disease, cardiac or brain infarction, herpes or adenovirus infection, diabetes and viral hepatitis. The present sequence represents the human Acinus protein. 78; A novel polypeptide which induces chromatin aggregation but is not involved in DNA fragmentation used for the regulation of apoptosis and screening of potential apoptosis inhibitors 329 PRRKAKESKTREYYEKQFPEIRKQREQQERFQRVGQRGAGLSATIARSEHEISEIIDGLS 388 389 EQENNEKQMRQLSVIPPMMFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHEKEIF 448 -----sllpp----elels 199 449 KDKFIQHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARP 508 SQEEKVEEKEE-----DKAEKTEKKEEEKKDEEEKDEKE---DSKENTKEKDKID 555 581; Gaps DB 21; Length 1341; Indels Query Match 2.5%; Score 317.5; DB 21; Best Local Similarity 19.8%; Pred. No. 4e-09; Matches 338; Conservative 208; Mismatches 584; Disclosure; Page 60-67; 99pp; Japanese. 1341 AA; Sequence 200 181

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AAY85657 standard; Protein; 1341 AA.

RESULT 37
AAY85657
ID AAY856

oy ob	556 GTAEETEEREQATPRGRKTANSQGRRKGRITRSMINEAAAASAAAAATEEP 607
oy Oy	360mkttspleeerelkssgglke
qq	383kskspspprltedrkkaslvalpeqtaseeetppplltkeassp 426
oy g	720 EENPEDSEVEAVKPSEDSPENAISRGNIEPRAVELEPITETAPSISPSLAVP 770 : :
δ d	STKPAEDESVETQVNDSISAETAEQMDVD-QQEHSAEEGSVCDPPPATKADSVD
3 &	ULAGESPAGNYPEESVIPTYAASELAGYSSAYAUIEPESUISAY TOTAL PUPLAILEETA VEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATC
a à	538 lakgiteecikqpsleqkegirashtilpshrikqsadssssrs 582 884 sanenungebendampangkegirapagirusegiranginipolioupayipoliyo
g 8	services and the services of t
ç g	944 TPCNIPIGTPVSGYALYQRHIKAMHESALLEEQRQRQEQIDLECRSSTSPCGTSKSPNRE 1003
3 8	THE PARTY OF THE P
2 2	1004 WEVIQHENDITINEEGVRLYTKPIREPFLIPSEKTYNSEKPSFINGGSIS 1058   :     :   :   :   :   :     :
Οy	QGTPGTYLTSHNQASYTQET   : :
g	ergspkkce-
oy Op	1119 PEGLLVRAQHEGVVRGTAGAIQEGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGIP 1178  11 :     :     :
δ	1179 TEALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIKNAREGTRSPRTA 1238
q	
δ d	HEISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIMQ
<u>a</u>	-essipksikrkisvysatkgypagn
2 6	1299 GIFFATITEFEDGLAXYRAINKESFFIKAFEGALINGKYNGITTIKEMGKSIHELFK 1350 838sdtegggpgrkrrwgastattgkpsisitt 868
δy	IEGS
qq	
Qy	1417 MPPLEIVPENIKVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIY 1476
qq	899edeterngddgthdkglkicrtvtqvvpaegqenggr 935
δ	1477 DDTSARRTPVSYQNTMSRGSPMMNRTS-DVTIPPNKSTNHE-RKSTLTPTQRESIPAK 1532
qq	ď
δλ	
q	sgvsitiddpvrtaqvpspprgkisnivhisnlvrpf
οy	1590 QLSPTPGYPSQYQLYAMENTRQTILNDYITSQQMQVNLRPDVARGLSPREQPLGLPY 1646

1075 pgsn-----pkflc----adyaegdeldyhrgllvdrpsetkteeggiprplhpp 1120 1697 SMSPGHPTHLAAAASAERE---RERERERERERIAAASSDLYLRPGSEQPGRPGSHGY 1753 1754 VRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMPLPAGGPSISQGLPASR 1813 1647 PATRGIIDLINMPPTILVPHPGGTSTPPMDRITYIPGTQITFP-----PRPYNSA 1696 1874 EKRSVQCLYTSSAFPSGKPQPHS----SVVYSEAGKDKGPPPKSRYEEELRTRGKTTITA 1929 Acute lymphoblastic leukemia gene; ALL-1; chromosome 11; treatment; translocation breakpoint mapping; chromosomal abnormality; diagnosis; human; acute lymphocytic; myelomonocytic; monocytic; myelogenous; leukemia; Drosophila; trithorax; homology region; zinc finger domain; cysteine-rich. 1021..1221 /note= "Region of homology to Drosophila trithorax" 1462..1570 /note= "Region of homology to Drosophila trithorax" 3348..3562 /note= "Region of homology to Drosophila trithorax" 1814 YNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEV Detection and treatment of acute leukaemia(s) - using prods. derived from oligo:nucleotide sequences within the  $\mathtt{ALL}\text{-}1$  gene of 1930 ANFIDVIITRQIASDKDARERGSQSSDSSSS 1960 1315 -----erdridtkrhsrsrs 1331 AAR38470 standard; Protein; 3910 AA. Location/Qualiflers (UYJE-) UNIV JEFFERSON THOMAS 91US-0805093. 92US-0888839. 92US-0971094. 92WO-US10930 (first entry) Canaani E, Croce CM; WPI; 1993-214090/26. N-PSDB; AAQ43526. ALL-1 protein. 11-DEC-1991; 27-MAY-1992; 30-OCT:1992; 08-NOV-1993 Homo sapiens 09-DEC-1992; WO9312136-A 24-JUN-1993 AAR38470; Region Region Region RESULT 38 AAR38470 ID AAR3 Key g 셤 g g g ŏ δ ò ò ò

chromosome

This sequence is encoded by the acute lymphoblastic leukemia (ALL-1) gene of chromosome 11. The ALL-1 gene was isolated by translocation breakpoint mapping. Fragments of the ALL-1 cDNA may be used to identify chromosomal abnormalities within the ALL-1 gene. These fragments may be used in the treatment and diagnosis of human leukemias auch as acute lymphocytic, myelomonocytic, mnoncytic and myelogenous leukemia. ALL-1 protein shows three regions of homology to the Drosophila trithorax protein. These regions of homology to the Drosophila trithorax protein. These regions show 64%, 66% and 82% similarity respectively, to the Drosophila gene. The third region of homology constitutes the extreme C-terminus of the two proteins, both proteins end in an identical sequence. The first homology region is cysteine-rich and contains sequence motifs analogous to four zinc finger domains (3-6) within the trithorax gene. The second region of homology is also cysteine-rich and corresponds to zinc fingers 7 and 8 the Drosophila gene. The multiple conserved cysteines and of the multiple conserved cysteines and thistidines at the 3' end of the motifs allow two or three arrangements of the putative fingers. The structure of these cysteine-rich domains appears to be unique to the trithorax and ALL-1 genes. Disclosure; Page 29-50; 90pp; English. 3910 AA; Sequence 

Gaps 153; ---KVYHENIKTNQVMRKKLI---LFFKRRNHARKQREQKICQRYDQLMEAW 318 452 882 ditsvtlgdttavktkilikkgrgnlektnldlg-ptapslekektlclstpssstvkhs 940 70 SL-LSEFHPGSDRPQ---ERRISYEPFHPGPSPVD---HDSLESKRPRLEQVSDSHFQRV 122 421 svdtstdsqaseeiqvlpeersdtpevhp-plpisqspenesndrrsrrysvsersfgsr 479 123 SAAVLPLVHPLPEGLRASADAKKDPAFGGKHEAPSSPISGQPCGDDQNASPSKLSKEELI 182 183 QSMDRVDREIAKVEQQILKLKKKQQQLEEEAAKPP----EPEKPVSPPPVEQKHRSIV- 236 -----QIIYDENRKKAEEA---HKIFEGLGPKVELPLYNQPSDT----- 272 607 asgtaasarlfsplhsgtrfdmhkrspllraprftpseahsr------ifesv 653 EKKVDRIENNPRRKAKESKTREYYEKQFPEIRKQREQQERFQRVGQRGAGLSATIARSEH 378 710 ppssvssslsisvsplatsalnptftfpshsltqsgesaekngrprkqtsa-paepfsss 768 nkresrkekrkkgseigsssalypvgrvskekvvgedvatsssakkatgrkkssshdsgt 881 769 sptplfpwftpgsgtergrnkdkapeelskdr-----dadksvekdksrerdrereke 821 13 FSTEQSRYPPHSVQ--YTFPNTRHQQEFAVPDYRSSHLEVSQASQLLQQQQQQLR-RRP 69 -------EQENNEKQMRQLSVIPPMMFDAE Query Match 2.5%; Score 316; DB 14; Length 3910; Best Local Similarity 17.7%; Pred. No. 2e-08; Matches 581; Conservative 367; Mismatches 1067; Indels 1264; 412 QRRVKF-----INMNGLMED--PMKVYKDRQFMNVWTDHEKEIFKDKF--------IQHPKNFGLIASYLERKSVPDCVLYYYLTKKNE----------NYKALVRRNYGKRRGRNQQIARPSQEEKVEEK 379 EISEIIDGLS------237 g g g g g g ò ò g ò ò ò õ g ò ò

Qy	518	Æ.
qq	941 tss	igsmlaqadklpmtdkrvasllkkakaqlckiekskslkqt-dqpkaqqqesdsset 999
Qy	565 EQA	EQATPRGRKTANSQGRRKGRITRSMTNEAAAASAAAA 602
QQ	1000 svr	
Qy	603 ATE	ATEEPPPLIPPPEPISTEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAKWVGTKSEAQC 662
qq	1058	trnkapqeppvkk
Qy	699	KNFYFNYKRRHNLDNLLQQHKQKTSRKPR 691
qq	1106 gvc	gvctncldkpkfggrnikkqcckmrkcqnlqwmpskaylqkqakavkkkekksktsek-k 1164
Oy	692 EER	EERDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSEDSP 738
đ	1165 dsk	. : :   . :
δλ	739 ENA	ENATSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAE 794
đ	1225 ttp	
δ	795 QMD	QMDVDQQEHSAEEGSVCDPPPATKADSVDVEVRVPENHASKVEGDNTKERDLDRASEKVE 854
qq	1270	
Οy	855 PRD	PRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDV-DGEPERQRMFPMD 902
q	1287 prps:	sipvkqkpkekekpppvnkqenagtlnilstlsngnsskqkipadgvhrirvdfked 1346
Οy	903 SKP	SLLNPIGSILVSSPLKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTPVSGYAL
qq	; 1347 cea	: :               : :
δλ	961	ORHIKAMHESALLEEQRQRQEQID
qa	1384 vyc	ycqvccepfhkfcleenerpledqlenwccrrckfchvcgrqhqatkqllecnkcrnsy 1443
Qy	992 SP-	1006
q	1444 hpeci	jpnyptkptkkkvwictkcvrckscg-sttpg
ογ	1007	1026
qq	1503 kgnfc	ifcplcdkcyddddyeskmmqcgkcdrwvhskcenlsgtedemyeilsnlpesvaytc 1562
ΟŊ	1027 TRP	KTTVASEKPSFIMGGSISOGTP
qq	1563 vnc	vncterhpaewrialekelqislkqvltallnsrttsh-llryrqaakppdln 1614
ογ	1087 SLG	SLGLPRQQESAKSATLPYIKQEEFSP- 1112
qq	1615	-peteesipsisspegpdppvltevskqddqqpldlegvkrkmdqgnytsvlefsdd 1670
δy	1113	GLLVRA
qq	1671 ivk	ivkiiqaainsdgggpeikkansmvksffirgmervfpwfsvkksrfwepnkvssnsgml 1730
ογ	1140	QEGSITRGTP-TSKISVESIPSLRGSITQGTPALPQTGIPT 1179
qa	1731 pna	navlppsldhnyaqwqereenshteqpplmkiipapkpkgpgepdsptplhppt 1786
ΟŊ	1180 EAL	EALVKGSISRMPIEDSSPEKGREE1215
QC	1787 ppi	 ppilstdrsredspelnpppgjednrgcalcltygddsandagrllyiggnewthvncal 1846
Οy	1216 -SG	SGHILSYD-NIKNAR
Q	1847 wsa	wsaevfedddgslknyhmavirgkqlrcefcqkpgatvgccltsctsnyhfmcsrakncv 1906

oy oy	2914 2061 2955		VSSQTPV	: : :  :  vdptpeghmtpdhfigghmd -QQPPTSTFONSPSALVS             Iqvpvsptvpiqn	atpdhfi STFQNSI 11	: :	RTKTSNI	  adhiss  SNRYSPESQ  :     -qkyvpnst	adhissppcgsve XSPESQAQSVHHQ       yvpnst	2954 2113 2992
QY Dp	2114	RPGSRVSPENLYDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVHEKQDSLLLLSQRGA 	LVDKSRGS	RPGKSPER    dspgp	SHVSSI   : :     sqisne	KSPERSHVSSEPYEPISPPQVPVVHEKQ       : : :   : dspgpsqisnaavq-ttpphlkpatek-	VPVVHI : : :	EKQDSL    	LLLLSORGA  ::::	2173 3026
QY Dp	3027	EPAEGRNDARSPGSISYLPSFFT-KLENTS :	SPGSISYL :   vlqtl	PSFFT-KI  :  : pngvtgki	CENTS	GSISYLPSFFT-KLENTSPMVKSKKQEI 	KKQEIFI : : :	RKLNSS    1gpm	-PMVKSKKQEIFRKLNSSGGGDSDMA 	2227 3074
Qy Dp	2228 3075	AAQPGTEIF   glnp	NLPAVTTSGSVSSRG	SVSSRG : :  psaskgll	1pmshhc	HSFADPA(	ASNLGLI	EDIIRK.	-HSFADPASNLGLEDIIRKALMGSFDD 	2277 3116
QY	2278 3117	KVEDHGVVI : nis	OPMGVVPG    ::   ppsgllig	TANTS : vqpppddpq	SVVISGA ::     111vses	MSQPMGVVPGTANTSVVTSGETRREEGDPSPHSGG 	PSPHG :  :vatps	SGGVCK        sglk	PSPHSGGVCKPKLISKSN :	2331 3168
oy Op	2332	SRKSKSPIPGQGYLGTERPSSV- :  :	QGYLGTER : sst	GTERPSSVSSVHSEGDYHRQTP :   ::       -sstpsniapsdvvsnmtlinftp	SVHSEGI       Vsnmt	GW.	AWEDRP	SSTGST	TOFPYNPLT::  :  :   sqlpnhp-s	2389 3208
Oy Dp	2390	MRML :   11d1	SSTPPTPIACAPSAVNQA   :  : :: gslntsshrtvpniikrs	VNQAAPHC : :: ikrs	OONRIWI ::   -kssimy		2428 3243			
RESULT AAR664 ID A XX AC A XX		stan	rd; Protein;	39	10 AA.					
X X B	22-AU	G-1995 (acute	(first entry lymphocytic	ry) c leukae	) leukaemia-1)	protein.				
KKKK	Acute ly chromoso t(9:11);	Acute lymphoblastic leukaem chromosomal translocation; t(9:11); t(11:17); ALL-1; A	stic leuka nslocation 7); ALL-1;	: leukaemia; acute nonl ccation; abnormality; d ALL-1; AF-4; AF-9; AF-	acute ormalit AF-9;	nonlymphoblastic y; detection; t( AF-17; chimeric	blast ion; t		leukaemia; :11); gene; probe	
v s o v ×	Ношо	sapiens.								
FF	Key Protei	ein	Location 348.39	Location/Qualifiers 3483910 //note= "in the disc residues st	fiers disclo	iers disclosure, numbering s starts from Met 348	abering Aet 348	of	amino acid	73.0
FFF	Region	uo	13691569 /note= "cy Dr	stein osoph	ne-rich rec	ich region c trithorax,	of home	- <u> </u>   Se		
FFF	Domain	in	13721397 /label= zir /note= "hon	200		S of	2	~	:	
TH TH	Domai	i n	14171447 /label= zir /note= "hom	0,00		to zinc finger		domain ,	4 of	
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FT	Domain		/label= zinc_finger /note= "homologous t	537 zinc_fi "homolog	finger ogous to	to zinc finger		domain (	go of	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            flededydppikiarlestpnsr---fsapscgsse-ksaaasghssgmssdssrsssp 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SL-LSEFHPGSDRPQ---ERRTSYEPFHPGPSPVD---HDSLESKRPRLEQVSDSHFQRV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAAVLPLVHPLPEGLRASADAKKDPAFGGKHEAPSSPISGQPCGDDQNASPSKLSKEELI 182
                                                                                                                                    trithorax
both
                                                                                                                                                                                                                                                                                                                                                                                                                  The ALL-1 cDNA was obtained from a series of overlapping clones spanning 14.7 kb, isolated by screening a human fibroblast library and a K562 library. The sequence revealed a single, long ORF predicting a protein of approx. 4000 amino acids. The predicted amino acid sequence includes regions of homology with the Drosophila trithorax gene which contain zinc finger domains. The multiple conserved cysteines and histidines at the 3' end of the motifs allow two or three arrangements of the putative fingers. The ALL-1 gene on chromosome 11 is involved in a series of chromosomal translocations which are associated with certain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSTEQSRYPPHSVQ--YTFPNTRHQQEFAVPDYRSSHLEVSQASQLLQQQQQQLR-RRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           svdtstdsqaseeiqvlpeersdtpevhp-plpisgspenesndrrsrrysvsersfgsr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------pptiplaspflpastapmqgkrksilr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----QIIYDENRKKAEEA---HKIFEGLGPKVELPLYNQPSDT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QSMDRVDREIAKVEQQILKLKKKQQQLEEEAAKPP----EPEKPVSPPPVEQKHRSIV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 581; Conservative 367; Mismatches 1067; Indels 1264;
"cysteine-rich region of homology to
Drosophila trithorax, contg. sequence
motifs analogous to zinc fingers"
                                                        of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3910;
                                                    /note- "homologous to zinc finger domain 7
Drosophila trithorax"
                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                 /note= "homologous to zinc finger domain
Drosophila trithorax"
                                                                                                                                  /note= "region of homology to Drosophila located at extreme C-terminus of
                                                                                                                                                                                                                                                                                                                                                    New acute lymphocytic leukaemia gene prods. - used for diagnosis and treatment of leukaemias, partic. acute lymphoblastic or nonlymphoblastic leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 2.5%; Score 316; Similarity 17.7%; Pred. No. 20
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 65; Page 62-79; 207pp; English
                                           zinc_finger
                                                                                       /label= zinc_finger
                                                                                                                                                           proteins"
                                                                                                                                                                                                                                                                        (UYJE-) UNIV JEFFERSON THOMAS
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                                 Domain
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1444 hpeclgpnyptkptkkkvwictkcvrckscg-sttpgkgwdaqwshdfslchdcaklfa 1502 ------LQPAPHQLITNLPEGVRLPT 1026 -----KYVYHENIKTNQVMRKKLI---LFFKRRNHARKQREQKICQRYDQLMEAW 318 eptfrwtslkhsrsepqyfssakyakeglirkpifdnfrpp---pl--tpedvgfasgfs 606 EKKVDRIENNPRRKAKESKTREYYEKQFPEIRKQREQQERFQRVGQRGAGLSATIARSEH 378 tlpsnrtsagtsssgvsnrkr--rkvfspirseprspshsmrt--rsgrlssselsplt 709 ---EQENNEKQMRQLSVIPPMMFDAE 411 710 ppssvssslsisvsplatsalnptftfpshsltqsgesaeknqrprkqtsa-paepfsss 768 : || |:| ::| | ::| tsigsmlaqadklpmtdkrvasllkkakaq1ckiekskslkqt-dqpkaqgqesdsset 999 -----RITRSMTNEAAAAAAA 602 ------KNFYFNYKRRHNLDNL-------LQQHKQKTSRKPR 691 EERDVSQCESVAS----TVSAQEDEDIEASNE-----EENPEDSEVEAVKPSEDSP 738 ENATSRGN----TEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAE 794 QMDVDQQEHSAEEGSVCDPPPATKADSVDVEVRVPENHASKVEGDNTKERDLDRASEKVE 854 PRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDV-DGEPERQRM-----FPMD 902 ------LE---CRSST 991 sptplfpwftpgsqtergrnkdkapeelskdr----dadksvekdksrerdrereke 821 nkresrkekrkkgseigsssalypvgrvskekvvgedvatsssakkatgrkkssshdsgt 881 ditsvtlgdttavktkilikkgrgnlektnldlg-ptapslekektlclstpssstvkhs -----EEDKAEKTEKKE----EEKKDEEEKDEKEDSKENTKEKDKIDGTAEETEER QRRVKF-----INMNGLMED--PMKVYKDRQFMNVWTDHEKEIFKDKF----------NYKALVRRNYGKRRGRNQQIARPSQEEKVEEK--------SKPSLLNPTG--SILVSSPLKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTPVSGYALY 1347 ceaenvwemgglgiltsvp-----assghvef ATEEPPPPLPPPPEPISTEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAKMVGTKSEAQC -----IQHPKNFGLIASYLERKSVPDCVLYYYLTKKNE--asgtaasarlfsplhsgtrfdmhkrspllraprftpseahsr--------CGTSKSPNREWEV------ORHIKAMHESALLEEQRQRQEQID------EQATPR----GRKTANSQGRRKG----EISEIIDGTS----941 265 1058 1106 1165 607 654 112 697 882 518 603 692 739 795 1270 1287 273 453 486 663 855 903 1001 961

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a		kgnfcplcdkcyddddyeskmmqcgkcdrwvhskcenlsgtedemyeilsnlpesvaytc 1	1562
οy		н	1086
qq	1563 vn	vncterhpaewrlalekelgislkqvltallnsrttsh-llryrgaakppdln 1	1614
οy	1087 SL	SLGLPRQDESAKSATLPYIKQEEFSP- 1 :	1112
QQ	1615	peteesipsrsspegpdppvltevskqddqqpldlegvkrkmdqgnytsvlefsdd l	1670
οy	1j13		1139
QQ	1671 iv	ıvkiiqaainsdggqpeikkansmvksffirqmervfpwfsvkksrfwepnkvssnsgml	1730
οy	1140		1179
Q	. 1731 pn	pnavlppsldhnyaqwqereenshteqpplmkkiipapkpkgpgepdsptplhppt 1	1786
٥y	1180 EA		1215
qq	1787 pp	 ppilstdrsredspelnpppgiednrgcalcltygddsandagrllyiggnewthvncal l	1846
٥y	1216 -5		1229
qq	1847 ws	aevfedddgslknvhmavirgkqlrcefcqkpgatvgccltsctsnyhfmcsrakncv	1906
δy	1230		1262
g	1907 fl	flddkkvycgrhrdlikgevvpengfevfrrvfvdfegislrrkflnglepenihmmi	1964
οy	1263 SP		1301
Ωp	1965 gs	::   ::   ::     :	2024
οy	1302 RA		1347
QQ	: 2025 ns	:	2076
οy	1348 GR		1399
qq	2077 yh		2132
٥y	1400	VSSGP	1456
qq	2133 sr		2173
οy	1457 SV		1502
QQ	2174 at	:      :	2233
οy	1503 SD		1562
Op	2234 as	asdlvskssslkgektkvlsskssegsahnvaypgipklapqvhnttsrelnvs 2	2287
ΟŽ	1563 HL		1605
OD	2288 ki	kigsfaepssvsfsskealsfphlhlrgqrndrdqhtdstqsansspdedtevktlklsg 2	2347
οy	1606 ME		1632
q	2348 ms		2406
οy	1633		1652
Dp	2407 de	devltpeymggrpcnnvssdkigdkglsmpgvpkappmgvegsakelgaprkrtvkvtlt 2	2466
٥y	1653	IDDTHAMPTILVPHPGTS	1671
QQ	2467 pl	: :             plkmenesgsknalkesspasplqiestsptepisasenpgdgpvagpspnntscqdsgs 2	2526
δÿ	1672		1711
QQ	2527 nn	nnyqnlpvqdrnlmlpdgpkpqedgsfkrryprrsararsnmffgltplygvrsy 2	2581

οy	1712		174
qa	2582	:       :	263
QY	1750	SHGYVRSPSPSVRTQETMLQQRPSVFQGT-NGTSVITPLDPTAQLRIMPLPAGGPSISQG	180
qq	2640	shnlfreeeqcdlpkisqldgvddgtesdtsvtattrkssqipkrngkengten	269
ΟŸ	1809	LPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRS 	185.
Q	2694	pkmdnchsvsrvktgggdsleaglsslessrrvh	275
δλ	1858	YTSSAFPSGKPQPHSSVVYSEAGK	190
qq	2754	stpsdknlldtyntellksdsdnnnsddcgnilpsdimdfvlkntpsmgal	280
οy	1906	RGSQSSDSSSS	196
q	2805	gespessssellnlgeglgldsnrekdmglfevfsqqlpttepvdssvsssi	285
Οy	1962	SSHRYETPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQAEN	200
qq	2857		291
Qy	2005	OOLPPSSQAEGMGQVPRTHRLITL	206
QQ	2914	dpallspgadhissppcgsve	295
δλ	2061	QDFARNOVSSQTPQQPPTSTFQNSPSALVSTPVRTKTSNRYSPESQAQSVHHQ	211
q	2955	gghgnngdltrnsstpglgvpvsptvpignqkyvpnst	2993
ΟŊ	2114	PYEPISPPQVPVVHEK	217
qq	2993		302
δλ	2174	EPAEQRNDARSPGSISYLPSFFT-KLENTSPMVKSKKQEIFRKLNSSGGGDSDMA	222
QO	3027	qplyvlqtlpngvtqkiqltssvsstpsvmetntsvlgpmgggltltt	307
δλ	2228	AAQPGTEIFNLPAVTTSGSVSSRGHSFADPASNLGLEDIIRKALMGSFDD	227
qq	3075	glnpslptsqslfpsaskgllpmshhqhlhsfpaatqssfpp	311(
ογ	2278	KVEDHGVVMSQPMGVVPGTANTSVVTSGETRREEGDPSPHSGGVCKPKLISKSN	233
qq	3117	is in the state of the second	316
οy	2332	GYLGTERPSSVSSVHSEGDYHRQTPGWAWEDRPSSTG	238
qq	3169	trknkklapsstpsniapsdvvsnmtlinftpsqlpnhp-s	320
Οy	2390	MRMLSSTPPTPIACAPSAVNQAAPHQQNRIWEREPAPLL 2428	
qq	3209	idlgsintsshrtvpniikrskssimyfepapll 3243	
RESU	RESULT 40		
<u>.</u> 8	AAR92100	100 standard; Protein; 1719 AA.	
S S S	AAR92	2100;	
, E	19-MAY	.Y-1996 (first entry)	
X DE	Нитап	RIZ allele D283.	
KKK	Retin cell diagn	Retinoblastoma protein-interacting zinc finger; RIZ; cell proliferation; tumour; cancer; neuroblastoma; melanoma; diagnosis; therapy.	
× so	Ношо	Homo sapiens.	

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1015 ITNLPEGV-----RLPTTRPTRPPPPLIPSSKTTVASEKPSFIMGGSISQGTPGTYLTS 1068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GL-----GVVRGTAGAIQE-GSITRGTPTSK 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -KGREEAASKGHVIYE-----GKSGHILSYDN-----IKNAREGTRSPRTAHE 1240
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                                 NLLQQHKQKTSRKPREERDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPS-- 734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 sepdftsanmrdsaegpkedeekpsasalegpatlg---evasgevppelatpapawepg 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid encoding mammalian retinoblastoma protein-interacting zinc finger - used to identify cell proliferation modulating agents for treatment of tumours, esp. neuroblastoma and melanoma, also used
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Matches 359; Conservative 255; Mismatches 704; Indels 631;
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/label=_Zinc_finger(4-6)
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18-AUG-1994;
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Human; Rb-interacting zinc finger; RIZ; retinoblastoma; heart disease; cell proliferation; cell differentiation; tissue repair; transcription requlator; breast cancer; gene therapy; melanoma; neuroblastoma; leukaemia; Parkinson's disease; Huntingdon's disease; Alzheimer's disease; paralysis; motor neurone disorder; chromosome 1p36;
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The present sequence is a mutant human retinoblastoma (Rb)-interacting zinc finger (RIZ) protein, encoded by allele D283. RIZ is a nuclear phosphoprotein that acts as a cell differentiation factor. RIZ can modulate cell growth by binding to Rb protein, which is involved in regulating cell proliferation. In addition, RIZ can act to regulate transcription. RIZ functions to maintain cells in the G1 phase of the cell cycle, by interacting with Rb through the cr2 domain of RIZ. RIZ protein is a PR domain protein and is present primarily in the cell cycles. RIZ gene mutations may be implicated in various cancers such a melanoma, neuroblastoma, leukaemia and breast cancer, and so the RIZ gene may be used in gene therapy for these disorders. Since RIZ protein is implicated in cell cycle arrest, inhibition of RIZ activity may be useful in neurodegenerative disorder therapy e.g. for Parkinson's, Huntingdon's or Alzheimer's disorder therapy is or motor neurone disorders, or cardiac disorders e.g. for heart disease, where the ability to induce neural/ cardiac tissue proliferation would be useful. The human RIZ gene is located on chromosome lp36. The RIZ D283 allele is thought to occur two times more frequently in the human population than the RIZ B283 allele (AAA60123 and AAB1213).
                                                                                                                                                                                                                                                                                                                                New PR domain peptides comprising amino acid sequences from, for example retinoblastoma-interacting zinc finger, or egl-43 proteins, for regulating gene transcription and controlling cell proliferation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: the present sequence is not shown in the specification but is derived from the human RIZ allele D283 sequence given in Figure 9 (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 vymwevyypnlgwmcidatdpekgnwlryvnways---geegnlfpleinraiyyktlkp 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 420 MNGLMED----PMKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNFG-LIASYLERKSVPDC 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        506 ARPSQEEKVEEKEEDKAEKTEKKEEEKKDEEEKDE-----KEDSKENTKEKDKIDGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -PEPISTEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAKWVGTKSEAQCKNFYFNYKRRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     559 EETEEREQATPRGRKTANSQGRRKGRITRSMTNEAAAASAAAAAATEEPPPPLPPP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           475 V----LYY-----YLTKKNENYKALVRRNYGKRRGRNQQI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative 252; Mismatches 712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.5%; Score 311; DB 21;
18.8%; Pred. No. 1.3e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page -; 91pp; English.
                                                                                                                                                                                             (LJOL-) LA JOLLA CANCER RES FOUND
                                                                                          95US-0516859
                                                                                                                                   94US-0292683
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                                                                                                                                                                                                                                                                       WPI; 2000-410879/35.
N-PSDB; AAA60124.
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                                                                                                                                                                                                                                                                                                                                                                                          differentiation
                                                                                        18-AUG-1995;
                                                                                                                                                   06-MAR-1995;
              US6069231-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372;
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733 308	790 347	847 397	901 444	961 499	1011 555	1065 · 607	1117 666	1149 723	1197 783	1237 843	1297 896	1357 926	1417 962	1477 1005	1537 1037	1596 . 1078	1644	1130
4 NLDNLLQQHKQKTSRKPREERDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKP :::  ::         :  :  :  :  :  :  :  :	4 SEDSPENATSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISA ::		RASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDV-DGEPERQRMFPM-	DSKPSLLNPTG          dssppslgpdc	RHIKAMHESALLEEQRQRQEQIDLECRSSTSPCGTSKSPNRER    : :	2 HQLITNLPEGVRLPTTRPPPPLIPSSKTTVASEKPSFIMGGSISQGTPGTY : :   :	5 LTSHNQASYTQETPKPSVGSISLGLPRQQESAKSATLPYIKQEEFSPRSQNS :	QPEGLGVVRGTAGALGE-GSITRGTP	0 TSKISVESIPSLRGSITQGTPALPQTGIPTEALVKGSISRMPIEDSSP	B EKGREEAASKGHVIYEGKSGHILSYDNIKNAREGTRSPRT	A HEISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIM	3 QGTPRATTESFEDGLKYPKQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHEIPRQ 	DILTQESRKTPEVVQSTRPIIEGSISQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSRGM   :     :     :     :     :       :       :         :         :         :	PPLEIVPENIKVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYD		VDPVVS-HSPEDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPG		!lsaissvvssgdnleaslpmisfkqeeleneglkpreepqsaaeqdvvvqet
674 263	734	791	398	902	962	1012	1066	1118	1150	1198	1238	1298	1358 927	1418	1478	1538	1597	1079
දු දු	O. Db	O.Y	oy Db	oy a	Oy Dp	O.Y	oy D	oy Dp	Oy Db	O.Y	oy Dp	oy ob	oy B	g g	g ç	g ç	οy.	g

δλ	1645	PLTNMPPTILVPHPGGT 1670
Ob	1131	finknfvcnvcespflsikdltkhlsihaeewpfkcefcvqlfkdktdlsehrfllhgvgn 1190
δy	1671	STPPMDRITYIPGTQITFPPRRPYNSASMSPGHPT 1704
QQ	1191	ifvcsvckkefaflcnlqqhqrdlhp-dkvcthhefesqtlrpqnftdpskahve 1244
ογ	1705	HLAAAASAERERERERERERERERAASSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQ 1764 
đ	1245	hmqslpedpletskeeeelndsseelyttikimasgiktkdpdvrlg 1291
Οy	1765	EI
qa	1292	lnqhypsfkpppfgyhhrnpmgigvtatnftthnipqtfttairctkcgkgvd 1344
Οy	1808	GLPASRYNTAADALAALVDAAASAPQMDVSKTKESKH
q	1345	dkkrytpkknpvplk
οy	1845	EAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYT 1883
q	1403	rlnfsvelskmssn-klklnalkkknqlvqkailqknksakqkadlknacessshicpyc 1461
Οy	1884	SSAFP-SGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVIITRQIA 1942
QQ	1462	nreftyigslnkhaafscpkkplsppkk1489
δλ	1943	SDKDARERGSQSSDSSSSLSSHRYETPSDAIEVISPASSPAPPQEKLQTYQPEVVKA 1999
g	1490	kvshsskkgghsspassdknsnsnhrrrtadaei
Qy	2000	
QQ	1536	rarssgpt-qvplpsssfrskqnvkfaasvkskkpsssslrnsspirmakit-hve 1589
Qy	2057	QIITQDFARNQVSSQTPQQPPTSTFQNSPSALVSTPVRTKTSNRYSPESQAQS 2109
qa	1590	
RES	RESULT 42	
E PAK	79054 AAR79054	9054 standard; Protein; 2441 AA.
ž S	AAR79054	3054;
X E	19-7	19-JAN-1996 (first entry)
YY E	CREB	CREB binding protein.
KKK	CREB	CREB binding protein; inhibition; promotion; activation; cAMP; cyclic adenosine monophosphate; reporter gene; reporter construct;
×	Take C	סני בערנטו במרנטו, בשמוניו במרנטוו, מכני עמנוניו.
s ×	Unknown	own .
N X	W0952	WO9521940-Al.
: 교	17-AC	17-AUG-1995.
PF	01-FE	-FEB-1995; 95WO-US01325.
PR	10-FE	10-FEB-1994; 94US-0194468.
EA X	(SALK	( ) SALK INST BIOLOGICAL STUDIES.
PI	Mont	Montminy MR;
R R	WPI; N-PSE	WPI; 1995-293136/38. N-PSDB; AAQ99456.
X	Ident	identification of a compound having properties characteristic of CBP

Identification of a cpd. (I) which inhibits and/or promotes activation of CAMP and mitogen responsive genes comprises monitoring expression of a reporter in response to (I), relative to expression of reporter in the absence of (I), where exposure of (I) is performed in the presence of (I), where exposure of (I) is performed in the presence of (I), a signal dependent transcription; (2) a polypeptide comprising at least maino acid residues 461-661 of this sequence (ARRY9054); and (3) a reporter construct comprising a reporter gene under the control of a signal dependent transcription factor. The method can be used to identify a compound which has the binding and/or activation properties of CREB binding protein or the transcription activation characteristic of a signal dependent which inhibits and/or promotes the activation of cAMP and mitogen Claim 1; Page 32-39; 46pp; English transcription factor responsive genes 

Sequence

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Gaps 122; 331 vgivptqaiatgptadpekrkliqqqlvlllhahkcqrreqan---gevracs1p--- 382 635 LRRRPSLLSEFHPGSDRPQERRTSYEPFHPG--PSPVDHDSLESKRPRLEQVSDSHF--- 119 321 -----hcrt---mknvl----nhmthcqapkacqvahcassrqiishwknctr 423 623 919 plnggdsst------pnlpkga----astsgptppasgalnpgagkgvg 159 322 VDRIENNPRRKAKESKTREYYEKQFPEIRKQREQQERF------QRVGQRGAGLSATI 373 421 422 GLMEDPMKV-----YKDRQFMNVWTDHEKEI---FKDKFIQHPKNFGLIASYLERKSVPD 473 474 CVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEKVEEKEE-----DKAEKTEK 527 KEEE-----KKDEEEKDEKEDSKENTKE--KDKIDGTAEETEEREQATPRGRKTANSQGR 580 -----ilgnqpalpasgaqppvippaqsvrppngplplpvnrmqvsqgmnsfnpmsl 728 7 PPNQGAFSTEQSRYPPHSVQYTFPNTRHQQEFAVPDYRSSHLEVSQASQLLQQQQQQQ-- 64 | | :| | :| | :| | grgrgagmpgatssvlaetltqvspqmag-haglntaqaggmtkmgmtgttsp lvtsspatsqtgpgic---mnanfnqthpgllnsnsghslmnqaqqqqqqvmngslgaa ---PSSPISGQPCGDDQNASPSKLSKEELIQSMDRVDREIAKVEQQILKLKKKQQQLEEE AAKPPEPEKPVSPPPVEQKHRSIVQ----IIYDENRKKAEEAHKIFEGLGPKVELPLYNQ PSDTKVYHENIKTNQVMRKKLILFFKRRNHARKQREQKICQ-----RYDQLMEAWEK--K hdcpvclplknasd------krnqqtilgspasgiqntigsvgagqqnat 374 ARSEHEISEIIDGLSEQE----NNEKQMRQLSVIP---PMMFDAEQRRVKFINMN slsn---pnpidpssmgrayaalglpymngpgtglgpgqypgggpagppahg---gmrtln RKGRITRSMTNEAAAAAAAAAATEEPP-----PPLPPPPEPISTEPVETSRWTEEEMEV Length 2441; 992; Indels 859; Query Match 2.4%; Score 309.5; DB 16; Best Local Similarity 18.7%; Pred. No. 2.4e-08; Matches 495; Conservative 304; Mismatches 992; ORVSAAVLPLVHPLPEGLRASADAKK - - - - DPAFGGKHEA - - -121 65 160 120 216 269 383 424 578 528 624 581 677

ζ	030 ARNGEVERGKRWAALARM***VGIRSEAUCRNFIFNIARRHNDUNDLLUURT-ISKRFR 0	160
QQ	729 gnvqlpqapmgpraaspmnhsvqmnsmasvpgmaispsrmpqppnmmgthannimaqapt 7	788
δy	692 EERDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAV 7	731
QQ		847
ģ	32 KPSEDSP	772
g	848 ppvtqsplhptpppastaagmpslqhptapgmtppqpaaptqpstpvssgqtpt-ptpgs $^9$	906
δy	73 KPAEDESVETQVNDSISAETAEQMDVDQQEHSAEGSVCDP	817
qq	907 vpsaagtgstptvgaaagagv-tpgpgtpvgppsvatpgssgggptpvhtgppgtpl 9	962
δy	818KADSVDVEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQS 8	875
qq	tddtdepte	1013
δy	876 DNDSSATCSADEDVDGEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAA 9	935
QQ	vkeetdtregksepmeveekkpevk	1057
δy	936 VIPPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEQRQRQEQIDLECRS-STSPC 9	994
Dp	- Sd	1079
δλ	995 GTSKSPNREWEVLQPAPHQLITNLPEGVRLPTTRPTRPPPPLIPSSKTTVASEKPSF 1	1051
g	slpfrqpvdpqllgipdyfdivknpmdls	1137
ΟŸ	NQASYTQETPKPSVGSI	1086
Dp	1138 tikrkidtggygepwgyvddvrlmfnnawlynrktsrvykfcsklaevfegeidpvmgsl 1	1197
οy	SQNSQPEGLLVRAQHEGVVRGTA-GAIQEGSIT	1145
Dp	ب -	1251
Qγ	PQTGIPTEALVKGSISRMPIEDSSPEKGREEAA	1205
QQ	1252 lgdapsgpqttiskdqfekkndtldpepfvdckecg l	1288
ογ	1206 SKGHVIYEGKSGHILSYDNIKNAREGTRSPRTAHEISLKRSYESVEGN 1	1253
qq	1289 rkmhqicvlhydiiwpsgfvcdnclkktgrprkenkfsakrlqttrlgnhledr 1	1342
ò	1254 IKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIMQGTPRATT 1	1305
οg	ksrfvdsgemsesfpyrtk	1395
δy	GAITKGKPYDGITTIKEMGRSIHEIPRQDILT	1361
Ω		1425
ΟŸ	1362 QESRKTPEVVQSTRPIIEGSISQGTPIKFDN-NSGQSAIKHNVKSLI 1	1407
g	gcvyisyldsihffrprclrta	1469
ογ	1408TGPSKLSRGMPPLEIVPENIKVVERGKYEDVKAGE 1	1442
qq	1470 ahiwacppsegddyifhchppdqkipkpkrlqewykmldkafaeriindykdifkqane 1	1529
δ	1443 TVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNT 1	1491
а	vleesikeleqeeeerkkeestaasetpegsggdskna	1586
οy	1492 MSRGSPWMNRT-SDVTIPPNKSTNHERKSTLIPTORESIPA 1 :     :     :	1531
qq	1587 kkknnkktnknkssisrankkkpsmpnvsndlsqklyatmekhkevffvihlhagpvist 1	1646
ΟŊ	1532 KSPVPGVDPVVSHSPFDPHHRGSTAGEVYWS1	1562

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teneckhhvetrwhetveedydleineyntkshthkmvkwglglddegssggepgskspg 1766
                                                                                                              -----PTPGYPSQYQLYAM 1606
                                                                                                                                          esrrlsigrcigslvhacgcrnancslpscgkmkrvvghtkgckrktnggcpvckglial 1826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse; nuclear CREB binding protein; CBP; transcription factor; cyclic AMP; response element; non-insulin dependent diabetes mellitus; GAL4 response element.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --ASDKDARERGSQSSDSSSSLSS----HRYETPSDAIEVISPAS-SPAPPQEKLQTYQ 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSQAEGMGQVPRTHRLITLADHI -- CQIITQDFARNQVSSQTPQQPPTSTFQNSPSALVS 2090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REQPLGLPYPATRGIIDLINMPPTILVPHPGGTSTP-PMDRI-TYIPGTQITFPP----
                                                                                                                                                                                                                                                                                                       -RPYNSASMSPGHPTHLAAAASAEREREREREKERERERIAAASSDLYLRPGSEQPGRPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             namgagvprpgvpppgpamgglnpqgg----alnimnpghnpnmtnmnpgyremvrrgll
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                                                                                                         1587 FQRQLS------
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2413 tpnrsalsse 2422
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The present sequence is the mouse nuclear CREB binding protein (CBP). CREB is the cyclic AMP (CAMP) response element binding protein. CBP cooperates with upstream activators which are involved in transcription activation. Signal transduction by cAMP appears to be involved in the aetiology of non-insulin dependent diabetes mellitus (NIDDM), and so inhibition of cAMP signal transduction, which would lead to gene transcription inhibition, may be a possible target for therapy. To identify possible cAMP activation inhibitors, the expression of a reporter construct comprising a GAM response element operatively linked to a reporter gene can be monitored. Any test compounds which reduce reporter gene expression would be a cAMP activation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plnggdsst------pnlpkga----astsgptppasgalnpgagkgvg 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying compounds which disrupt CREB : CBP complex for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene in
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llarity 18.6%; Pred. No. 2.4e-08;
Conservative 306; Mismatches 993; Indels 859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    diabetes, involves monitoring the expression of a reporter ge response to exposure of the compound, in a modified host cell
                                                                                        /note= "Unspecified residue encoded by CGN'
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                                           Location/Qualifiers 377
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. Оу	2 QESRKTPEVVQSTRPI
đ	prolrtavyheiligyleyvkkl
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අ	fkgane
δŏ	TVRSRHTSVVSGGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNT   :   :   :
<b>Q</b>	dritsakelpyfegdfwpnvleesikelegeeeerkkeestaasetpegsggdskna 1
οy	1492 MSRGSPMMNRT-SDVTIPPNKSTNHERKSTLTPTQRESIPA 1531
QQ	1587 kkknnkktnknkssisrankkkpsmpnvsndlsqklyatmekhkevffvihlhagpvist 1646
οy	1532 KSPVPGVDPVVS1SPFDPHHRGSTAGEVXWS
qq	1647 gppivdpdpllscdlmdgrdafltlardkhwefsslrrskwstlcmlvelhtggqdrfvy 1706
ολ	1563BPAAAAYL 1586
qq	1707 tcneckhhvetrwhctvcedydlcincyntkshthkmvkwglglddegssggepgskspg 1766
ογ	1587 FORQLSPTPGYPSQYQLYAM 1606
QQ	1767 esrrisiqrciqslvhacqcrnancslpscqkmkrvvqhtkgckrktnggcpvckqlial 1826
ογ	1607VILRPDVARGL-SP 1637
q	1827 ccyhakhcqenkcpvpfclnikhnvrqqqiqhclqqaqlmrrrmatmntrnvpqqslpsp 1886
δλ	PATRGIIDLTNMPPTILVPHPGGTSTP-PM
QQ	1887 tsappgtptqqpstpqtpqppaqpqpspvnmspagfpnvartqpptivsa 1936
οy	1691 -RPYNSASMSPGHPTHLAAAASAERERERERERERERERERERAASSDLYLRPGSEQPGRPG 1749
QQ	1937 gkptngvpappppagpppaaveaargiereagggghlyraninngmppgrdgmgtpg 1993
ογ	1750 SHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMPLPAGGPSISQGL 1809
q	1994 sqmtpvglnvprpnqvsgpvmssmppgqwqqapipqqqpmpgm 2036
οy	1810 PASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLKSRSAAVSEQQQLEQK 1869
οg	2037 prpvmsmqaqaavagprmpnvqpnrsispsa-lqdllrtlkspsspqqqqq 2086
δλ	YTSSAFYTSSAF
qq	2087 vlnilksnpglmaafikgrtakyvangpgmgpgpggggggggggmgpggpglggggggggggggg
Qy	1899 VYSEAGKDK-GPPPKSRYEEELRTRGKTTITAANFIDVIITRQI- 1941
qq	2144 namqagvprppppppamgglnpqgqalnimnpghnpnmtnmnpqyremvrrqll 2199
Oy	DAIEVI
qq	2200 qhqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqq
0y	1994 PEVVKANQAENDPTRQYEGPLHHYRPQGESPSPQQQLPP 2032
qq	2254 piggssmggmaapmgglggmggpglgadstpniggalggrilggggmkggigspggpnpm 2313
δy	2033 SSQABGMGQVPRTHRLITLADHICQIITQDFARNQVSSQTPQQPPTSTFQNSPSALVS 2090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           finger (RIZ) protein, encoded by allele D283. RIZ is a nuclear phosphoprotein that acts as a cell differentiation factor. RIZ can modulate cell growth by binding to Rb protein, which is involved in regulating cell proliferation. In addition, RIZ can act to regulate transcription. RIZ functions to maintain cells in the G1 phase of the cell cycle, by interacting with Rb through the cr2 domain of RIZ. RIZ protein is a PR domain protein and is present primarily in the cell nucleus. RIZ gene mutations may be implicated in various cancers such as melanoma, neuroblastoma, leukaemia and breast cancer, and so the RIZ gene may be used in gene therapy for these disorders. Since RIZ protein is implicated in cell cycle arrest, inhibition of RIZ activity may be useful in neurodegenerative disorder therapy e.g. for Parkinson's,
                                                                                                                                                                                                                                                                  Human; Rb-interacting zinc finger; RIZ; retinoblastoma; heart disease; cell proliferation; cell differentiation; tissue repair; transcription regulator; breast cancer; gene therapy; melanoma; neuroblastoma; leukaemia; parkinson's disease; Huntingdon's disease; Alzheimer's disease; paralysis; motor neurone disorder; chromosome 1p36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for
                present sequence is the human retinoblastoma (Rb)-interacting zinc
                                                                                                                                                                                                                                         Human Rb-interacting zinc finger (RIZ) protein encoded by allele D283
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2091 TPVRTKTSNRYSPESQAQSVHH-----QRPGSRVSPENLVDKSRGSRPGKS-
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/label- PR_domain
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95US-0399411.
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06-MAR-1995;
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times more frequently in the human population than (AAA60123 and AAB12113).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sepdftsanmrdsaegpkedeekpsasalegpatlg---evasgevppelatpapawepg 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PISTEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAKMVGTKSEAQCKNFYFNYKRRHNLD 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLLQQHKQKTSRKPREERDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPS-- 734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cdekpedlle----epkttseetledcsevtpamgiprtk----- 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQMDVDQQEHSAEEGSVCDPPPATKADSVDVEVRV -- PENHASKVEGDNTKERDLDRAS 850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----afgtginrrrherrheaglkrkpsqtlqpsedladgkasgenvaskddss 447
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                                                                                                                                                                          Query Match 2.4%; Score 309; DB 21; Length 1719; Best Local Similarity 18.5%; Pred. No. 1.6e-08; Matches 344; Conservative 247; Mismatches 664; Indels 600;
to occur two E283 allele
                                                                                        1719 AA;
thought t
                                                                                        Sequence
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δo.	RPIIEGSISQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSRGM
q	930 pgsgfpap-tvestpdvcpsspalqtpslssgq
δ	KVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPK
qq	966 -1iptdpssppcppvltvatppppllptvplpapssasp 1005
Qy	1481 ARRIPVSYQNTMSRGSPMANRTSDVIIPPNKSTNHERKSTLTPTQRESIPAKSPVPGVDP 1540
qq	snataqsplpilsptvspspspipp
δŏ	VVS-HSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPS
g G	1041 lmsaaspgpptlssssssssssssssssssp 1078
οy	1600 QYQLXAMENTRQTILNDYITSQQMQVNLRPDVARGLSPREQPLGL 1644
qq	1079lsaissvvssgdnleaslpmisfkgeeleneglkpreepgsaaegdvvvgetfnk 1133
Qy	1645PYPATRGII
qq	1134 nfvcnvcespflsikdltkhlsihaeewpfkcefcvqlfkdktdlsehrfllhgvgnifv 1193
δδ.	1671STPPMDRITYIPGTQITFPPRPXNSASMSPGHPTHLA 1707
qq	1194 csvckkefaflcnlgqhgrdlhp-dkvcthhefesgtlrpqnftdpskahvehmg 1247
οy	ERERIAAASSDLYLRPGSEQPGRPGSHGYV
QQ	
ογ	1768 LQQRPSVFQGINGTSVITPLDPTAQLRIMPLPAGGPSISQGLP 1810
ΩĐ	
Qγ	1811 ASRYNTAADALAALVDAAASAPQMDVSKTKESKH 1844
qq	
δ	RLEENLRSRSAAVS
q	1406 fsvelskmssn-klklnalkkknglvgkailgknksakgkadlknacessshicpycnre 1464
Οy	1887 FP-SGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVIITRQIASDK 1945
QQ	1465 ftyigsinkhaafscpkkpisppkkkvs 1492
δλ	1946 DARERGSQSSDSSSLSSHRYETPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQA 2002
q	1493 hsskkgghsspassdknsnsnhrrtadaeikmgsmqtplgktrar 1538
QY	2003 ENDPTRQYEGPLHHYRPQQESPSPQQQLPPSSQAEGMGQVPRTHRLITLADHICQII 2059
QQ	1539 ssgpt-qvplpsssfrskqnvkfaasvkskkpsssslrnsspirmakit-hvegkk 1592
Qy	2060 TODFARNQVSSQTPQQPPTSTFQNSPSALVSTPVRTKTSNRYSPESQAQS 2109
qa	
RESI	RESULT 45
AAW TD	140058 AAW40058 standard; Protein; 2441 AA.
X X	ААМ40058;
563	20-JUL-1998 (first entry)
SES	Cellular transcriptional factor CBP.
K W	Cellular transcriptional factor; CBP; P/CAF; human; transcription;

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This polypeptide sequence comprises CBP, a global transcriptional coactivator that is involved in the regulation of various DNA-binding transcriptional factors. The invention relates to a novel human p300/CBP associated cofactor. P/CAF (see AAW40052), that modulates transcription through binding to p300 and CBP (see AAW40058). The region (see AAW40060) of CBP that binds to P/CAF is claimed. The invention provides methods of screening for compounds that inhibit or stimulate the transcription modulating and histone acetyltransferase activity of P/CAF and p300/CBP. Inhibitors can be used e.g. to inhibit thy TAF-mediated than transcription in the treatment of HIV infection. Stimulators can be used e.g. to inhibit the cation factor MyoD to promote muscle differentiation factor MyoD to promote muscle differentiation. The products can also be used to inhibit the cell cycle progression inducing effect of an occoprotein which binds p300/CBP in a subject.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 lvtsspatsqtgpgic----mnanfnqthpgllnsnsghslmnqaqqqqaqvmngslgaa 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated p300/CBP-associated factor, P/CAF - used to develop products for modulating transcription, e.g. for treating HIV infection or cancers or for promoting muscle differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.4%; Score 308.5; DB 19; Length 2441; Best Local Similarity 18.5%; Pred. No. 2.7e-08; Matches 489; Conservative 305; Mismatches 1005; Indels 843;
histone acetyltransferase; HIV; infection; cancer; therapy; muscle differentiation.
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Misc-difference 377
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N-PSDB; AAV10093.
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156 ---PSSPISGOPCGDDQNASPSKLSKEELIQSMDRVDREIAKVEQQILKLKKKQQQLEEE

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321	373	421	521 473	577	527	623	280	919	635	128	691	88/	731	847	772	906	817	862	875	1013	935	1057	994	1079	1051	1137	1086	1197	1145	1251	1205	1288
9 PSDTKVYHENIKTNQVMRKKLILFFKRRNHARKQREQKICQRYDQLMEAWEKK   :	VDRIENNPRRKAKESKTREYYEKQFPE 	ARSEHEI	stsnpnpidpssmgrayaaigipymndpdcdidpdvpgdgdpaqppang GLMEDPMKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNFGLIASYLE	:        :   :  algnnpmsvpaggittdqqppnlisesalptsl	CVLYYYLTKKNEN	taappsstgvrkgwhehvt	KEEEKKDE	rmenlvayakkvegdmyesansrdeyyhllaekiykiqkeleekrrtrlhk	RKGRITRS	TIGNGPALPAS	AKKGL	gaver pearpage	EERDVSQCESVASTVSAQEDEDIEASNEEENPED	$^{ m 9}$ qnqflpqnqfpsssgamsvnsvgmgqpaaqagvsqgqepgaalpnplnmlapqasqlpc-		ppvtqsplhptpppastaagmpsl	KPAE	vpsaaqtqstptvhaaaqaqv-tpqpqtpv	KADSVDVEV	Ø	DNDSSATCSADEDVDGEPERQRMFPMDSKPSLLNPTGSILV	skgeprsemme	VIPPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLE		GTSKSPNREWEVLOPAPHQLITNLPEGV	gprkkifkpeelrgalmptlealyrgdpeslpfrgpvdpgllgipdyfdivknpmdls	IMGGSISQGTPGTYLISHNQASYTQETPKPSVGS	tikrkldtggygepwgyvddvrlmfnnawlynrkts	SLGLPRQOESAKSATLPYIKQEEFSPRSQNSQPE	gyccgrkyefspqtlccygkqlctiprdaayysyqnryhfcgkcfteiggenvt	RCTPTSKISVESIPSLRGSITQGTPALPQTGIPTEALVKGSISRMPI	
373	322	374	408	522	474	578	528	624	581	10	636	67/	692	789	732	848	773	907	818	963	876	1014	936	1058	995	1080	1052	1138	1087	1198	1146	7671
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Qy	1206 SKGHVIYEGK	SGHILSYDNI INAREGTRSPRTAHEISLKRSYESVEGN 1253
q	1289 rkmhqic	gfvcdnclkktgrprkenkfsakrlqttrlgnhled
ΟY	1254 IKQGMSMRES	EGLICRALPRGSPHSD
Q	1343 vnkflrrqnh	ktvevkpgi
Qy	1306 ESFEDG	1311
q	1396 alfafeeidgvdvcff	${\tt gmhvqdtaliaphqiqgcvyisyldsihffrprclrt}$
δλ	1312LKYPKQIKRE	S
q	1456 igyleyvkkl	tahiwacppsegddyifhch
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q	1572 asetpegs	gdsknakkknnkktnknkssisrankkpsmpnvsndlsgkl 1622
δŏ	1432 RGKYEDVKAG	RGKYEDVKAGETVRSRHTS-VVSSGPSVLRSTLHEAPKAQLSPGIYDD 1478
В	1623 yatmekhkev	ffylhlhagpvistqppivdpdpllscdlmdgrdafltlardkh 1676
ΟŸ	1479TSARRTP	1491
q	1677 wefsslrrsk	:
Qγ	1492 MSRGSPMM	MSRGSPMMBXIPPNKSTNHERKSTLTPTQRESIPAKSPV 1535
đ	1737 kshthkmvkw	
δλ	1536 PGVDPVV	PGVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAAYLFQRQLS 1592
a	1794 pscqkmkrvv	htkgckrktnggcpvckqllalccyhakhcqenkc 1839
δλ	1593 PTPGYPSQYQ	PTFCYPSQYQLYAMENTRQTILNDYITSQQMQVNLRPDVARGL-SPREQPLGLP 1645
q	1840 pvpfc	nikhnvrqqqiqhclqqaqlmrrrmatmntrnvpqqslpsptsappgtp 1894
δŏ	1646 YPATRGIIDL	YPATRGIIDL/INMPPTILVPHPGGTSTP-PMDRI-TYIPGTQITFPPRPYNSAS 1697
qq	1895	-tqqpstpqtpqppaqpqpspvnmspagfpnvartqpptivsagkptnqvp 1944
δλ	1698 MSPGHPTHLA	MSPGHPTHLAAAASAERERERERERERERIAAASSDLYLRPGSEQPGRPGSHGYVRSP 1757
qq	1945 appppagppp	naveaargiereaggghlyraninngmppgrdgmgtpgsg 1995
οy	1758 SPSVRTQETM	SRYN
ф	1996mtpvgl	yasgpvmssmppgqwqqapipqqqqpmp
ολ	1818 ADALAALVDA	ASAPQMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRS 1877
q	2038 rpvmsmqaqa	gprmpnvqpnrsispsa-l
Οy	1878 VOCLYTSSAF	SSVVYSEAGKD 1906
qq	2095 pqlmaaf	kqrtakyvanqpgmqpqpglq
οy	1907 K-GPPPKSRY:	K-GPPPKSRYEEELRTRGKTIITAANFIDVIITRQIASDKDA 1947
đ	2152 rpgvpppgpa	ghnpnmtnmnpqy
ογ	1948 RERGSQSSDSSSSLSS-	HRYETPSDAI
qq	2208 qqqqqqqqqqnsaslag	mag
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                                                                                                                                                                                                                                                                                                                                                                                                                                         197339 seqs, 20590346 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                              US-09-522-753-11
12643
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 94, Appli Sequence 94, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli		3 195 (026 CTING OLECULES AND METHODS 30
1 US-08-195-487-4 1 US-08-466-390-4 1 US-08-466-390-4 1 US-08-470-950-4 1 US-08-483-224-4 1 US-08-687-200-94 8 US-08-066-64-94 1 US-08-05-06482-2 8 DS-08-800-644-94 1 US-08-227-536-2 1 US-08-227-536-2 1 US-08-227-536-2 2 US-08-287-536-2 4 DS-07-853-913-4 5 US-08-399-411-2 6 US-08-399-411-2 6 US-08-399-411-2 6 US-08-369-411-2 6 US-08-369-411-2 6 US-08-368-3 6 US-08-368-3 7 US-08-368-3 6 US-08-368-3 7 US-08-368-3 7 US-08-368-3 8 US-08-368-3 8 US-08-368-3 9	ALIGNMENTS	FLED INTERA S AND RELATED M P.C. Suite 3100 % Version #1. 652 6/246001
28 286.5 2.3 2101 29 286.5 2.3 2101 30 285.5 2.3 2101 31 285.5 2.3 2101 32 285.5 2.3 2101 33 285.5 2.3 2101 34 284 2.2 1898 35 284 2.2 2419 36 284 2.2 2419 37 284 2.2 2419 38 276.5 2.2 2419 40 274.5 2.2 1706 41 274.5 2.2 1706 42 274.5 2.2 1706 43 270.5 2.2 1706 44 258 2.0 1185 45 256.5 2.0 1898		RESULT 1  US-08-372-652-5  Sequence 5, Application US/08372652  Patent No. 5932699  GENERAL INFORMATION: PAPLICANT: Seol, Wongi APPLICANT: Choi, Huenge-Sik TITLE OF INVENTION: RETINIOD X TITLE OF INVENTION: RETINIOD X TITLE OF INVENTION: POLYPEPTIDE NUMBER OF SEQUENCES: 17 CORRESPONDENCE ADDRESS: ADDRESSE: Fish & Richardson STREET: 225 Franklin Street, CITY: Boston STATE: MA COUNTRY: USA COMPUTER: IBM PC COMPAILDLE OPERATING SYSTEM: PC-DOS/MS-D SOFTWARE: Patentin Release #1 COMPUTER: IBM PC COMPAILDLE OPERATING SYSTEM: PC-DOS/MS-D SOFTWARE: Patentin Release #1 COMPUTER: IBM PC COMPAILDLE OPERATION NUMBER: US/08/372 FILING DATE: 13-JAN-1995 ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul T REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 0078 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION NUMBER: 30,162 TELESX: 50154 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: G19 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA
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1819 DALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSV 1878

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Query Match 22.8%; Score 2885.5; DB 2; Length 619; Best Local Similarity 90.1%; Pred. No. 2.4e-171; Matches 562; Conservative 27; Mismatches 28; Indels 7;

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                                                                                  RQIASDKDARERGSQSSDSSSSLSSHRYETPSDAIEVISPASSPAPPQEKLQTYQPEVVK 1998
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APPLICANT: Choi, Hueng-Sik
TITLE OF INVENTION: RETINOID X RECEPTOR-INTERACTING
TITLE OF INVENTION: POLYPEPTIDES AND RELATED MOLECULES AND METHODS
CORRESPONDENCE ADDRESS:
                                                                                                121 RQIASDKDARERGSQSSDSSSSLSSHRYETASDAIEVISPASSPAPPQEKPQAYQDWYK
                                                                                                                                                      181 ANQAENESTRQYEGPLHHYRSQOESPSPQQOPPLPPSSQSEGMGQVPRTHRLITLADHIC
                                                                                                                                                                                                             ANTSVVTSGETRREEGDPSPHSGGVCKPKLISKSNSRKSKSPIPGQGYLGTERPSSVSSV
|:|||||| | ||:||||||| ASTSVVTSSEARRDEGEPSPHA-GVCKPKLINKSNSRKSKSPIPGQSYLGTERPSSVSSV
                           1879 QCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVIIT
                                                                                                                                         ANQAENDPTROYEGPLHHYRPQQESPSPQQQ--LPPSSQAEGMGQVPRTHRLITLADHIC
                                                                                                                                                                                                                                                  2117 SRVSPENLVDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVHEKQDSLLLLSQRGAEPA
                                                                                                                                                                                                                                                                                                         EQRNDARSPGSISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGGDSDMAAAQPGTEIF
DALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQKNLEVEKRSV
                                        2057 QIITQDFARNQVSSQTPQQPPTSTFQNSPSALVSTPVRTKTSNRYSPESQAQSVHHQRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2357 HSEGDYHRQTPGWAWEDRPSSTGSTQFPYNPLTMRMLSSTPPTPIACAPSAVNQAAPHQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NRIWEREPAPLLSAQYETLSDSDD 2440
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/372,652
FILING DATE: 13-JAN-1995
ATTÓRNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Moore, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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PCT-US95-16311-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 QIITQDFARNQV----PSQPSTSTFQTSPSALSSTPVRTKTSSRYSPESQSGTVLHPRPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.8%; Score 2885.5; DB 5; Length 619; 90.1%; Pred. No. 2.4e-171; tive 27; Mismatches 28; Indels 7;
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/246001
TELECOMMUTCATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPRAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2417 NRIWEREPAPLLSAQYETLSDSDD 2440
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APPLICANT: ALBERTSEN, HANS
APPLICANT: ANAND, RAKESH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             596 NRIWEREPAPLLSAQYETLSDSDD
                                                                                                       TELEX: 200154
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 619 amino acids TYPE: amino acid STRANDEDNESS: single
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CARLSON, MARY
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PCT-US95-16311-5
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1311 IGTRSAEDPVSEVPAVSQHPRTKSSRLQGSSLSSESARHKAVEFPSGAKSPSKSGAQTPK 1370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      396 QMRQLSVIPPMMFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHE--KEIFKDKFI 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      347 PEIRKQREQQE-RFQRVGQRGAGLSATIARSEH-------EISEIIDGLSEQENNEK 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       454 QHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.9%; Score 368; DB 1; Length 2843; ilarity 19.4%; Pred. No. 4.3e-14; Conservative 281; Mismatches 797; Indels 66
                                                                                                                            TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 94
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/741,940
FILING DATE: 19920109
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: RAGAN, SAZAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 31,141
REFERENCE/DOCKET NUMBER: 1107.035574
TELECOMMUNICATION INFORMATION:
TELEFNI: 202-508-9100
                                                                                                                                                                                                                ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, NW
CITY: Washington
    HEDGE, PHILIP J.
JOSLYN, GEOFF
KINZLER, KENNETH
MARKHAM, ALEXANDER F.
                                                                                    NAKAMURA, YUSUKE
THLIVERIS, ANDREW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2843 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-07-741-940-2
                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                 TMPPSRSKTPPP----PPQTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQ-RVQVLPDA 1485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --SLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTE--LTSNQQSA---NKTQAI 1913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QEGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGIPTEALVK-------G 1185
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----RDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSE--DSPEN 740
                                                                               741 A--TSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDV 798
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                                                                                                                                                                 DQQEHSAEE----GSVC-----DPPPATKADSVDVEVR----VPEN-HASKVEGDN
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                                                                      1622 QMQVNLRPDVA---RGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRI 1678
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1562 SHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITSQ 1621
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TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
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                                      ---DSTPSRPAQQPL--
                                                                                                                                             1679 TYIPGTQITFPPRPYNSASMSPGHPTHLAAAASAERERERER
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CARLSON, MARY
GRODEN, JOANNA
HEDGE, PHILIP J.
JOSLYN, GEOFF
KINZLER, KENNETH
MARKHAM, ALEXANDER F.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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THLIVERIS, ANDREW
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner &
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1088 KFQPHFG------QQECVSPY----RSRGANGSETNRVGSNHGINQNVSQSLCQE-1132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 454 QHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEK 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1542 PKESNENOEKEAEKTIDSEKDLL------DDSD-----DDDIEILEECIIS 1581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    396 QMRQLSVIPPMMFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHE--KEIFKDKFI 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           689 KPREE-----RDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSE--DSPEN 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347 PEIRKOREQQE-RFQRVGQRGAGLSATIARSEH------EISEIIDGLSEQENNEK 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        514 VEEKEEDKAEKTEKK--EEEKKDEEEKDEKEDSKENTKEKDKIDGTAEETEEREQATPRG 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R------KTANSQGRRKGRITRSMTNEAAAS------AAAAAATEEPPPPLPPP 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          615 PEPISTEPVET-----SRWT-----EEEMEVAKKGLVEHGRNWAAIAKM--- 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  654 VGTKSE------QKTKNFYFNYKRRHNLDNLLQQHK-------QKTSR 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      741 A--TSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDV 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  799 DQQEHSAEE----GSVC-----DPPPATKADSVDVEVR----VPEN-HASKVEGDN 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   891 -----GEPERQRMF---PMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVI 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1430 IMPPSRSKTPPP---PPQTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQ-RVQVLPDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           841 TKE--RDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDVD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 368; DB 1; Length 2843;
Pred. No. 4.3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 418; Conservative 281; Mismatches 797; Indels
                      PatentIn Release #1.0, Version #1.25
2.9%; Score 368;
                                                                                                                                                                                                                                                                                                                                                                                                         2843 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.48;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-289-548A-2
                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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DEKLQTYQPEVVKANQAENDPTRQYEGPLH 2015
:::|||||:|::|::|
KTLIYQMAPAVSK---TEDVWVRIEDCPIN 2667
                                                                                                    ...--SQAEGMGQVPRTHRLITLADHI 2055
: | | | | | | : : : : : CDSKDNQAKQNVGNGSVPM--RTVGLENRL 2722
                                                                                                                                      SOMATIC MUTATIONS OF APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                   Beckett
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; MOLE US-08-452	TOPOLOGY: linear MOLECULE TYPE: protein 3-452-654-2
Query Ma Best Loc Matches	Match 2.9%; Score 368; DB 1; Length 2843; Local Similarity 19.4%; Pred. No. 4.3e-14; es 418; Conservative 281; Mismatches 797; Indels 664; Gaps 98;
Qy 347	PEIRKOREQOE-REORVGORGAGLSATIARSEHEISEIIDGLSEOENNE
Db 981	
Qy 396 Db 1041	OMRQLSVIPPMMFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHEKEIFKDKFI 453
Oy 454	QHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEK 513 :
_	VEEKEEDKAEKTEKK EEEKKDEEKDEKEDSKENTKEKDKIDGTAEETEEREGATPRG 571 ::       :     :       :
57	RKTANSQGRKGRITIRSMTNEAAAASAAAAATEEPPPLPPP 614
Qy 615 Db 1251	PEPISTEPVETSRWTEEBMEVAKKGLVEHGRNWAAIAKM 653
Oy 654 Db 1311	VGTKSEOKTSR 688 :  :  :  :  :  :  :  :  :
Qy 689 Db 1371	) KPREERDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSEDSPEN 740
Qy 741 Db 1430	. ATSRGNTEPAVELEPTTETAPSTSPSIAVPSTKPAEDESVETQVNDSISAETAEQMDV 798 
Qy 799 Db 1486	DQQEHSAEEGSVCDPPPATKADSVDVEVRVPEN-HASKVEGDN 840
Oy 841 Db 1542	TKERDLDRASEKVEPRDEDL/VVAQOINAQRPEPQSDNDSSATCSADEDVD 890    :::   ::
Oy 891 Db 1582	GEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVI 937
Qy 938 Db 1634	PPMVSCTPCNIPIGTPVSGYALYORHIKAMHE 969 
Oy 970 Db 1694	SAL
Oy 1008 Db 1754	QPAPHQLITNLPEGVRLPTTRPTRPPPPLI
Qy 1039 Db 1811	SSKTTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQETP 1079

2140 SGISLGSPF------HLTPDQEEKPFTSNKGPRILK-----PGEKSTLETKK 2180 1787 LDPTAQLRIMPLPAGGPSISQGLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEA 1846 KPSVGSISLGLPRQQESAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVRGTAGAI 1139 --SLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTE--LTSNQQSA---NKTQAI 1913 : | | | | : : | : | | | 1. :: | | | 1. :: | | | | 1. :: | | | | 1914 AKQPINRGQPKPILQKQS------TFPQSSKDIPDRGAATDEKLQNFAIENTPVCFSHNS 1967 SLSSLSDIDQENNNKENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSL 2027 --LSYDN-----IKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPL 1269 2028 SSLSIDSEDDLLQECISSAMPKKKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPD 2087 1270 EGLICRALPRGSPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYPKQIKRESPPIRAFE 1329 SE---HGLSPDSENFDWKAIQEGANSIVSSLHQAAAAAC----LSRQASSDSDSILSLK 2139 1330 GAITKGKPYDGITTIKEMGRSIHEIPRQDILTQESRKTPEVVQSTRPIIEGSISQGTPIK 1389 1390 FDNNS-GQSAIKHNVKSLITGP----SKLSRGM-PPLEIVPENIKVVERGKYEDVKAGET 1443 1444 VRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTS 1503 1504 DVTIPPNKSTNHERKSTLTPT-ORESIPAK-SPVPGVDPVVSHSPFDPHHRGSTAGEVYW 1561 1562 SHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITSQ 1621 -----SR 2319 1622 OMQVNLRPDVA---RGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRI 1678 2320 PIQSPGRNSISPGRNGISPPNK------LSQLPRT-SSPSTASTKSSGSGKM 2364 1679 TYIPGTQITFPPRPYNSASMSPGHPTHLAAAASAERERERERE-------KERER 1726 2365 SY-----TSPGROMSQONLT--KQTGLSKNASSIPRSESASKGLNOMNNGNGANKKVEL 2416 1727 ERIAAASSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITP 1786 2450 --PILR-RKLEESASFESLS---PSSRPASPTRSQAQTPVLSPSLPDMSLS-THSSVQAG 2502 2503 GWRKLPPNL---SPTIEYNDGRPAKRHDIAR-----SHSESPSRLPINRSGTWKREHS 2552 1905 KDKGPPPKSRYEEELRTRGKTTITAAN-----FIDVIITRQIASDKDARERGSQSSD 1956 2553 KHSSSLP--RVSTWRRTGSSSSILSASSESSEKAKSEDEKHVNSISGTKQSKENQVSAKG 2610 1957 SSSSLSSHRYE-TPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGPLH 2015 2016 HYRPQQESPSPQQQLPP------S055 2668 NPR---SGRSPIGNIPPVIDSVSEKANPNIKDSKDNQAKQNVGNGSVPM--RIVGLENRL 2722 2056 CQIITQDFARNQVSSQTPQQPPT--STFQNSPSALVST---PVRTKTSNRYSPESQAQSV 2110 ------RTMIH----IPGV-----RNSSSTSPVSKKGP 2251 1847 A--RLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAG 1904 2181 IESESKGIKGGKKVYKSLITGKVRSNSEISGOMKOPLO---ANMPSISRG-----2417 SRMSSTKSS-----GSESD------RSERPVLVRQSTFIKEAPS---------PIEDSSPEKGREEAASKGHVIYEGKSGHI-1140 QEGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGIPTEALVK-SISRM-----1080 1861 1968 1220 1186 2088 2228 2306 셤 ò 쉽 ŏ Q ŏ ρp δλ Ω δ DP OY DP OY DP 0y 0y 0y qq ò g O g y qq ò g δý q ŏ δ qq g δ 셤 à

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2723 TSFIQVD------APDQKGTEIKPGQNNPVPVSETNESPIVERT-----PFSSSSSS 2768
                                                                                     2769 KHSSPSGTVAARVTPFNY-----NPSPRKSSADSTSARPSQIP-TPVNNNTKKDS 2818
                                                      2111 HHQRP----GSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVH--EKQDS 2164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          454 QHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEK 513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  347 PEIRKQREQQE-RFQRVGQRGAGLSATIARSEH------EISEIIDGLSEQENNEK 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  396 QMRQLSVIPPMMFDAEQRRVKFINMNGLMEDPMKVYKDRQFWNVWTDHE--KEIFKDKFI 453
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Best Local Similarity 19.4%; Pred. No. 4.3e-14;
Matches 418; Conservative 281; Mismatches 797; Indels 664; Gaps
                                                                                                                                                                                           Sequence 2. Application US/08370235A
Patent No. 5910418
GENERAL INFORMATION:
APPLICANT: VOGELSTEIN, BERT
APPLICANT: HILL, DAVID E.
APPLICANT: JOHNSON, KAREN A.
TITLE OF INVENTION: ANTIBODIES AND ASSAYS FOR DERMINING
TITLE OF INVENTION: ANTIBODIES AND ASSAYS FOR DERMINING
TITLE OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRIE

21P: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/370,235A

FILING DATE: 01-0AN-1995

FILING DATE: 01-0AN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.48688
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508 9100
TELEFAX: 202 508 9299
                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1001 G STREET, N.W. CITY: WASHINGTON STREET, N.W. CITY: WASHINGTON STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202 508 9299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2843 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-370-235A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
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US-08-370-235A-2
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q	1191	QKQSFSFSKSSSGQSSKTEHMSSSSENTSTPSSNAKRONQLHPSSAQSRSGQPQKAATCK 1250
οy	615	PEPISTEPVETSRWT
Ωp	1251	VSSÍNQETIQTYCVEDTPICFSRCSSLSSLSSAEDEIGCNQTTQEADSANTLQIAEIKGK 1310
οy	654	TKSE
qq	1311	:  :   IGTRSAEDPVSEVPAVSQHPRTKSSRLQGSSLSSESARHKAVEFPSGAKSPSKSGAQTPK 1370
ΟY	689	KPREERDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSEDSPEN 740
qq	1371	SPPEHYVQETPLMFSRCTSV-SSLDSFESRSIASSVQSEPCSGMVSGIISPSDLPDSPGQ 1429
Øλ	741	AISRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDV 798
qa	1430	TMPPSRSKTPPPPPQTAQTKREVPKNKAPTAEKRESGFKQAAVNAAVQ-RVQVLPDA 1485
ΟŊ	1 664	DQQEHSAEEGSVCDPPPATKADSVDVEVRVPEN-HASKVEGDN 840
qq	1486	DILLHFATESTPDGFSCSSSLSALSLDEPFIQKDVELRIMPPVQENDNGNETESEQ 1541
ολ	841	VAQQINAQRPEPQSDNDSSATCS
qq	1542	PKESNENQEKEAEKTIDSEKDLLDDSDDDDDIEILEECIIS 1581
οy	891	GEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVI 937
đ	1582	AMPTKSSRKGKKPAQTASKLPPPVARKPSQL-PVYKLLPSQNRLQPQKHVSFT 1633
οy	938	PPMVSCTPCNIPIGTPVSGYALYQRHIKAMHE 969
qq	1634	PGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQSGEFEKRDTIPTE 1693
ολ	970	NREW]
đ	1694 (	GRSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKPFRVKKIMDQVQQA 1753
δλ	1008	QPAPHQLITNLPEGVRLPTTRPTRPPPLI
đ	1754	SASSSAPNKNQLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKNNLNAERVFSDNKD 1810
ολ	1039	SSKTTVASEKPSFIMGGSISQGTPGTYLLSHNQASYTQETP 1079
qa	1811	SKKQNLKNNSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSRND 1860
Qy	1080	KPSVGSISLGLPRQQESAKSATLPYIKQEEFSPRSQNSQPEGLJVRAQHEGVVRGTAGAI 1139
qq	1861	SLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQQSANKTQAI 1913
Qγ	1140	IPSLRGSITQGTPALPQTGIPTEALVK
qq	1914	AKQPINRGQPKPILQKQSTFPQSSKDIPDRGAATDEKLQNFAIENTPVCFSHNS 1967
ΟŊ	1186	SISRM1219
qq	1968	SLSSLSDIDQENNNKENEPIKETEPPDSQGEPSKPQASGYAFKSFHVEDTPVCFSRNSSL 2027
ΟÝ	1220	LSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPL 1269
đ	2028	SSLSIDSEDDLLQECISSAMPKKKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPD 2087
ΟŊ	1270	EGLICRALPRGSPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYPKQIKRESPPIRAFE 1329
qa	2088	VSSLH(
οy	1330	GAİTKGKPYDGITTIKEMGRSIHBIPRQDILIQESRKTPEVVQSTRPIIBGSISQGTPIK 1389
q	2140	SGISLGSPFPGERSTLETKK 2180
Qy	1390	FDNNS-GQSAIKHNVKSLITGPSKLSRGM-PPLEIVPENIKVVERGKYEDVKAGEF 1443

McKie & Beckett

: Banner, Birch, 1001 G Street, NW

STREET: 1001 G St CITY: Washington STATE: D.C.

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                                     1444 VRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTS 1503
                                                                                                                 DVTIPPNKSTNHERKSTLTPT-QRESIPAK-SPVPGVDPVVSHSPFDPHHRGSTAGEVYW 1561
                                                                                                                                    SHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITSQ 1621
                                                                                                                                                                                                                                                                   1622 QMQVNLRPDVA---RGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRI 1678
                                                                                                                                                                                                                                                                                             :| | | | : :: | | : | | SY-----TSPGRQMSNGNGANKKVEL 2416
                                                                                                                                                                                                                                                                                                                                                                                                                    1727 ERIAAASSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITP 1786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1787 LDPTAQLRIMPLPAGGPSISQGLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEA 1846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1847 A--RLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAG 1904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2503 GWRKLPPNL---SPTIEYNDGRPAKRHDIAR-----SHSESPSRLPINRSGTWKREHS 2552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1905 KDKGPPPKSRYEEELRTRGKTTITAAN-----FIDVIITRQIASDKDARERGSQSSD 1956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2553 KHSSSLP--RVSTWRRTGSSSSILSASSESSEKAKSEDEKHVNSISGTKQSKENOVSAKG 2610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2611 TWRKIKENEFSPINSTSQTVSSGATNGAESKTLIYQMAPAVSK---TEDVWVRIEDCPIN 2667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----SSQAEGMGQVPRTHRLITLADHI 2055
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                                                                           ----RNSSSSTSPVSKKGP
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GENE IN COLORECTAL CANCER IN HUMANS
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                                                                           ----RTMIH-----IPGV--
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ANAND, RAKESH
CRALSON, MARY
GRODEN, JOANNA
HEDGE, PHILIP J.
JOSLIN, GEOFF
KINZLER, KENNETH
MARKHAM, ALEXANDER F.
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Patent No. 535275
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, HANS
APPLICANT: ANNON, RAKESH
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1040 Q------SPSQNERWARPKHIIEDEIKQSEQRQSTTYPVYTESTDDKHL 1086
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1087 KFQPHFG-----QQECVSPY----RSRGANGSETNRVGSNHGINQNVSQSLCQE-
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                                                                                                                SUFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/741,940
FILING DATE: 19920109
CLASSIFICATION
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                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTONEY AGENTION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REPERENCE/DOCKET NUMBER: 1107.035574
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
COUNTRY: USA
ZIP: 20001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2842 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                          202-508-9299
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STRANDEDNESS: single
TOPOLOGY: linear
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CLONE: APC
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741 ATSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDV 798 	DQQEHSAEEGSVCDPPPATKADSVDVEYRVPEN-HASKVEGDN	841 TKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDVD 890     :::   :  :  :  :  :  :  :  :  :  :	891GEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVIP 938 :  :	ALYORHIKAMHES ::: IIESPPNELAAGEGVRGGAOSGEFERRDIIPTEG	ALLEEQRQRQEQIDLECRSSTSPCGTSKSPNREWEVL	QPAPHQLITNLPEGVRLPTTRPTRPPPLIPS                     ASSAPNKNQLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKNNLNAERVFSDNKD	1040 SKTTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQETPK 1080	1081 PSVGSISLGLPRQQESAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVRGTAGAIQ 1140                         1 1860 -SLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQQSANKTQAIA 1913	1141 EGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGIPTEALVKGS 1186	1187 ISRM	1220 -LSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPLE 1270	1271 GLICRALPRGSPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYPKQIKRESPPIRAFEG 1330 101	1331 AITKGKPYDGITTIKEMGRSIHEIPRODILIQESRKTPEVVOSTRPIIEGSISOGTPIKF 1390 11	1391 DNNS-GQSAIKHNVKSLITGPSKLSRGM-PPLEIVPENIKVVERGKYEDVKAGETV 1444 ::	1445 RSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTSD 1504	1505 VTIPPNKSTNHERKSTLTPT-QRESIPAK-SPVFGVDPVVSHSPFDPHHRGSTAGEVYWS 1562 1	1563 HLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTLLNDYITSQQ 1622 	1623 MQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRIT 1679
Oy Db	Q Pb	Oy Dp	Q D	6 6	Oy Dp	Oy Dp	9 0	Qy Db	Q Q	Oy Dp	OY Db	oy Db	oy B	oy Op	9. Pb	Oy Op	Q.	οy

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-------LSQLPRT-SSPSTASTKSSGSGKMS 2364
                                                      GHPTHLAAAASAERERERERE------KERERE 1727
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                  ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTARTION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.46943
                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 202-508-9100
                                                                                                                                                          TELEFAX: 202-500-522
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2842 amino acids
                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: APC
US-08-289-548A-7
                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
CLASSIFICATION: 435
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δλ	939PMVSCTPCNIPIGTPVSGYAL	YQRHIKAMHES 970
q	1634 GDDMPRVYCVEGTPINFSTATSLSDLTI	ESPPNELAAGEGVRGGAQSGEFEKRDTIPTEG 1693
ΟŊ	971 AL	ISPCGTSKSPNREWEVL 1007
q	Db 1694 RSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKPFRVKKIMDQVQQA	AMPKGKSHKPFRVKKIMDQVQQAS 1753
δy	QY 1008QPAPHQLIINLPEGVRLPTTRPTRPPPPLI	1039 1039
QQ	Db 1754 ASSSAPNKNQLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKNNLNAERVFSDNKDS	RVRKNADSKNNLNAERVFSDNKDS 1810
QY	1040	QGTPGTYLTSHNQASYTQETPK 1080
qa	Db 1811 KKONLKNNSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTP	PIEGTPYCFSRND 1859
QY	1081	LVRAQHEGVV
qq	Db 1860 -SLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTE	SHTELTSNQQSANKTQAIA 1913
ΟŊ	1141 EGSITRGTPTSKISVESIPSLRG	IPTEALVKGS 1186
đ	1914 KQPINRGQPKPILQKQS	TFPQSSKDIPDRGAATDEKLQNFAIENTPVCFSHNSS 1967
δλ	1187 ISRMPIEDSS	VIYEGKSGHI 1219
QQ	Db 1968 LSSLSDIDQENNNKENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSL	SGYAPKSFHVEDTPVCFSRNSSLS 2027
δy	1220 -LSYDNIKNAREGTRSPRTAHEI	SLKRSYESVEGNIKQGMSMRESPVSAPLE 1270
qq	Db 2028 SLSIDSEDDLLQECISSAMPKKKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDS	PRNMGGILGEDLTLDLKDIQRPDS 2087
٥y	QY 1271 GLICRALPRGSPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYPKQIKRESPPIRAFEG	SFEDGLKYPKQIKRESPPIRAFEG 1330
q	Db 2088 EHGLSPDSENFDWKAIQEGANSIVSSLHQAAAAAC-	ACLSRQASSDSDSILSLKS 2139
Οy	1331 AITKGKPYDGITTIKEMGRS	IPEVVQSTRPIIEGSISQGTPIKF 1390
q	Db 2140 GISLGSPFHLTPDQEERPFTSNKGPRILK-	SPRILKPGEKSTLETKKI 2180
οy	1391 DNNS-GOSAIKHNVKSLITGP	SKLSRGM-PPLEIVPENIKVVERGKYEDVKAGETV 1444
q	Db 2181 ESESKGIKGGKKVYKSLITGKVRSNSEISGQMKQPLQ	2ANMPSISRG 2226
ΟŊ	1445 RSRHTSVVSSGP	SVLRSTLHEAPKAQLSPGIXDDTSARRTPVSYQNTMSRGSPMMNRTSD 1504
qq	2227RTM	RNSSSSTSPVSKKGPP 2251
οy	1505	DPVVSHSPFDPHHRGSTAGEVYWS 1562
qq	2252	:
Qy	QY 1563 HLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITSQQ	SQYQLYAMENTRQTILNDYITSQQ 1622
q	2305	AQQPLSRP 2319
Qy	1623 MQVNLRPDVA	-RGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRIT 1679
qq	2320 IQSPGRNSISPGRNGISPPNK	LSQLPRI-SSPSTASTKSSGSGKMS 2364
οy	1680 YIPGTQITFPPRPYNSASMSP	REREREKERERE 1727
qq	2365 YTSPGRQMSQQNLT-	- KQTGLSKNASSIPRSESASKGLNQMNNGNGANKKVELS 2416
δy	1728	ZETMLQQRPSVFQGTNGTSVITPL 1787
qq	2417	-RSERPVLVRQSTFIKEAPS 2448
δy	1788 DPTAQLRIMPLPAGGPSISQG	CVDAAASAPQMDVSKTKESKHEAA 1847
qq	2449 -PTLR-RKLEESASFESLS	-PSSRPASPTRSQAQTPVLSPSLPDMSLS-THSSVQAGG 2502

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                                                                                                                                   SSSLSSHRYE-TPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGPLHH 2016
1848 --RLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGK 1905
                                                                 1906 DKGPPPKSRYEEELRTRGKTTITAAN-----FIDVIITRQIASDKDARERGSQSSDS 1957
                                                                                                                                                         2017 YRPQQESPSPQQQLPP-------S050AEGMGQVPRTHRLITLADHIC 2056
                                                                                                                                                                                                                              2057 QIITQDFARNQVSSQTP-QQPPTSTFQNSPSALVS-TPVRTKTSNRYSPESQAQSVHHQR 2114
                                2503 WRKLPPNL---SPTIEYNDGRPAKRHDIAR-----SHSESPSRLPINRSGTWKREHSK
                                                                                     2553 HSSSLP--RVSTWRRTGSSSSILSASSESSEKAKSEDEKHVNSISGTRQSSKENQVSAKGT
                                                                                                                                                                                                                                                                                             2723 SFIQVDAPDQKGTEIKPGQNNPVPVSETNESSIVERTPFSSSSSKHSSPSGTVA----
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                                                                                                                                                                                                                                                                                                                                                                  2778 -- ARVIPFNY------NPSPRKSSADSTSARPSQIP-IPVNNNTKKRDS 2817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CARLSON, MAXY
APPLICANT: GRODEN, JOANNA
APPLICANT: GRODEN, JOANNA
APPLICANT: JOSLYN, GEOFE
APPLICANT: MARKHAM, GEOFE
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: THILYPERIS, WHOREM
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 25-MAY-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION:
TELEPHONE: 202-508-9100
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APPLICATION NUMBER: US 07/741,940
FLILNG DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-452-654-7; Sequence 7, Application US/08452654; Sequence No. 5691454; Patent No. 5691454; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Kagan, Sarah A. REGISTRATION NUMBER: 32,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALBERTSEN, HANS
ANAND, RAKESH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2842 amino acids
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ADDRESSEE: Banner, B
STREET: 1001 G Stree
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COMPUTER READABLE FORM:
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COUNTRY:
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| 1310 IGTRSAEDPVSEVPAVSQHPRTKSSRLQGSSLSSESARHKAVEFSSGAKSPSKSGAQTPK 1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 980 PSIESYSEDDESKFCSYGOYPADLAHKIHSANHMDDNDGELDTPINYSLKYSDEOLNSGR 1039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1370 SPPEHYVQETPLMFSRCTSV-SSLDSFESRSIASSVQSEPCSGMVSGIISPSDLPDSPGQ 1428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1581 AMPTKSSRKAKKPAQTASKLPPPVAR-----KPSQLPVYKLLPSQNRLQPQKHVSFTP 1633
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                                                                                                                                                                                                                                                                                                                                                                                                                                          347 PEIRKQREQQE-RFQRVGQRGAGLSATIARSEH------EISEIIDGLSEQENNEK 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    396 QMRQLSVIPPMMFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHE--KEIFKDKFI 453
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                                                                                                                                                                                                                                                                                                                                                                                       Indels 648; Gaps
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                                                                                                                                                                                                                                                                                                                          Length 2842;
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                                                                                                                                                                                                                                                                                                                   Query Match 2.9%; Score 365; DB 1; L. Best Local Similarity 19.0%; Pred. No. 6.6e-14; Matches 409; Conservative 288; Mismatches 807;
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                       TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                        IMMEDIATE SOURCE
STRANDEDNESS:
                                                                                                                                                                                             ; CLONE: 1
US-08-452-654-7
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8	RESULT US-08- 1. Sequ Pate Pate N A A A A A A A A A A A A A A A A A A A	44 44 F F Z O		G. G. &.	I INF	; ; M US-08- Quer Best Matc
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1080 1859 1140 1913 1186	1219 2027 1270 2087 1330 2139	1390 2180 1444 2226 1504 2251	1562 2304 1622 2319			1957 2610 2016 2667
1040 SKTTVASEKPSF	1187 ISRMPIEDSSPEKGREEAASKGHVIYEGKSGHI	1331 AITKGRPYDGITTIKEMGRSIHEIPRQDILTQESRKTPEVVQSTRPIIEGSISQGTPIKF	1505 VTIPPNKSTNHERKSTLTPT-QRESIPAK-SPYPGVDPVVSHSPEDPHHRGSTAGEVYWS  1   1   1   1   1   1   1   1   1   1		DPTAQLRIMPLPAGGPSISGGLPASR     :   :   :   :   :	1906 DKGPPPKSRYEEELRTRGKTTITAANFIDVIITRQIASDKDARERGSGSSDS 1957
04 04 04 04	6 6 6 6 6	60 60 60 60 60 60 60 60 60 60 60 60 60 6	6 6 6 6	6 6 6 6 6	6 6 6 6	40 A

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-----SSQAEGMGQVPRTHRLITLADHIC 2056
                                                                                                                                                                                                                                                                                    2057 QIITQDFARNQVSSQTP-QQPPTSTFQNSPSALVS-TPVRTKTSNRYSPESQAQSVHHQR 2114
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APPLICANT: THLYTERIS, ANDREW
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APPLICANT: THLYTERIS, ANDREW
APPLICANT: THLYTERIS, ANDREW
ANDRESSE: 102
CORRESPONDENCES: 102
CORRESPONDENCE ADDRESS: 102
CORRESPONDENCE ADDRESS: 102
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APPLICANT: ALBERTSEN, HANS
APPLICANT: ANAND, RAKESH
APPLICANT: GRODEN, JOANNA
APPLICANT: HEDGE, PHILIP J.
APPLICANT: JOSLYN, GEOFF
APPLICANT: KINZLER, KENNETH
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: MARKHAM, ALEXANDER F.
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ent No. 5783666
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TELEFAX: 202-508-9299
2017 YRPQQESPSPQQQLPP----
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-452-655B-2
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3 8	306	FOLESTOSEUDESAR COTOGET FAULARIA LASANARMUUNUGELUTYLATA SLATSUEQLNÖGK. OMBOT CYTEDDMMEDNARODEDUYETANANGT MEDIDMYTYGYDDARARIIMAHIB YRTTRANAFIT
5 g	1041	
ογ	454	QHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEK 513 : :
g	1088	KFQPHFGQQECVSPYRSRGANGSETNRVGSNHGINQNVSGSLCQE-1132
کا را د	514	VEEKEEDKAEKTEKKEEEKKDEEKDEKEDSKENTKEKDKIDGTAEETEEREQATPRG 571 ::       :       :         :         :
3 8	573	IEDUNKINISEKISEEEQNEEEEKRINISININ EERKHVUQVIDISLKIAIDIKSS
<u>8</u> 5	1191	FS
ò	615	PEPISTEPVETWAALAKM 653
q	1251	VSSINQETIQTYCVEDTPICFSRCSSLSSLSSAEDEIGCNQTTGEADSANTLQIAEIKEK 1310
Oy	654	VGTKSEQCKNFYFNYKRRHULDNLLQQHKQKTSR 688
g	1311	SAEDPV
oy D	689	KPREERDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSEDSPEN 740
}	741	
<u>2</u> 8	1430	A-TSANGNIERAVELEPTIETAPSISPELAVETIKPÄEDESVETQVNDSISAETAEQMDV /98 
οy	799	DQQEHSAEEGSVCDPPPATKADSVDVEVRVPEN-HASKVEGDN 840
g	1486	DILLHFATESTPDGFSCSSSLSALSLDEPFIQKDVELRIMPPVQENDNGNETESEQ 1541
οχ	841	/AQQINAQRE
q	1542	PKESNENOEKEAEKTIDSEKDLLDDSDDDDIEILEECIIS 1581
δy	891	GEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVIP 938
Q	1582	AMPTKSSRKAKKPAQTASKLPPPVARKPSQLPVYKLLPSQNRLQPQKHVSFTP 1634
ογ	939	PMVSCTPCNIPIGTPVSGYAL
Д	1635	GDDMPRVYCVECTPINESTATSLSDLTIESPPNELAAGEGVRGGAQSGEFEKRDTIPTEG 1694
δy	971	AL
q	1695	RSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKPFRVKKIMDQVQQAS 1754
οy	1008	
a	1755	ASSSAP
ογ	1040	
g	1812	KKQNLKNNSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSRND 1860
οy	1081	PSVGSISLGLPRQQESAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVRGTAGAIQ 1140
g	1861	-SLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQQSANKTQAIA 1914
ογ	1141	Д
a	1915	KQPINRGQPKPILQKQSTFPQSSKDIPDRGAATDEKLQNFAIENTPVCFSHNSS 1968
δ	1187	ISRMPIEDSSPEKGREEAASKGHVIYEGKSGHI 1219

E---HGLSPDSENFDWKAIQEGANSIVSSLHQAAAAAC----LSRQASSDSDSILSLKS 2140 :| : | : | : | : | : | III |: ISSLSDIDQENNNKENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLS 2028 --IKNAREGTRSPRTAHEISLKRSYESVEGNIKQCMSMRESPVSAPLE 1270 1271 GLICRALPRGSPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYPKQIKRESPPIRAFEG 1330 2321 IQSPGRNSISPGRNGISPPNK------LSQLPRT-SSPSTASTKSSGSGKMS 2365 AITKGKPYDGITTIKEMGRSIHEIPRQDILIQESRKTPEVVQSTRPIIEGSISQGTPIKF 1390 DNNS-GQSAIKHNVKSLITGP----SKLSRGM-PPLEIVPENIKVVERGKYEDVKAGETV 1444 1445 RSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTSD 1504 -----RNSSSSTSPVSKKGPP 2252 1505 VTIPPNKSTNHERKSTLTPT-QRESIPAK-SPVPGVDPVVSHSPFDPHHRGSTAGEVYWS 1562 1563 HLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITSQQ 1622 ----DSTPSRPAQQPL-----SRP 2320 MQVNLRPDVA---RGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRIT 1679 YIPGTQITFPPRPYNSASMSPGHPTHLAAAASAERERERERE------KERERE 1727 Y-----TSPGRQMSQONLT--KQTGLSKNASSIPRSESASKGLNQMNNGNGANKKVELS 2417 RIAAASSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPL 1787 RMSSTKSS----GSESD----- ZA49 DPTAQLRIMPLPAGGPSISQGLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAA 1847 --RLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGK 1905 1958 SSSLSSHRYE-TPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGPLHH 2016 2612 WRKIKENEFSPINSTSQIVSSGAINGAESKTLIYQMAPAVSK---TEDVWVRIEDCPINN 2668 ----SSQAEGMGQVPRTHRLITLADHIC 2056 DKGPPPKSRYEEELRTRGKTTITAAN-----FIDVIITRQIASDKDARERGSQSSDS 1957 2669 PR---SGRSPTGNTPPVIDSVSEKANPNIKDSKDNQAKONVGNGSVPM--RTVGLENRLN 2723 2057 QIITQDFARNQVSSQTP-QQPPTSTFQNSPSALVS-TPVRTKTSNRYSPESQAQSVHHQR 2114 2554 HSSSLP--RVSTWRRTGSSSSILSASSESSEKAKSEDEKHVNSISGTKQSKENQVSAKGT 2724 SFIQVDAPDQKGTEIKPGQNNPVPVSETNESSIVERTPFSSSSSSKHSSPSGTVA----2115 PGSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVH--EKQDS 2164 2017 YRPQQESPSPQQQLPP-----LSYDN----1969 1220 2089 1331 1391 2253 1623 1680 2366 1728 2418 1788 2450 1848 1906 2228 2306 2779 δ δŏ g 셤 δ 6 Q ò 8 δ QQ δ g δŏ g g οχ g g g g g Db ò ŏ δ ò οý à Qγ ò a Qy g

RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2843;
                                                                                                                                                                                                                                     TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.9%; Score 365; DB 1;
Best Local Similarity 19.0%; Pred. No. 6.6e-14;
Matches 409; Conservative 288; Mismatches 807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PELLING DATE: 25-MAY-1995
CLASSIFICATION NUMBER: US/08/452,655B
FILING DATE: 25-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,548
FILING DATE: 12-AUG-1994
PRIOR APPLICATION NUMBER: US 08/289,548
FILING DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                       ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, NW
CITY: Washington
Sequence 7, Application US/08452655B Patent No. 5783666 GENERAL INFORMATION:
                                                                                                                                                                                   MARKHAM, ALEXANDER F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32,141
                                                     ALBERTSEN, HANS
ANAND, RAKESH
CARLSON, MARY
GRODEN, JOANNA
HEDGE, PHILIP J.
JOSILYN, GEOFF
KINZLER, KENNETH
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THLIVERIS, ANDREW
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INFORMATION FOR SEQ ID NO: 7:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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US-08-452-655B-7
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1251 VSSINQETIQTYCVEDTPICFSRCSSLSSLSSAEDEIGCNQTTQEADSANTLQIAEIKEK 1310
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                                                                                                                                                                                                                                        1191 OKOSFSFSKSSSGOSSKTEHMSSSSENTSTPSSNAKRONQLHPSSAQSRSGOPOKAATCK 1250
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514 VEEKEEDKAEKTEKK--EEEKKDEEEKDEKEDSKENTKEKDKIDGTAEETEEREQATPRG 571
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                                                                                                                                                                   1391 DNNS-GQSAIKHNVKSLITGP----SKLSRGM-PPLEIVPENIKVVERGKYEDVKAGETV 1444
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                                                                             2141 GISLGSPF-----PGEKSTLTSNKGPRILK-----PGEKSTLETKKI
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US-08-450-582-2
; Sequence 2, Application US/08450582
; Patent No. 6114124
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GRODEN, JOANNA
HEDGE, PHILIP J.
JOSLYN, GEOFF
KINZLER, KENNETH
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ANAND, RAKESH
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APPLICANT: ALBERT
APPLICANT: ANAND,
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APPLICANT: G
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KFQPHFG------QQECVSPY----RSRGANGSETNRVGSNHGINQNVSQSLCQE-1132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    396 QMRQLSVIPPMAMFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHE--KEIFKDKFI 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  347 PEIRKQREQQE-RFQRVGQRGAGLSATIARSEH------EISEIIDGLSEQENNEK 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      454 QHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEK 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          514 VEEKEEDKAEKTEKK--EEEKKDEEEKDEKEDSKENTKEKDKIDGTAEETEEREQATPRG 571
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Matches 409; Conservative 288; Mismatches 807; Indels 648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.9%; Score 365; DB 3; Length 2843;
19.0%; Pred. No. 6.6e-14;
APPLICANT: NAKAMUKA, 1000...
APPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS (
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUM
                                                                                                                                                                                                                                                                                                                                                                                                            Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: RAGAN, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.49964
TELEPHONE: 202-508-9190
TELEPHONE: 202-508-9199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/452,655
FILING DATE: 25-MAY-1995
APPLICATION NUMBER: US 08/289,548
FILING DATE: 12-AUG-1994
                                                                                                                      STREET: 1001 G Street, NW CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,582
                                                                                                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                   TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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ΟŸ	654	VGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSR 688	-
qq	1311	:  :    IGTRSAEDPVSEVPAVSQHPRTKSSRLQGSSLSSESARHRAVEFSSGAKSPSKSGAQTPK 1370	
QY	689		,
<b>Q</b> :	1371		
g 5	1430	ATSKANIERAVELERTTETARSTSPSTARVETKAEDESVETQVNDSLSAETARGNDV 798 	
οy	799	DQQEHSAEEGSVCDPPPATKADSVDVEVRVPEN-HASKVEGDN 840	
qq	1486		
oy .	841	TKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDVD	
a d	1542	PKESNENQEKEAEKTIDSEKDLLDDSDDDSDDDSD	
දු පු	1582	GEPERQRAMFPMDSKPSLINPTGSILVSSPLKPPRLDLPQLQHRAAVIP 938GE	
δλ	939	PMVSCTPCNIPIGTPVSGYALYORHIKAMHES 970	
Q	1635	GDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQSGEFEKRDTIPTEG 1694	
Qy	971	AL	
QD	1695	RSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKPFRVKKIMDQVQQAS 1754	
δλ	1008	QPAPHQLITNLPEGVRLPTTRPTRPPPLI	
Q	1755	ASSSAPNKNQLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKNNLNAERVFSDNKDS 1811	
δy	1040	SKITVASEKBSFIMGGSISQGTPGTYLTSHNQASYTQETPK 1080	
qq	1812	KKONLKNNSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSRND 1860	
Oy	1081	PSVGSISLGLPRQQESAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVRGTAGAIQ 1140	
qq	1861	-SLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQQSANKTQAIA 1914	
δλ	1141	EGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGIPTEALVKGS 1186	
QQ	1915	KQPINRGQPKPILQKQSTFPQSSKDIPDRGAATDEKLQNFAIENTPVCFSHNSS 1968	•
οy	1187	ISRM	
Op	1969	LSSLSDIDQENNNKENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLS 2028	
Qy	1220	-LSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPLE 1270	
qq	2029	SLSIDSEDDLLOECISSAMPKKKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDS 2088	
δλ	1271	GLICRALPRGSPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYPRQIKRESPPIRAFEG 1330	
QQ	2089	EHGLSPDSENFDWKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKS 2140	
οy	1331		
QQ	2141	GISLGSPFHLTPDQEERPFTSNKGPRILKPGEKSTLETKKI 2181	
Qy	1391		
qq	2182	ESESKGIKGGKKVYKSLITGKVRSNSEISGQMKQPLQANMPSISRG 2227	
δy		RSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTP  : :	
Ω	222B	RTMIHIPGVRNSSSSTSPVSKKGPP 2252	_

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2253 LKTPASKSPSEGQTATTSPRGAKPSVKSELSPVARQTSQIGGSSKAPSRSGSR----- 2305
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                                                                                        1563 HLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITSQQ 1622
                                                                                                                                   -----SRP 2320
                                                                                                                                                                              1623 MQVNLRPDVA---RGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRIT 1679
                                                                                                                                                                                                                                                                                                      2366 Y-----TSPGRQMSQQNLT--KQTGLSKNASSIPRSËSASKGLNQMNGNGANKKVELS 2417
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APPLICANT: ALBERTSEN, HANS
APPLICANT: CARLSON, MARY
APPLICANT: GARLSON, MARY
APPLICANT: GROEF, PHILIP J.
APPLICANT: MIXLER, KENNETH
APPLICANT: MIXLER, KENNETH
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2779 -- ARVIPENY------NPSPRKSSADSTSARPSQIP-TPVNNNTKKRDS 2818
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STREET: 1001 G Street, NW
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Sequence 7, Application US/08450582
Patent No. 6114124
GENERAL INFORMATION:
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CITY: Washington
STATE: D.C.
COUNTRY: USA
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| 1311 IGTRSAEDPVSEVPAVSQHPRTKSSRLQGSSLSSESARHKAVEFSSGAKSPSKSGAQTPK 1370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  514 VEEKEEDKAEKTEKK--EEEKKDEEEKDEKEDSKENTKEKDKIDGTAEETEEREQATPRG 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      615 PEPISTEPVET-----WAAIAKM 653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          572 R-----KTANSQGRRKGRITRSMTNEAAAAS------AAAAAATEEPPPPLPPP 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                347 PEIRKQREQQE-RFQRVGQRGAGLSATIARSEH------EISEIIDGLSEQENNEK 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1088 KFQPHFG------QQECVSPY----RSRGANGSETNRVGSNHGINQNVSQSLCQE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       807; Indels 648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2843;
                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.9%; Score 365; DB 3; Best Local Similarity 19.0%; Pred. No. 6.6e-14; Matches 409; Conservative 288; Mismatches 807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGTKSE-----AQCKNFYFNYKRRHNLDNLLQQHK---
                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/452,655
FILING DATE: 25-MAY-1995
PILING DATE: 12-AG-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AGG-1991
ATTONNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
                                                                                                                                                                                                                                                                                                                                                                         NAME: Kagan, Sarah A. RECISTRATION NUMBER: 32,141
REFERNCE/DOCKET NUMBER: 1107.49964
TELECOMMUNICATION: TELEPHONE: 202-508-9100
                             PC-DOS/MS-DOS
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2843 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
YES
                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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; ANTI-SENSE: NO
US-08-450-582-7
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1081 PSVGSISLGLPRQQESAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVRGTAGAIQ 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1635 GDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAOSGEFEKRDTIPTEG 1694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1755 ASSSAPNK---NOLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKNNLNAERVFSDNKDS 1811
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                                                                                                                                                                                                                                                                                                                                                                1582 AMPTKSSRKAKKPAQTASKLPPPVAR-----KPSQLPVYKLLPSQNRLQPQKHVSFTP 1634
741 A--TSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDV 798
                                                   1430 TMPPSRSKTPPP---PPQTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQ-RVQVLPDA
                                                                                                    DQQEHSAEE----GSVC-----DPPPATKADSVDVEVR----VPEN-HASKVEGDN
                                                                                                                                                                                                                                                            1542 PKESNENQEKEAEKTIDSEKDLL------DDSD-----DDDDIEILEECIIS
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1812 KKQNLKNNSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTP--YCFSRND------
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---KERERE 1727
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                                                                                                 2366 Y-----TSPGROMSQONLT--KOTGLSKNASSIPRSESASKGLNOMNNGNGANKKVELS
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                                                           1680 YIPGTQITFPPRPYNSASMSPGHPTHLAAAASAEREREREF
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SOFTWARE: FastSEQ for Windows Version 2.0
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..yelstein, Bert
...tllCANT: Sparks, Andrew
TITLE OF INVENTION: Beta Catenin, TC
TITLE OF INVENTION: Interact to Preve
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner
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APPLICATION NUMBER: US/08/821,355A
FILING DATE: 20-MAR-1997
CLASSIFICATION: 514
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Patent No. 5851775
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APPLICANT: Barker, Nick
APPLICANT: Clevers, Hans
APPLICANT: Korinek, Vladimir
APPLICANT: Morin, Patrice
APPLICANT: Knicer, Kenneth
APPLICANT: Sparks, Andrew
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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APPLICATION NUMBER:
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US-08-821-355A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.9%; Score 365; DB 2; Length 2973;
Best Local Similarity 19.0%; Pred. No. 7.1e-14;
Matches 409; Conservative 288; Mismatches 807; Indels 648; Gaps
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                                            NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32,145
REFERENCE/DOCKET NUMBER: 1107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELERX: 97430 BMB UT
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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FILING DATE: ATTORNEY/AGENT INFORMATION:
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; 음	RSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKPFRVKKIMDQVQQAS	DD 2554 HSSSLP-
ογ	1008 QPAPHQLITNLPEGVRLPTTRPTRPPPLI	1958
ą	1755 ASSSAPNKNQLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKNNLNAERVFSDNKDS 1811	7107
දු පු	1040 SKTTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQETPK 1080   :	Db 2669 PRSGR
δλ	PSVGSISLGLPRQQESAKSATLPYIKQEEFSPRSQNSQPBGLLVRAQHEGVVRGTAGAIQ  :  :	Qy 2057 QIITQDFP   1   Db 2724 SFIQVDAE
g	-SLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQQSANKTQAIA	
දු පු	1141 EGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGIPTEALVKGS 1186  1       : :   : :   : :     : :       : : :         : : :         : :	2779
S G	1187 ISRM PIEDSSPEKGREEAASKGHVIYEGKSGHI 1219 	RESULT 15 US-09-003- <b>687A-7</b> ; Sequence 7, Appl
ογ		; Patent No. 59986 ; GENERAL INFORM; : APPLICANT: E
අ	2029 SLSIDSEDDLLQECISSAMPKKKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDS 2088	APPLICANT
S G	1271 GLICRALPRGSPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYPKQIKRESPPIRAFEG 1330 2089 EHGLSPDSENFDWKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKS 2140	APPLICANT: P APPLI
λ 6	VVQSTRPIIEGSISQGTPIKF :::         ILKPGEKSTLETKKI	APPLICANT: 5 TITLE OF INVE TITLE OF INVE NUMBER OF SEC
è e	IKVV)	CORRESPONDENC CADDRESSEE: CATREET: 10 CITY: Wash
ž f	1445 RSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRIPVSYQNTMSRGSPMMNRTSD 1504   :	STATE: DC     STATE: DC
े हें	VIIPPNKSTNHERKSTLTPT-QRESIPAK-SPVPGVDPVVSHSPFDPHHRGSTAGEVYWS	COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER:
3 6 8	HLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITSQQ 	CURRENT APPLI CURRENT APPLI APPLICATION FILING DATE CLASSIFICAL
oy Oy	TILVPHPGGTSTPPMDRIT	PRIOR APPLICA APPLICATION FILING DATE ATTORNEY/AGEN
O.y	1680 YIPGTQITFPPRPYNSASMSPGHPTHLAAAASAEREREREKERERE 1727	) NAME: Kaga ; REGISTRATIC ; REFERENCE/E ; TELECOMMUNICA
<u>ک</u> ۾	1728 RIAAAASSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVPQGTNGTSVITPL 1787                           1	; TELEPHONE: ; TELEFAX: 2 ; TELEX: 974 ; INFORMATION FOR
oy Op	1788 DPTAQLRIMPLPAGGPSISQGLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAA 1847 1	; SEQUENCE CHAR; ; LENGTH: 29 ; TYPE: amin ; STRANDEDNES
à g	1848RLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGK 1905 1	; TOPOLOGY: ; MOLECULE TYPE US-09-003-687A-7
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--RVSTWRRTGSSSSILSASSESSEKAKSEDEKHVNSISGTKQSKENQVSAKGT 2611
                                                                                      IRYE-TPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGPLHH 2016
                                                                                                                                      -----SSQAEGMGQVPRTHRLITLADHIC 2056
KSRYEEELRTRGKTTITAAN-----FIDVIITRQIASDKDARERGSQSSDS 1957
                                                                                                                                                                                                         FARNQVSSQTP-QQPPTSTFQNSPSALVS-TPVRTKTSNRYSPESQAQSVHHQR 2114
                                                                                                                                                                                                                                                                                             PENLVDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVH--EKQDS 2164
                                                                                                                                                                                                                                                                                                                                                                                                                                                Barker, Nick

Clevers, Hans

Clavers, Hans

Corinek, Vladimir

Morin, Patrice

Kinzler, Kenneth

Vogelstein, Bert

Sparks, Andrew
INVENTION: Beta Catenin, TCF-4, and APC
INVENTION: Interact to Prevent Cancer

SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYSTEM: DOS
FastSEO for Windows Version 2.0
LICATION DATA:
ON NUMBER: US/09/003,687A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agan, Sarah A
TION NUMBER: 32,145
TE/DOCKET NUMBER: 1107.05064
TICATION INFORMATION:
TE: 202-508-9100
97430 BMB UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCES: 11
BNCE ADDRESS:
E. Banner & Witcoff, Ltd.
1001 G Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATION:
ICATION DATA:
ION NUMBER: 08/821,355
ATE: 20-MAR-1997
GENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              plication US/09003687A
8600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TADABLE FORM:
TPE: Diskette
: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SS: single
linear
PE: No. 5998600e
                                                                                                                                      SPSPQQQLPP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARACTERISTICS:
2973 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  no acid
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OHZ	Query Ma Best Loc Matches	<pre>// Match 2.9%; Score 365; DB 2; Length 2973; Local Similarity 19.0%; Pred. No. 7.1e-14; hes 409; Conservative 288; Mismatches 807; Indels 648; Gaps 94;</pre>	
Óλ	347	PEIRKQREQQE-REQRYGQRGAGLSATIARSEHEISEIIDGLSEQENNEK 395	
g	981	PSIESYSEDDESKECSYGQYPADLAHKIHSANHMDDNDGELDTPINYSLKYSDEQLNSGR 1040	
δŏ.	396	QMRQLSVIPPMMFDAEQRRVKFINMNGLMEDPMKVXKDRQFMNVWTDHEKEIFKDKFI	
Q Q	1041		
oy Oy	1088	QHPKNFGLIASYLERKSVPDCVLYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEK 513 :	
ÓΫ	514	VEEKEEDKAEKTEKKEEEKKDEE	
qq	1133	-:  :   :   :   :     :   -   -   -   -	
δŏ	572	RKTANSQGRKKGRITRSMINEAAAASAAAAATEEPPPPLPPP :         : :   : :   : :   : :	
qq	1191	QKQSFSFSKSSGQSSKTEHMSSSSENTSTPSSNAKRQNQLHPSSAQSRSGQPQKAATCK 1250	
Qy Db	615 1251	PEPISTEPVETWAAIAKM 653	
δ	654	VGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSR 688	
qq	1311	:    :     :	
S S	689	KPREERDVSQCESVASTVSAQEDEDIEASNEEBNPEDSEVEAVKPSEDSPEN	
3	13/1	SFFERT VQETFLMF SKCTSV - SSLDSFESKSTASSVQSEFCSGMVSGTLSFSDLFUSFGQ	
o S	741	ATSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDV 798	
ογ	799	DQQEHSAEEGSVCDPPPATKADSVDVEVRVPEN-HASKVEGDN 840	
q	1486		
δλ	841	TKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSD	
QQ	1542	PKESNENQEKE	
δλ	891	GEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVIP 938	
qq	1582	AMPTKSSRKAKKPAQTASKLPPPVARKPSQLPVYKLLPSQNRLQPQKHVSTP 1634	
ογ	939	PMVSCTPCNIPIGTPVSGYALYQRHIKAMHES 970	
QQ	1635	GDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQSGEFEKRDTIPTEG 1694	
οy	971	AL	
qq	1695	RSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKPFRVKKIMDQVQQAS 1754	
οχ	1008	OPAPHQLITNLPEGVRLPTTRPTRPPPPLI	
qq	1755	ASSSAPNKNQLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKNNLNAERVFSDNKDS 1811	
Qy	1040	SKTTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQETPK 1080	
qq	1812	KKONLKNNSKDFNDKLPNNEDRVRGSFAFDSPHHYTPI	
οy	1081		
ą	1861	-SLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQQSANKTQAIA 1914	

δ ć	1141	EGSITRGIPTSKISVESIPSLEGSITQGTPALPQTGIPTEALVKGS 1186
3 8	1107	DIENCEDENZA CONTRACTOR DE LA CONTRACTOR
S Q	1969	LENGUATE PER PER PER PER PER PER PER PER PER PE
οy	1220	-LSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPLE 1270
ф	2029	SISIDSEDDILQECISSAMPKKKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDS 2088
Qγ	1271	GLICRALPRGSPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYPKQIKRESPPIRAFEG 1330
g	2089	EHGLSPDSENFDWKAIQEGANSIVSSLHQAAAAACLSRQASSDSSILSLKS 2140
Qy Dp	1331	ALTKGKPYDGITTIKEMGRSIHEIPRQDILIQESRKTPEVVQSTRPIIEGSISQGTPIKF 1390   1   1   1   1   1   1   1   1   1
Qy	1391	- 1
g	2182	::
οy	1445	RSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTSD 1504
qq	2228	RIMIHIPGVRNSSSTSPVSKKGPP 2252
δy	1505	VIIPPNKSINHERKSILIPI-QRESIPAK-SPVPGVDPVVSHSPEDPHHRGSIAGEVYWS 1562
QQ	2253	LKTPASKSPSEGQTATTSPRGAKPSVKSELSPVARQTSQIGGSSKAPSRSGSR 2305
δλ	1563	HLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITSQQ 1622
qq	2306	STPSRPAQQPLSRP 2320
Qγ	1623	PLGLPYPATRGIIDLTNMPPTIL
QQ	2321	IOSPGRNSISPGRNGISPPNKLSQLPRT-SSPSTASTKSSGSGKMS 2365
δλ	1680	IPGTQITEPPRPYNSASMSPGHPTHLAAAASAERERERE
qq	2366	YTSPGRQMSQQNLTKQTGLSKNASSIPRSESASKGLNQMNNGNGANKKVELS 2417
ογ	1728	RIAAASSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPL 1787
οp	2418	RMSSTKSSGSESD
οÿ	1788	RIMPLPAGGPSISQG
qq	2450	- PTLR-RKLEESASFESLSPSSRPASPIRSQAQIPVLSPSLPDMSLS-THSSVQAGG 2503
δλ	1848	VEKRSVQCL
q	2504	WRKLPPNLSPIIEYNDGRPAKRHDIARSHSESPSRLPINRSGTWKREHSK 2553
δy	1906	DKGPPPKSRYEEELRTRGKTTITAANFIDVIITRQIASDKDARERGSQSSDS 1957
qq	2554	HSSSLPRVSTWRRTGSSSSILSASSESSEKAKSEDEKHVNSISGTKQSKENQVSAKGT 2611
ΟŊ	1958	SSSLSSHRYE-TPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQAENDFTRQYEGPLHH 2016
QQ	2612	
δλ	2017	YRPQQESPSPQQQLPPSOQESPSPQQVPRTHRLITLADHIC 2056
qq	2669	PRSGRSPTGNTPPVIDSVSEKANPNIKDSKDNQAKQNVGNGSVPMRTVGLENKLN 2723
δy	2057	QIIIQDFARNQVSSQIP-QQPPISTFQNSPSALVS-TPVRFKTSNRYSPESQAQSVHHQR 2114
Q	2724	SFIQYDAPDQKGTEIKPGQNNPVPVSETNESSIVERTPFSSSSSKHSSPSGTVA 2778
Qy	2115	PGSRVSPENLYDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVHEKQDS 2164

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1251 VSSINQETIQTYCVEDTPICFSRCSSLSSAEDEIGCNQTTQEADSANTLQIAEIKEK 1310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1430 IMPPSRSKTPPP---PPQTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQ-RVQVLPDA 1485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEPISTEPVET-----WAAIAKM 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGTKSE------AQCKNFYFNYKRHNLDNLLQQHK------QKTSR 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KPREE-----RDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSE--DSPEN 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    741 A--TSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDV 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         799 DQQEHSAEE----GSVC-----DPPPATKADSVDVEVR----VPEN-HASKVEGDN 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    347 PEIRKQREQQE-RFQRVGQRGAGLSATIARSEH-------EISEIIDGLSEQENNEK 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           396 QMRQLSVIPPMMFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHE--KEIFKDKFI 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            454 QHPKNFGLIASYLERKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : :| | | :: :| 1 | :: :| 1.088 KFQPHFG-----QQECVSPY----RSRGANGSETNRVGSNHGINQNVSQSLCQE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   514 VEEKEEDKAEKTEKK--EEEKKDEBEKDEKEDSKENTKEKDKIDGTAEETEEREQATPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R-----KTANSQGRRKGRITRSMTNEAAAS------AAAAAATEEPPPPLPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.9%; Score 365; DB 4; Length 2973; Best Local Similarity 19.0%; Pred. No. 7.1e-14; Matches 409; Conservative 288; Mismatches 807; Indels 648;
2779 -- ARVIPENY-------NPSPRKSSADSTSARPSQIP-TPVNNNTKKRDS 2818
                                                                                                                                                                                                                                   APPLICANT: VOGGISTAIN. Bert
TITLE OF INVENTION: Beta Catenin, TCF-4, and APC Interact to
TITLE OF INVENTION: Prevent Cancer
FILE REFERENCE: 1107.75741
CURRENT APPLICATION NUMBER: US/09/136, 605A
CURRENT FILING DATE: 1999-03-20
EARLIER APPLICATION NUMBER: 09/801, 355
EARLIER APPLICATION NUMBER: 09/903, 687
EARLIER PILING DATE: 1999-01-06
EARLIER PILING DATE: 1999-01-06
SARLIER FILING DATE: 1999-01-06
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 7
LENGH: 2973
                                                                                                                           Sequence 7, Application US/09136605A Patent No. 6140052
                                                                                                                                                                                              APPLICANT: He, Tong-Chuan APPLICANT: Kinzler, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-136-605-7
                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      654
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oy d	841 TKE 11 1542 PKE	TKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDVD	890
0y	91	SKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVI	
qq	1582 AMF	:  :	1634
δy	686		970
g	1635 GDI	GDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQSGEFEKRDTIPTEG	1694
Oy	971 AL-	LEEQRQRQEQIDLECRSSTSPCGTSKSPNREWEVL	1001
Op	1695 RSI	RSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKPFRVKKIMDQVQQAS	1754
Οy	1008	OPAPHQLITNLPEGVRLPTTRPTRPPPPLI	1039
Ob	1755 ASS	ASSSAPNKNQLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKNNLNAERVFSDNKDS	1811
Qy	1040 SKT	GTPGTYLTSHNQASYTQETPK	1080
Op	1812 KKC	KKONLKNNSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSRND	1860
οy	1081 PSV	SVGSISLGLPRQQESAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVRGTAGAIQ	1140
qq	1861 -SI		1914
δy	1141 EGS	EGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGIPTEALVKGS	1186
QQ	1915 KQF	KQPINRGQPKPILQKQSTFPQSSKDIPDRGAATDEKLQNFAIENTPVCFSHNSS	1968
δy	1187 ISRM	AMPIEDSSPEKGREEAASKGHVIYEGKSGHI	1219
q	1969 LSS	SLSDIDQENNNKENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLS	2028
Qy	1220 -LS	SYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPLE	1270
Ωp	2029 SLS	SLSIDSEDĢILQECISSAMPKKKRPSRLKGDNEKHSPRNWGGILGEDLTLDLKDIQRPDS	2088
QY	1271 GLI	GLICRALPRGSPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYPKQIKRESPPIRAFEG	1330
ф	2089 E	HGLSPDSENFDWKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKS	2140
Qy	1331 AIT	AITKGKPYDGITTIKEMGRSIHBIPRQDILIQESRKIPEVVQSTRPIIEGSISQGTPIKF	1390
qq	2141 GIS	SLGSPFPGEKSTLETKKI	2181
Qy	1391 DNN	Σ	1444
QQ	2182 ESE	ESESKGIKGGKKVYKSLITGKVRSNSEISGQMKQPLQANMPSISRG	2227
ò	1445 RSF	RSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTSD	1504
QQ	2228	RNSSSSTSPVSKKGPP	2252
Qy	1505 VT	VIIPPNKSTNHERKSTLTPT-QRESIPAK-SPVPGVDPVVSHSPFDPHHRGSTAGEVYWS	1562
QQ	2253 LKT	LKTPASKSPSEGQTATTSPRGAKPSVKSELSPVARQTSQIGGSSKAPSRSGSR	2305
Oy	1563 HLF	HLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITSQO	1622
qq .	2306	STPSRPAQQPLSRP	2320
δλ	1623 MQV	MQVNLRPDVARGLSPREQPLGLPYPATRGIDLTNMPPTILVPHPGGTSTPPMDRIT	1679
qq	2321 108	IQSPGRNSISPGRNGISPPNKLSQLPRT-SSPSTASTKSSGGKMS	2365
οy	1680 YIF	PGHPTHLAAAASAEREREREREKERERE	1727
Ωp	2366 Y	TSPGROMSQONLTKQTGLSKNASSIPRSESASKGLNOMNNGNGANKKVELS	2417

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MOLECULE TYPE: protein US-08-061-376-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       383 IIDGLS-----
 unknown
 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Evans, Glen A.
APPLICANT: Djabali, Malek
APPLICANT: Djabali, Licia
APPLICANT: Selleri, Licia
APPLICANT: Parry, Pauline
TITLE OF INVENTION: CHARACTERIZATION OF A CHROMOSOME 11023
TITLE OF INVENTION: TRANSLOCATION BREAKPOINT ASSOCIATED WITH ACUTE LEUKEMIAS
CORRESPONDENCE: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                      2016
                                                                                                                                  1905
                                                                                                                                                                                                                                     2611
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1728 RIAAASSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPL 1787
                                                                                          -PTLR-RKLEESASFESLS---PSSRPASPTRSQAQTPVLSPSLPDMSLS-THSSVQAGG 2503
                                                                                                                                                                                                  1906 DKGPPPKSRYEEELRTRGKTTITAAN------FIDVIITRQIASDKDARERGSQSSDS 1957
                                                                                                                                                                                                                                                                                                                                      2017 YRPQQESPSPQQQLPP--------SGQAEGMGQVPRTHRLITLADHIC 2056
                                                                                                                                                                                                                                                                                                                                                            HSSSLP--RVSTWRRTGSSSSILSASSESSEKAKSEDEKHVNSISGTKQSKENQVSAKGT
                                                                                                                                  1848 -- RLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGK
                                                                                                                                                                                                                                                                    1958 SSSLSSHRYE-TPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGPLHH
                                                                                                                                                                                                                                                                                         2612 WRKIKENEFSPTNSTSQTVSSGATNGAESKTLIYQMAPAVSK---TEDVWVRIEDCPINN
                                                                                                                                                                                                                                                                                                                                                                                                      2057 QIITQDFARNQVSSQTP-QQPPTSTFQNSPSALVS-TPVRTKTSNRYSPESQAQSVHHQR
                                                                1788 DPTAQLRIMPLPAGGPSISQGLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAA
                                                                                                                                                                 2504 WRKLPPNL---SPTIEYNDGRPAKRHDIAR-----SHSESPSRLPINRSGTWKREHSK
                                                                                                                                                                                                                                                                                                                                                                                                                                     2724 SFIQVDAPDQKGTEIKPGQNNPVPVSETNESSIVERTPFSSSSSKHSSPSGTVA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2779 -- ARVIPENY-----NPSPRKSSADSTSARPSQIP-IPVNNNTKKRDS 2818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2115 PGSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVH--EKQDS 2164
                               2418 RMSSTKSS----GSESD-----RSERPVLVRQSTFIKEAPS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/061,376 FILING DATE: 13-MAY-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P41 9387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-061-376-5
; Sequence 5, Application US/08061376
; Patent No. 6175000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION UNDABER: 31,192
REFERENCE/DOCKET NUMBER: P41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3969 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (619)546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
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STATE: California
COUNTRY: USA
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497 VLPEERSDIPEVHPPLPISQSPENESNDRRSRRYSVSERSFGSRITKKLSTLÅSAPQQQT '556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             338 HLQKKIRQLSDKALEGLSQLGLFLLQKGQMQ-----PLLSNSYRGQKKGAQKKIEKEA-- 390
                                                                                                                                                                                                                                                                                                                                                                                       94 PGPSPVDHDSLESKRPRLEQVSDSHFQRVSAAVLPLVHPLPEGL----RASADAKKDP- 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                   391 -----AQLQGRKVK-----TQVKNIRQFIMPVVSAISSRIIKTPRRFIEDEDYDPP 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 -AFGGKHEAPSSPISGQPCGDDQNAS----PSKLSKEELIQSMDRVDREI---AKVEQQ 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         672 AASARLFSPLHSGTRFDMHKRSPLLRAPRFTPSEAHSR-------IFESVTLPS 718
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                                                                                                                                                                                          278 LSPSSLSLRQGSFKZEGRGYKLZTERKASINRKDKDPFGLLIILNWKSPRKSGKTRKEHL 337
                                                                                                                              --PDYRSSHL 48
                                                                                                                                                                                                                                                         49 E------VSQASQLLQQQQQQLRRRPSLLSEFHPGSDRPQERRTSYEPFH 93
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Query Match 2.6%; Score 329; DB 4; 1
Best Local Similarity 17.5%; Pred. No. 1.8e-11;
Matches 593; Conservative 378; Mismatches 1089;
                                                                                                                                 1 MSSSGYPPNQGAFSTEQSRYPPHSVQYTFPNTRHQQEFAV-
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695 1229	742	798 1330	858	1351	1411	961 1448	993	1004	1567	1033	1627	1093	1112	1735	1139	1795	1186	1851 .	1221 1911	1229	1971	1269	2029	1306	2089	1354 2141	1404	
663LAOHKQKTSRKPREERD  17 ST ST ST ST ST ST ST ST ST ST ST ST ST	696 VSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSEDSPENAT	743 SRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDV   1	DSVDVEVRVPENHASKVEGDNTKERDLDRAS	DLVVAQQINAQRPEPQSDNDSSATCSADEDV-DGEPE	GVHRI	907 LLNPTGSILVSSPLKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTPVSGYALYQ :		1449 VCCEFF HAR CLEENERFLEDQLENWCCKRCRCHCHCGKQHQAIRQLLECNNCKHNSYHPEC 994	LGPNY PTKPTKKKKVWICTKCVRCKSCG-STTPGKGWD	1005EVLQPAPHQLITNLPEGVRLPTTRPTRP	1568 CPLCDKCYDDDDYESKMMQCGKCDRWVHSKCENLSDEMYEILSNLPESVAYTCVNCTERH	1034 PPLIPSSKTTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQETPKPSVGSISLGLPRQ	QESAKSATLPYIKQEEFSP	:    :   1676 EESIPSRSSPEGPDPPVLTEVSKQDDQQPLDLEGVKRKMDQGNYTSVLEFSDDIVKIIQA	1113RSQNSQPEGLLVRAQHEGVVRGTAGAI	1736 AINSDGGQPEIKKANSMVKSFFIRQMERVFPWFSVKKSRFWEPNKVSSNSGMLPNAVLPP	OEGSITRGTP-TSKISVESIPSLRGSITOGTPALPOT		1187 ISRMPIEDSSPEKGREESGHILS	1222 YDNIKNAR	::   1912 DDDGSLKNVHMAVIRGKQLRCEFCQKPGATVGCCLTSCTSNYHFMCSRAKNCVFLDDKKV	1230EGTRSPRTAHEISLKRSYESVEGNIKOGMSMRESPVSAPL	1972 YCQRHRDLIKGEVVPENGFEVFRRVFVDFEGISLRRKFLNGLEPENIHMMIGSWTIDC	1270 BGLICRALPRGSPHSDLKERTVLSGSIMQGTPRATTE	VYTCK	1307SFEDGLKYPKQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHEI 1009 ENRITAHSPTSFTESSSKESQNTAEIISPPSPDRPPHSQTSGSCYYHVISKV	1355 PRQDILTQESRKTPEVVQSTRPIIEGSISQGTPIKFDNNSGQSAIKHNVK	
Oy 6	Oy 6 Db 12	Oy 7	0y 7	•		Oy 9 Db 14	6 4 5			0y 10	Db 15	Oy 10			0y 11	Db 17			Oy 11 Bb 18	0y 12	Db 19	0y 12	Db 19	0y 12	Dp 20	Oy 13 Db 20	0y 13	

qq		
δλ	1405	V-RSRH
qq	b 2198 SLSPQRSKL-RIMSPM	RIGNTYSRNNVSSVSTTGTATDLESS 2238
QY	1463	LHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTSDVTIPP 1509
qq	2239	SSNLQRTVVTVGNKNSHLDGSSSSEMKQSSASDLVSK 2298
Qy	1510	SHSPF
qq	b 2299 SSSLKGEKTKVLSSKSSEGSAHNVAYPGIPKLA	VAYPGIPKLAPOVHNTTSRELNVSKIGSFAE 2352
οy	1570	OLSPTPGYPSQYQLYAMENTRQT 1612
qq	2353	PSSVSFSSKEALSFPHLHLRGQRNDRDQHTDSTQSANSSPDEDTEVKTLKLSGMSN-RSS 2411
οy	1613	1632
qq	b 2412 IINEHMGSSSRDRRQKGKKSCKET	TFKEKHSSKSFLEPGQVTTGEEGNLKPEFMDEVLTPE 2471
οy	1633R	PREQPL GLPYPATRGI 1652
qq	2472	YMGQRPCNNVSSDKIGDKGLSMPGVPRAPPMQVEGSAKELQAPRKRTVKVTLTPLKMENE 2531
δλ	1653	TTLVPHPGGTSTP 1673
qq	b 2532 SQSKNALKESSPASPLOIESTSPTEPI	TEPISASENPGDGPVAQPSPNNTSCQDSQSNNYQNLP 2591
Qy	1674 PMDRITYIPGTQIT	SMSPGHPTHLAAAAS 1711
qq	2592 VQDRNLMLPD	:  :  :
Qy	1712 -	~
q	2647 Y	SSSTGKKRGKRSAEGQVDGADDLSTSDEDDLYYYNFTRTVISSGGEERLASHNLFRE 2704
δy	1757 P	NGTSVITPLDPTAQLRIMPLPAGGPSISQGLPASRYN 1815
qq	b 2705 EEQCDLPKISQLDGVDDGTESDTSVTATTRKSSQI	SDTSVTATTRKSSQIPKRNGKENGTENLKIDRPE 2758
οy	1816 TAADA	
qq	2759	DAGEKEHVTKSSVGHKNEPKMDNCHSVSRVKTQGQDSLEAQLSSLESSRRVHTSTPSDKN 2818
οy	1865 QLEQKTLEVEK	RSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPK 1912
g	b 2819 LLDTYNTELLKSDSDNNNSDDC-	GESPE 2867
QY	1913 S	IITRQIASDKDARERGS
Q	b 2868 SSSELLINLGEGLGLDSNREKDMGLFEVFSQQLPTTEPV	GLFEVFSQQLPTTEPVDSSVSSSISAEEQFE 2921
δλ	1966	z
q	2922	LPLELPSD-LSVLTTRSPTVPSQNPSRLAVISDSGEKRVTTTEKSVASSESDPALLSP 2978
Qy	y 2012 GPLHHYRPQQESPSPQQQLPPSSQAEGMGQVPRTHRLITLADHI	OAEGMGQVPRTHRLITLADHICQIITQDFARNQ 2067
q	b 2979 GVDPTPEGHMTPDHFIQGHMD	FIQGHMDADHISSPPCGSVEQGHGNNQ 3019
Qy	2068VSSQTPQQP-	-PTSTFQNSPSALVSTPVRTKTSNRYSPESQAQSVHHQRPGSRVS 2120
qq	3020 DLTRNSSTPG	
Qy	2121 P	ENLVDKSRGSRPGKSPERSHVSSEPYEPISPPQVPVVHEKQDSLLLLSQRGAEPAEQRN 2180
qa	3051	-DSPGPSQISNAAVQ-TTPPHLKPATEKLIVVNQNMQPLY 3088
ò	y 2181 DARSPGSISYLPSFFT-KLENTS	PMVKSKKQEIFRKLNSSGGGDSDMAAAQPGTE 2234

588 SMINEAAAASAAAAAAIEEPPPPLPPPEPISTEPVETSR 627 1	628 WTEE-EMEVAKKGLVEHGRNWAAIAKWYGTKSEAQCKNFYFNYKRRHNLDNLLQOHKQKT 686     :   :     :     :       :	687 SRRPREERDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVRPSEDSPENATSRGN 746	747 TEP AVELEPTTETAPSTSPSLAVPSTKPAEDESVE	782TQVNDSISAETAEQMDVDQQEHSABEGSVCDPPPATKAD-SVD 823	824 VEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLV 861 :	862 VAQQINAQRPEPQSDNDSSATCSADEDVDGEPERQ 896	897 RWFPMDSKPSLLINPTGSILVSSPLKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTPVSG 956 1     :     :     605 GVTPWASFKKMVTP	957 YALYORHIKAMHESALLEEQRQRQEQIDLECRSSTSPCGTSKSPNREWEVLQPAPHQLIT 1016 11	1017 NLPEGVRLPTTRPTRPPPPLIPSSKTTVASEKPSFIMGGSISQGTPGTXLISHNQASYTQ 1076	1077 ETPKPSVGSISLGLPRQQESAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVRGTA 1136   :  :  :  :  :  :  :  :  :  :  :  :  :	1137	1197 PEKGREEAASKGHVIYEGKSGHILSYDNIKNARBGTRSPRTAHEISLKRSYESVEGNI 1254 	1255 KQGMSMRESPVSAPLBGLICRALPRGSPHSDLKERTVLSGSIMQGTPRAT 1304   : :       : :   :   : :     : :   :	1305 TESFEDGLKYPRQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHE 1353 	1354 -IPRQDILTQESRKTPEVVQSTRPIIEGSISQGTPIKFDNNSGQSAIKHN 1402 	1403 -VKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVKA-GETVRSRHTSVVSSGP- 1456 1004 AVSQLTDSPDTTEEATPVQEVEGGVPD-IEEQERRTQEVLQAVAEKVKEESQLFGTGGPE 1062	1457 SVLRSTLHEAPKAQL-SPGIYDDTSARRTPVSYQNTMSRGSP-MMNRT 1502 
QV	oy da	da	Qy Dp	ζς Dp	Oy Oy	do do	<i>₹</i> 8	\$ A	Qy	& a	δ d	δ, 42 20	Qy Dp	λο d	ço d	yo da	. да 
3089	VMSQPMGVVPGTANTSVVTSGETRREEGDPSPHSGGVCKPKLISKSNSRKSKSP	IPGQGYLGTERPSSVSSVHSEGDYHRQTPGWAWEDRPSSTGSTGFPYNPLTWRMLSST 	PPTPIACAPSAVNQAAPHQQNRIWERPAPLL 2428  :: :: :	I VF NI IAKS NOS IMI FEFAFUL	pplicatic 41890 RMATION:		NUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower/233 South Wacker Drive	CITY: Chicago STATE: 1111nois COUNTRY: United States of America ZIP: 60606-6402		SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: BAPLICATION NUMBER: US/08/769,309A FILING DATE:	ы .	XEEE   XEEE	INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENTH: 1780 amino acids	TIVE: AMINO ACLU TOPOLOGY: 1 inear MOLECULE TYPE: protein -08-769-309A-5	Query Match 2.6%; Score 323.5; DB 1; Length 1780; Best Local Similarity 18.6%; Pred. No. 1.3-11; Matches 361; Conservative 273; Mismatches 741; Indels 565; Gaps 82;	NQOIARPSQBEKVEEKBEDKAEKTEKKEEEKKDEEEKDEKEDSKENT 548	KEKDKIDGTABETEEREQATPRGRKTANSQGRRKGRITR:: GRITR:::

us-09-522-753-11.rai

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amino acid
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                                                                           1661 TILVPHPGGTSTPPMDRITYI----PGTQITFPPR----PYNSASMSPGHPTHLAAAASA 1712
                                                                                                                                                                                          -----TVSREKVTEVALKGEGTEEAECKKDDALELQSHAKSPPSPVEREMVVQV 1339
                                                                                                                                                                                                                                                                                                                                                      ---KTKESKHEAAR 1848
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                                                                                                                                                                                                                                                                                                                      1395 PPCLGQEEAVCTKIQVOSSEASFTLTAAAEEEKVLGETA--NILETGETLEPAGAHLVLE 1452
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                                                                                                                 ------EQPLGLP-YPATRGIIDLTNMPP
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                                                        1561 WSHLPTQLDPAMPFHRA----LDPA----AAAYLFQRQLSPTPGYPSQYQLYAMENTRQT
                                                                                                                                                                                                                                 ERER-ERE----PGRPGSHGYVRSP
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APPLICANT: Scott, John D.,
APPLICANT: Nauct, Theresa M.
TITLE OF INVENTION: Protein Binding Domains of Gravin
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower/233 South Wacker Drive
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                   GLPASRYNTAA - - - - DALAALVDAAASAPQMDVS -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTY: United States of America ZIP: 66606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
                                                                                                              1613 ILNDYITSQOMQVNLRPDVARGLSPR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S-08-994-570-5
Sequence 5, Application US/08994570
Patent No. 6090929
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  628 WTEE-EMEVAKKGLVEHGRNWAAIAKMVGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKT 686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.6%; Score 323.5; DB 3; Length 1780; 18.6%; Pred. No. 1.3e-11; tive 273; Mismatches 741; Indels 565;
Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                    27866/33451
                                                    PARLICATION NUMBER: US/08/994,570
FILING DATE:
CLASSIFCATION:
ATCORANTION:
ATCORANT INFORMATION:
NAME: NO. 6090929and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33451
TELECOMUNICATION INFORMATION:
TELECHOME: 312-474-6300
TELEFRAX: 312-474-0448
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Matches 361; Conservative 273;
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SOFTWARE: Patentin ReleCURRENT APPLICATION DATA:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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QQ ·	1077 E	ETPKPSVGSISLGLPRQQESAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVRGTA 1136	OY 2010 YEGPEHI
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à	1 5021		RESULT 20 US-08-194-468-2
qq	832 E	PTGANEDDSDVPAVVPLSEYDAVEREKMEAQQAQKGAEQPEQKAATEVSKELSESQVHMM 891	; Sequence 2, App
ò	1305 1	TESFEDGLKYPKOIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHE 1353	; Patent No. 5750
! 7			; APPLICANT:
o a		5	; TITLE OF IN
οy	1354 -	-IPRODILTQESRKTPEVVQSTRPIIEGSISQGTPIKFDNNSGQSAIKHN 1402	; TITLE OF IN
අධ	952 F	PLPENREARGDIVVSEAELTPEAVTAAETAGPLGSEEGTEASAAEETTEMVS 1003	ž Ö
οy	1403 -	-VKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVKA-GETVRSRHTSVVSSGP- 1456	; ADDRESSEE ; STREET: '
ģ	1004 2	AVSOLTDSPDTTERATEVORVEGGVPD-TREORRETORVIAVARKVERSOLDGTGGPR 1062	CITY: LO
! .			COUNTRY
ά	145/ 5	SVLRSTLHEAPKAQL-SPGIYDDTSARRTPVSYQNTMSRGSP-MMNRT	; ZIP: 900
셤	1063	DVLOPVQRAEAERPEEQAEASGLKKETDVVLKVDAQEAKTEPFTQGKVVGQTTPESFEKA 1122	MEDIUM TY
δy	1503 8	SDVTIPPNKSTNHERKSTLTPTQRESIPAKSPVPGVDPVVSHSPFDPHHRGSTAGEVY 1560	COMPUTER
g	1123 E		SOFTWARE:
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δō	1561		; FILING DAY
Q O	1180	DAPGTTOKDEIVEIHEENEVHLVPVRGTEAEAVPAOKERPPAPSSF-VFOEETKEOS 1235	; ATTORNEY/AGI
ΟŊ	1613	ILNDYITSQOMQVNLRPDVARGLSPREQPLGLP-YPATRGIIDLTNMPP 1660	STF
qq	1236 F	KMEDTLEHTDKEVSVETVSILSKTEGTQEADQYADEKTKDVPFFEGLEGSID-TGI 1290	; REFERENCE; TELECOMMUNIC
ò	1661 1	TILVPHPGGTSTPPMDRITYIPGTOITFPPRPYNSASMSPGHPTHLAAAASA 1712	TELEPHONE
<b>3</b> :			; INFORMATION FO
QQ	1291	TVSREKVTEVALKGEGTEEAECKKDDALELQSHAKSPPSPVEREMVVQV 1339	SEQUENCE CH.
οy	1713 E	ERER-EREREKERERERIAAASSDLYLRPGSEQPGRPGSHGYVRSP 1757	, TYPE: am
q	1340 E	EREKTEAEPTHVNEEKLEHETAVTVSEEVSKQLLQTVNVPIIDGAKEVSSLEGSP 1394	MOLECULE TYL
Οy	1758	SPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMPLPAGGPSISQ 1807	US-08-194-468-2
q	1395	: :  :       :	Onerv Watch
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ολ	1808	GLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAAR 1848	Matches 495;
q	1453 F	EKSSEKNEDFAAHPGEDAVPTGPDCQAKSTPVIVSATTKKGLSSDLEGEKTTSLKWKSDE 1512	Oy 7 PPNQGAI
Qy	1849 I	LEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSG 1890	Db 121 PLNQGD
qq	1513 V		Qy 65 LRRRPS
Qγ	1891 K	KPOPHSSVVYSEAGKDKGPPPKSRYEE-ELRTRGKTIITAANFIDVIITRQIASDKDARE 1949	Db 160 LVTSSP
qq	1573 E	:   :   : :: :     :     :       :       :       :       :       :       :     :     :     :     :     :     :	Qy 120 ORVSAA
δy	1950 F	RGSQSSDSSSSLSSHRYETPSDAIEVISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQ 2009	Db 216 GRGRGAC
Ωp	1613 -	KEESESTAVGQAHSDISKDMSEASEKTMTVEVEGSTVNDQQ 1653	Qy 156PSSI

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Montainy, Marc R.
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Montainy, Marc R.
Montains ASSAYE FOR THE IDENTIFICATION OF
VERNICON: COMPOUNDS WHICH INHIBIT ACTIVATION OF CAMP AND MITOGEN
VENTION: RESPONSIVE GENES
VENTION: RESPONSIVE GENES
SOURCES:
NCE ADDRESS:
Pretty, Schroeder, Brueggemann & Clark
Pretty, Schroete, Suite 2000
SA Angeles
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TYPE: Floppy disk

TYPE: Floppy disk

TYPE: TBM PC compatible

TWO SYSTEM: PC-DOS/MS-DOS

TWO SYSTEM: PC-DOS/MS-DOS

APPLICATION DATA:

TYPE: 10-FEB-1994

APPLICATION 435

AGENT INFORMATION:

Reiter, Stephen E.

Reiter, Stephen E.

REITER, Stephen E.

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Page 27

330	268 382	321	373	421 521	473	527 623	580	635	691 788	731	772 906	817 962	875 1013	935	994	1051	1086	1145
	AAKPPEPEKPVSPPPVEQKHRSIVQIIYDENRKRAEEAHKIFEGLGPKVELPLYNQ	PSDTKVYHENIKTNQVMRKKLILFFKRRNHARKQREQKICQRYDQLMEAWEKK ::   :   :   :   :   :   :   :   :   :	VDRIENNPRRKAKESKTREYYEKOFPEIRKOREGOERFORVGGRGAGLSATI 	ARSEHEISEIIDGLSEQENNEKQMRQLSVIPPMMFDAEQRRVKFINMN :	GLMEDPWKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNFGLIASYLERKSVPD	CVLYYYLTKKNENYKALVRRNYGKRRGRNQOIARPSQEEKVEEKEEDKAEKTEK	KEEEKKDEEEKDEKEDSKENTKEKDKIDGTAEETEEREGATPRGRKTANSGGR :	RKGRITRSMTNEAAAASAAAAAATEEPPPPLPPPEPISTEPVETSRWTEEEMEV :	AKKGLVEHGRNWAAIAKMVGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQK-TSRKPR   :	EERDVSQCENPEDSEVEAU : : :   :	KPSEDSP	KPAEDESVETQVNDSISAETAEQMDVDQQEHSAEEGSVCDPPPRT	KADSVDVEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQS	DNDSSATCSADEDVDGEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAA :     :     ::   :     ::       ::	VIPPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEQRQRQEQIDLECRS-STSPC	GTSKSPNREWEVLQPAPHQLITNLPEGVRLPTTRPTRPPPPLIPSSKTTVASEKPSF 	IMGGSISQGTPGTYLTSHNQASYTQETPK	SIGLPRQOESAKSATLPYIKQEEFSPRSONSQPEGLLVRAQHEGVVRGTA-CAIQEGSIT
275	213	269	322	374	422	474 578	528	581	636	692	732	773	818 963	876 1014	936 1058	995	1052 1138	1087
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qq	1198 GYCCGRKYEFSPQTLCCYGKQLCTIPRDAAYYSYQNRYHFCGKCFTEIQGENVT 1251
οy	1146 RGTPTSKISVESIPSLRGSITQGTPALPQTGIPTEALVKGSISRMPIEDSSPEKGREEAA 1205
qq	1252 IGDDPSQPQTTISKDQFEKKNDTLDPEPFVDCKECG 1288
Qy	1206 SKGHVIYEGKSGHILSYDNIKNAREGTRSPRTAHEISLKRSYESVEGN 1253
οp	1289 RKMHQICVLHYDIIWPSGFVCDNCLKKTGRPRKENKFSAKRLQTTRLGNHLEDR 1342
δ d	4 IKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIMQGTPRATT 130
Q (	VNKFLRRQNHPEAGEVFVRVASSDKTVEVKPGMKSRFVDSGEMSESFPYRTK
δ, i	5 ESFEDGLKYPKQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHEIPRQDILT 136
අ	ALF
ΟŊ	1362 QESRKTPEVVQSTRPIIEGSISOGTPIKFDN-NSGQSAIKHNVKSLI 1407
QQ	1426IQGCVYISYLDSIHFFRPRCLRTAVYHEILIGYLEYVKKLVYVT 1469
δλ	1408YGPSKLSRGMPPLEIVPENIKVVERGKYEDVKAGE 1442
qq	1470 AHIWACPPSEGDDYIFHCHPPDQKIPKPKRLQEWYKKMLDKAFAERIINDYKDIFKQANE 1529
οy	1443 TVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSXQNT 1491
q	1530DRLTSAKELPYFEGDFWPNVLEESIKELEQEEEERKKEESTAASETPEGSGGDSKNA 1586
ΟŸ	1492 MSRGSPMMNRT-SDVTIPPNKSTNHERKSTLTPTQRESIPA 1531
q	1587 KKKNNKKTNKNKSSISRANKKKPSMPNVSNDLSQKLYATMEKHKEVFFVIHLHAGPVIST 1646
Οÿ	1532 KSPVPGVDPVVSHSPFDPHHRGSTAGEVYWS1562
qq	1647 QPPIVDPDPLLSCDLMDGRDAFLTLARDKHWEFSSLRRSKWSTLCMLVELHTQGQDRFVY 1706
ΟŸ	1563HLPTQLDPAMPFHRAL
q	1707 ICNECKHHVETRWHCTVCEDYDLCINCYNTKSHTHKMVKWGLGLDDEGSSQGEPQSKSPQ 1766
Qy	1587 FORQLSPTPGYPSQYQLXAM 1606
q	1767 ESRRLSIQRCIQSLVHACQCRNANCSLPSCQKMKRVVQHTKGCKRKTNGGCPVCKQLIAL 1826
ΟŻ	1607VILRPDVARGL-SP 1637
QQ	1827 CCYHAKHCQENKCPVPFCLNIKHNVRQQQIQHCLQQAQLMRRRMATMNTRNVPQQSLPSP 1886
Οy	1638 REQPLGLPYPATRGIIDLINMPPTILVPHPGGTSTP-PMDRI-TYIPGTQITFPP 1690
qq	1887 TSAPPGTPTQQPSTPQTPQPPAQPQPSPVNMSPAGFPNVARTQPPTIVSA 1936
Qy	1691 -RPYNSASMSPGHPTHLAAAASAERERERERERERERERERIAAASSDLYLRPGSEQPGRPG 1749
qq	1937 GKPTNQVPAPPPPAQPPPAAVEAARQIEREAQQQQHLYRANINNGMPPGRDGMGTPG 1993
οy	1750 SHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMPLPAGGPSISGGL 1809
q	1994 SQMTPVGLNVPRPNQVSGPVMSSMPPGQWQQAPIPQOQPMPGM 2036
δλ	1810 PASRYNTAADALAALVDAAASAPOMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQK 1869
q	2037 PRPVWSMQAQAAVAGPRMPNVQPNRSISFSA-LQDLLRTLKSPSSFQQQQQ 2086
QY	1870 TLEVEKRSVQCLYTSSAFSSV 1898
qq	2087 VLNILKSNPQLMAAFIKQRTAKIVANQPGMQPQPGLQSQPGMQPQPGHQQPSLQNL 2143
ΟŊ	1899 VYSEAGKDK-GPPPKSRYEEELRTRGKTIITAANFIDVIITRQI- 1941
qq	2144 NAMOAGVDRPGVDRDODDAMGGINDOGOAINTMDGHNDNMTNMNDOVDRWVDRDII 2119

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 --ASDKDARERGSQSSDSSSSLSS----HRYETPSDAIEVISPAS-SPAPPQEKLQTYQ 1993
                       2200 QHQQQQQQQQQQQQQQQQNSASLAGGMAGHSQFQQPQ-----GPGGYAPAMQQQRMQQHL 2253
                                                              P-----EVVKANQ----AENDPTRQ---YEGPLHHYRPQQESPSPQQQLPP 2032
                                                                                  2091 TPVRTKTSNRYSPESQAQSVHH-----2RPGSRVSPENLVDKSRGSRPGKS----- 2136
                                                                                                                                                                                                                2356 QPPHSSPSPRIQPQ---PSPHHVSPQTGTPHPGLAVTMASSMDQGHLGNPEQSAMLPQLN 2412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 LRRRPSLLSEFHPGSDRPQERRTSYEPFHPG--PSPVDHDSLESKRPRLEQVSDSHF--- 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 PLNQGDSST------PNLPKQA-----ASTSGPTPPASQALNPQAQKQVG 159
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                                                                                                                                                         2314 SPQQHMLSGQPQ-----ASHLPGQQIATS--LSNQVRSPAPVQSPRPQ-----S
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                                                                                                                            2033 SSQAEGMGQVPRTHRLITLADHI--CQIITQDFARNQVSSQTPQQPPTSTFQNSPSALVS
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                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Montminy, Marc R.
TITLE OF INVENTION: Methods for Treating Diabetes Mellitus
FILE REFERENCE: SALK1650-1
CURRENT PILING DATE: 1997-10-31
EARLIER APPLICATION NUMBER: US 194,468
EARLIER FILING DATE: 1994-02-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTEED for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.4%; Score 309.5; DB 3; Best Local Similarity 18.6%; Pred. No. 1.5e-10; Matches 492; Conservative 306; Mismatches 993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : LOCATION: (1)...(2441)
; OTHER INFORMATION: Xaa - Any Amino Acid
US-08-961-739-2
                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08961739A Patent No. 6063583
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2413 TPNRSALSSE 2422
                                                                                                                                                                                                                                                            2137 -PERSHVSSE 2145
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IYPE: PRT
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----NHMTHCQAPKACQVAHCASSRQIISHWKNCTR 423
                                                                       --QRVGQRGAGLSATI 373
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                                                                                                                                           -----KRNQQTILGSPASGIQNTIGSVGAGOQNAT
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                                                                       322 VDRIENNPRRKAKESKTREYYEKOFPEIRKOREQOERF--
--NGEVXACSLPHCRTMKNVL---
                                                                                                                                           HDCPVCLPLKNASD-----
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Oy 2033 SSQ Db 2314 SPQ Oy 2091 TPV Db 2356 QPP Oy 2137 -PE Db 2413 TPN	RESULT 22 US-08-459-568 ; Sequence 4, ; Patent No. ; GENERAL IN ; APPLICAN ; TITLE OF ; TITLE OF ; NUMBER O ; CORRESPO ; ADDRES	STREET COUNTR STATE: STATE: COUNTR COUNTR COMPUTER MEDIUM COMPUTER MEDIUM COMPUTER CORRENT COURRENT APPLIC	CLASSI PRIOR AP APPLIC FILING ATTORNEY NAME: REFERE TELECOM TELEPH	7, TOPOLO 7, MOLECULE 0S-08-459-568 OUERY MATCH BEST LOCAL MATCHER 34 QY 502 NQQ DD 1145 NPE QY 562 EER QY 562 EER QY 617 PIS DD 193 SEP
1254 IKOGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIMQGTPRATT 1305  1343 VNKFLRRQNHPEAGEVFVVVASSDKTVEVKPGMKSRFVDSGEMSSFPRTK 1395  1306 ESFEDGLKYPKQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRIEIRRQDILT 1361	1408  TGPSKLSRGMPPLEIVPENIKVVERGK	1532 KSPVPGVDPVVSHSPFDPHHRGSTAGEVYWS	1607	1810 PASRYNTAADALAALYDAAASAPOMDVSKTKESKHEAARLEENLRSKSAAVSEOOOLEGK 1869 1870 PRPUMSWQAQAAVAGPRMPNVQPINRSISPSA-LQDLLRTLKSPSSPQQQQQ 2086 1870 TLEVEKRSVQCLYTSSAF
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Similarity 18.5%; Pred. No. 9.7e-11;
144; Conservative 247; Mismatches 664; Indels 600; Gaps
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NAT: Huang, Shi
DF INVENTION: Retinoblastoma Protein - Interacting
OF INVENTION: Zinc Finger Proteins
OF SEQUENCES: 93
PONDENCE ADDRESS:
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ENTRA APPLICATION DATA:
PERMERS PATENTING NUMBER:

LING DATE:
ASSIRICATION DATA:
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ASSIRICATION DATA:
ASSIRICATION DATA:
TELNG DATE:
Campbell, Cathryn A.
GGISTRATION NUMBER: 31,815
FERENCE/DOCKET NUMBER: P-LJ 1264
COMMUNICATION INFORMATION:
LIEPRAX: (619) 535-9001
LIEFRAX: (619) 535-8949
LIEFRAX: (619) 535-8949
LIEFRAX: (619) 535-8949
MATION FOR SEQ ID NO: 4
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ST: 4370 La Jolla Village Drive, Suite 700
San Diego
S: California
RT: USA
92122
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JM TYPE: Floppy disk
JTER: IBM PC compatible
ATING SYSTEM: PC-DOS/MS-DOS
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NLLQQHKQQI     : : : : :         : : : :	1006 -HPCPSPLSNATAQSPLPILSPTVSPSPSPIPBVEP 1040 1541 VVS-HSPFDPHHRGSTAGEVYWSHLPTQLDPAMPEHRALDPAAAAYLFQRQLSPTPGYPS 1599
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--GTNGTSVITPLDPTAQLRIMPLPAGGPSISQGLP 1810
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                                                                                                                                                                                                                                                                               PISTEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAKMYGTKSEAQCKNFYFNYKRRHNLD 676
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                                                                                                                                                                                           145 NPEIAAAIEEERASARSKRSSPKSRK------GKKKSQENKNKGNKIQDIQLKT 192
                                                                                                                                                                                                                                                                                                           -------NACE------VN 264
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                                                                                                                                                                                                                                                                                                                                                                                          -EDSPENATSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETA 793
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                                                                                                                                                                 502 NQQIARPSQEEKVEEKEEDKAEKTEKKEEEKKDEEEKDEKEDSKENTKEKDKIDGTAEET
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                                                                                                                                        600;
                                                                                                            Length 1719;
                                                                                                           Query Match 2.4%; Score 309; DB 2; Length 17:
Best Local Similarity 18.5%; Pred. No. 9.7e-11;
Matches 344; Conservative 247; Mismatches 664; Indels
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                                                                                                                                                                                                                                                                                                        250 P---EP----DERLEA---
              1719 amino acids
SEQUENCE CHARACTERISTICS:
LENGTH: 1719 amino aci
                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                          amino acid
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US-08-399-411-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1541 VVS-HSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPS 1599
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| | | | :|: | | :
|----NPADG-TRSPSPCKSLEAQPDPDLG 929
                                                                                             1361 TQESRKTPEVVQSTRPIIEGSISQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSRGMPPL
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Patent No. 6069231
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Lanc Finger Proteins
NUMBER OF SEQUENCES: 106
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                                                                                                                                                          PGSGFPAP-TVESTPDVCPSSPALQTP---SLSSGQ---
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                         -----YNGIDLPVE-
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CORRESPONDENCE ADDRESS:

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Best Local Similarity 18.5%; Pred. No. 9.7e-11;
Matches 344; Conservative 247; Mismatches 664; Indels 600;
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
REFERENCE/POCKET NUMBER: P-LJ 1776
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/516,859A
FILING DATE: 18-AUG-1995
                                                                                                                                                    E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1719 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-516-859A-4
                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                        CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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1069 HN----QASYTQETPKPSVGSISLGLPRQQESAKSATLPYIKQEEFS----PRSQNSQPE 1120
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                                                                                                                                                                                                                                                                                       ....----LVRAQHE----GVVRGTAGAIQE-GSITRGTPTSK 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -KGREEAASKGHVIYE------GKSGHILSYDN------IKNAREGTRSPRTAHE 1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1301 PRATTESFEDGLKYPKQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHEIPRQDIL 1360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1361 TQESRKTPEVVQSTRPIIEGSISQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSRGMPPL 1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1421 EIVPENIKVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTS 1480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1541 VVS-HSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPS 1599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SIPPMDRI----TYIPGTQITFPPRPYNSASMSPGHPTHLA 1707
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--LEEQRQRQEQIDLECRSSTSPCGTSKSPNREWEVLQPAPHQL 1014
                                                                                                                                                                                                                                                                                                                             670 SISTTEAVSFHKEKSVYLSSKLKQLLQTQDKLTPPAGI---SATEIAKLGPVCVSAPASM 726
                                                                                                                                                                                                                                                                                                                                                                                                                                    727 LPVTSSRFKRRTSSPPSSPQHSPALRDFGKPSDGKAAWTDAGLTSKKSKLESHSDSPAWS 786
                                          503 RRVHERHLIPKGVRRKGGLEEPQPPAEQ----AQATQNVYVPSTEPEEGEADDVYIMDI
                                                                                             1015 ITNLPEGV-----RLPTTRPTRPPPLIPSSKTTVASEKPSFIMGGSISQGTPGTYLTS
                                                                                                                                             559 SSNISENLNYYIDGKIQTNNNT----SNCDVIEMESASADLYGINCLLTPVTVEIT
                                                                                                                                                                                                                      1153 ISVESI-----PSLRGSITQGTPALPQTGIP-----TEALVKGSISRMPIEDSSPE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 787 LSGRDERETVSPPCFDEYKMSKEWTASSAFSSVCNQQPLDLSSGVKQKAEGTGKTPVQWE
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965 KAMHESAL
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1406 F	FSVELSKMSSN-KLKLNALKKKNOLVOKAILOKNKSAKOKADLKNACESSSHICPYCNRE 1464
1887 FI     1465 F7	FP-SGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFIDVIITRQIASDK 1945 
	IEVISPASSPAPPQEKLQTYQPEVVKANQA
2003 ER	ENDPTRQYEGPLHHYRPQQESPSPQQQLPPSSQAEGMGQVPRTHRLITLADHICQII 2059 :
2060 TC	2060 TQDFARNQVSSQTPQQPPTSTFQNSPSALVSTPVRTKTSNRYSPESQAQS 2109 :  :    :  :
RESULT 25 US-08-046-585-5 ; Sequence 5, A ; Patent No. 54 ; GENERAL INFO	SULT 25 -08-046-585-5 Sequence 5, Application US/08046585 Patent No. 5453362 GENERAL INFORMATION: ADDITIONE
APPLICA APPLICA TITLE ( TITLE ( NUMBER	APPLICANT: Missol, Angus APPLICANT: Herr, Wisship TITLE OF INVENTION: A NOVEL EKARYOTIC TRANSCRIPTION PROTEIN: TITLE OF SEQUENCES: 15 OF SEQUENCES: 15
CORRESPOND ADDRESSES STREET: CITY: S: STATE: COUNTRY:	
ZIP: 941. COMPUTER REJ MEDIUM TYR COMPUTER: OPERATING	ZIP: 94111-4187 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PAtentin Release #1.0, Version #1.25
CURREN APPL FILLI CLAS: ATTORNI	~ ស៊ី២ដីន
NAME: REFERENCY REFERENCY TELEPHOI TELEPAX TELEX TELEX INFORMATION SEQUENCE (	NAME: OSMBAL, KACHARA A REGISTRATION NUMBER: 36,627 REFERENCE/DOCKET NUMBER: A-57503-1/RAO TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 398-3249 TELEFAX: (415) 398-3249 INFORMATION FOR SO ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 2035 amino acids
TYPE: AMIDO STRANDEDNESS TOPOLOGY: 1 MOLECULE TYPE: S-08-046-585-5	YTVE: amino acid STRANDEDNESS: single TOPOLOGY: linear LECULE TYPE: peptide 46-585-5
Query Match Best Local ( Matches 41)	tch 2.3%; Score 294.5; DB 1; Length 2035; al Similarity 19.5%; Pred. No. 9.8e-10; 412; Conservative 237; Mismatches 839; Indels 623; Gaps 98;
540 E	TOGTARRT-

ζ Q	584	RITRSMINEAAAAAAATEEPPPELPPPEPEISTEPVETSRWTEEEMBVAKKGLVEH	643 382
	. 4	CONTRAGED AND AND AND AND AND AND AND AND AND AN	100
A A	383	GENWAALANNYGINSEAUCKNETENIRKKHNIJNILUQHRUKISKRFREEKUVSUCESVA  :    :    ::   ::   ::   ::   ::   ::	406
ογ	704	PTTETAP   	761
ογ	762	STSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDVDQQEHSAEGSVCDPPPA	816
qq	456		495
Oy	817	RDLDRASEKVEPRDEDLVVAQQINAQRP	871
Ωp	496	TGTPLVTMRPASQAGKAPVTVTSLPAGVRMVVPTQSAQGTVIGSSP	541
δy	872		929
qq	542		591
δy	930	LQHRAAVIPPMVSCTPCNIPIGTPVSGYA-LYQRHIKAMHESALLEEQRQRQR 	981
qq	592	RMLKTAAAQVGTSVSSATNTSTRPIITVHKSGTVTVAQQAQ-	648
οy	982	QIDLECRSSISPCGISKSPNREWEVLQPAPHQLIINLPEGVRLPTIRP	1029
qq	649	SAVTGQAST	703
οy	1030	м -	1080
q	704	AGTILKLVTSADGKPTTITTTQASGA-GTKPTILGISSVSPSTTK	762
οy	1081	LPRQQESAKSAT-LPYIKQEEFSPRSQNSQPEGLL	1123
qq	763	SPITIITTKVMTSGTGAPAKIITAV	818
٥y	1124		1168
qq	819	PGTILRTVPMGGVRLVTPVTVSAVKPAVTTLVVKG	876
δλ	1169	YEGKSGHILSYDNIKNA	1228
qa	877	ITTLGTIATL	919
Qy	1229		1285
QQ	920	SSQVINP-TAITVSAAQTTLTAAGGLTT-PTITMQPVSQPTQVTLITA-PSGVEAQPVHD	916
φ	1286	YDGITT	1343
a a	977	TEQPIATVTIADSGQGDVQPGTVTLVCSNPPCETHETGTTNTATTTV	1033
οy	1344	SIHEIPRO-DILTQESRKTPEVVQSTRPIIEGSISQGTPIKFDNNSGQSAIK	1400
q	1034	VQFVCDRQEAAASLVTSTVGQQNGSVVRVCSNPPCETHETGTTNTA	1091
οy	1401	HNVKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVKAGETVRSRHTSVVSSGPSVLR	1460
qq	1092	THET	1114
δ.	1461	STLHEAPKAQLSPGIYDDTSARTPVSYQNTMSRGSPMMNRTSDVTIPPNKSTNH	1515
g	1115	ttamssvganhqrdarracaagtpavirisvatgaleaaqgsksqcq	1167
δ	1516	ERKSTLTPTQRESIPAKSPVPGVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFH:::	1575
ď	1168	TPOTE CATEGORIE AND THE CATEGO	1197

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1244 ---RSSVGAG-BPRMAPVCESLQGGSPSTTVTVTAL-EALLCPSATVTQVCSNPPCE--T 1296
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                                                                                                                                                                                                                                                                                                                                1625 VNLRPDVARGLSPREQPL--GLPYPATRGIIDLTNMPPTILVPHPGGT---STPPMDRIT 1679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1724 RERERIAAASSDLYLRPGSEQPGRPGSHGYVRS----PSPSVRTQETMLQQRPSVFQGT 1778
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Sequence 5, Application US/08393703 Patent No. 5585239

US-08-393-703-5

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287 EKEWKCTNTLACLNLDTMAWETILMDTLEDNIPRARAGHCAVAINTRLYIWSGRDGYRKA 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            644 GRNWAAIAKMYGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRKPREERDVSQCESVA 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AT-----ATSPTPNPVPS-VPANPPKSPAPAAAPAVQPLTQVGITLLPQAAPAP 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S42 QMSGWAALAAAAAATQKI------PPSSAPTVLSVPAGTTIVKTMAVTPGTTTLPA 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2035;
              APPLICANT: Wilson, Angus
APPLICANT: Herr, Winship
TITLE OF INVENTION: A NOVEL EKARYOTIC TRANSCRIPTION PROTEIN:
TITLE OF INVENTION: HOST CELL FACTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                       ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                      Query Match Carl Similarity 19.5%; Pred. No. 9.8e-10; Matches 412; Conservative 237; Mismatches 839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 540 EKEDSKENTKEKDKIDGTAEET ---EEREQATPRGRK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELES: 910 277299
INFORMATION FOR SEQ ID NO: 5:
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LENGTH: 2035 amino acids
: Lamarco, Kelly
: Wilson, Angus
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                                                                                                                                                          CITY: San Francisco
STATE: CA
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qq	:	1505
δ	NREWEVLQPAPHQLITNLPEGVRLPTTRP	Qy 1957 SSSLSSHRYETPSDAIEVISI  :  :    :    : Db 1559 QESAGSAVVATVVVQ
6 G	649 VYTTVVGGVTKTITLVKSPISVPGGSALISNLGKVMSVVQTKPVQTSAVTGQAST 703 1030TRPPPPLIPSSK-TTVASEKPSFIMGGSISQGTPGTXLTSHNQASYTQETPK 1080	Qy 2016 HYRPQQESPSPQQQLPPSSQAI
qq		1607
70 2		OY 2076 PPISTFONS
å å		Oy 2115 PGSRVSPENLVI
: 원	:   :   :   :	1713
ò á	TPALPQTGIPTEALVKGSISRMPIEDSSPEKGREEAASKCHVIYEGKSGHILSYDNIKNA 12	OY 2153 PQVPVVHEKQDSLLLLSQRGA :: Db 1773 AKLQAAA
6 6	0// 1ICVIILGIVIGIVSISLAGAGGHSISASLAIPLITLGIIAIL 919 1229 REGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSD 1285	Qy 2199 ENTSPMV
QQ	:     :  :  :	1819 KGINVMVTHYF
ογ	1286 LKERTVLSGSIMGGTPRATTESFEDGLKYPKQIKRESPPIRAFEGAITKGKPYDGITT 1343	OY 2225 DMAAAQPGTEIFNLPP ::: :: DD 1879 EISAFWTCLPGFPGAPC
QQ	977 LPVSILASPITEQPIATVIIADSGGGDVQPGTVTLVCSNPPCETHETGTINTATTTV 1033	2279
O.Y	1344 IKEMGRSIHEIPRQ-DILTQESRKTPEVVQSTRPIIEGSISQGTPIKFDNNSGQSAIK_1400 	
o d	1401 HNVKSLITGPSKLSRGMPDLEIVPENIKVVERGKYEDVKAGETVRSRHTSVVSSGPSVLR 1460 1092 TTATSNMAGOHGCSNPPCR	Qy 2327 ISKSNSRKSKSPIPGQGYLGTI   :          Db 1980 IFRIAARNEKGY
λō	RRTPVSYQNTMSRGSPMMNRTSDVTIPPNKSTNH	2387 PLTMRMLSSTP
q		Db 2017 PMSSPEMKSAP 2027
Qy Dp	1516   ERKSTLTPTQRESIPAKSPVPGVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFH	RESULT 27 PCT-US93-11721-5 ; Sequence 5, Application PC/TU
ογ	TPGYPSQYQLYAMENTRQTILI	GENERAL INFORMATION:  APPLICANT: Lamarco, Kelly
g	1198 -AREPGGRSPAFV-QLAPLSSKVRLSSPSIKDLPAGRHSHAVSTAAMT 1243	•
à à	1625 VNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRIT 1679 1244RSSVGAG-PPPMADVTFSI-GSSGWWTM1-PAIICPSAMWOVGNDPD1966	TITLE OF INVENTION: A COUNTY OF SEQUENCES: 15
δ	YIPGTQITFPPRPYNSASMSPGHPTHLAAAASAEREREREKE	STREET: 4 Embarcadero Co
Q	:      : ;     : :       : :       : :     : :     : : : : : : :     :	Car
Qy Dp	1724 RERERIAAASSDLYLRPGSEQPGRPGSHGYVRSPSPSYRTQETMLQQRPSVFQGT 1778   : : : :	COMPUTER READABLE FORM:  MEDIUM TYPE: Flored disj
οy	NGTSVITPLDPTAQLRIMPLPAGGPSISQGLPASRYNTAADALAALVDAAASAPQMDVSK	COMPUTER: IBM PC COMPACT COMPA
QQ	:::	; SOFTWARE: Patentin Releation CURRENT APPLICATION DATA:  APPLICATION NIMMED: DOT
oy g	1839 TKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSV 1898 	ris a
ογ	GPPPKSRYEEELRTRGKTTITAANFIDVIITRQIASDKDARERGSQSSD	; NAME: OSMan, Richard A ; REGISTRATION NUMBER: 36

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SPASSPAPPQEKL-QTYQPEVVKANQAENDPTRQYEGPLH 2015
AEGMGQVPRTHRLITLADHICQIITQDFARNQVSSQTPQQ 2075
                                                                                                                                                     AEAAAQAAATEEAQALA---IQAVLQ--AAQQAVMGTGEP 1652
                                                                                                                                                                                                              EGQEGQATTIPIVLTQQELAALVQQQQLQEAQAQQQHHL 1712
                                                                                                                                                                                                                                                                                                                                  AEPAEQRNDARSPGSISYLPSFFTK------L 2198
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----GPATQVR-------WLQETSKDSSGTKPANKR 2016
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                                                                                                                                                                                            ------PSALVSTPVRTKTSNRYSPESQAQSVHHQR 2114
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ease #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                              RITRSMTNEAAAAAAAAAATEEPPPPLPPPFEPISTEPVETSRWTEEEMEVAKKGLVEH 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRNWAAIAKWYGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRKPREERDVSQCESVA 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --SWGAVA----LOKYDI---PATA 406
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                                                                                                                                                                                                                                                                                                                                                                                        EKEWKCTNTLACLNLDTMAWETILMDTLEDNIPRARAGHCAVAINTRLYIWSGRDGYRKA 346
                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                               Length 2035;
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                                                                                                                                                                                                                                                                            Query Match 2.3%; Score 294.5; DB 5; Best Local Similarity 19.5%; Pred. No. 9.8e-10; Matches 412; Conservative 237; Mismatches 839;
                                                                                                                                                                                                                                                                                                                                                     540 EKEDSKENTKEKDKIDGTAEET --- EEREQATPRGRK----
FP-57503-1/RAO
             TELECOMMUNICATION INFORMATION:
TELEPACE: (415) 781-1989
TELEFAX: (415) 398-3249
TELER: 910 277299
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2035 amino acids
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                              SS: single
linear
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MOLECULE TYPE: peptide
PCT-US93-11721-5
                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
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LKERTVLSGSIMQGTPRATTESFEDGLKYPKQIKR--ESPPIRAFEGAITKGKPYDGITT 1343 IKEMGRSIHEIPRQ-DILTQESRKTPEVVQSTRPIIEGSISQ--GTPIKFDNNSGQSAIK 1400 VANLGG -- HPQPTQVQFVCDRQEAAASLVTSTVGQQNGSVVRVCSNPPCETHETGTTNTA 1091 HNVKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVKAGETVRSRHTSVVSSGPSVLR 1460 STLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTSDVT----IPPNKSTNH 1515 ERKSTLTPTQRESIPAKSPVPGVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFH 1575 VNLRPDVARGLSPREQPL--GLPYPATRGIIDLTNMPPTILVPHPGGT---STPPMDRIT 1679 ---RSSVGAG-EPRMAPVCESLQGGSPSTTVTVTAL-EALLCPSATVTQVCSNPPCE--T 1296 1680 YIPGTQITFPPRPYNSASMSPGHP-----THLAAAASA-----EREREREKE 1723 RERERIAAASSDLYLRPGSEQPGRPGSHGYVRS----PSPSVRTQETMLQQRPSVFQGT 1778 1404 -GTALLAPF-PTQRVCSNP-------PCETHETGTTHTATTVTSNMSSNQ-DPPP 1448 GTTNTATTAMSSVGANHQRDARR----ACAAGTPAVIRISVATGALEAAQGSKSQCQ 1167 1168 TRQTSATSTTMTVMATGAP-----1197 NCTSVITPLDPTAQLRIMPLPAGGPSISQGLPASRYNTAADALAALVDAAASAPQMDVSK 1838 AASDQGEV----ESTQGDSVNITSSSALTTTVSSTLTRAVTTVTQSTPVPQPSVPPPEEL 1504 1505 OVSPGPROOLPP-----ROLLQSASTALMGESAEVLSASQTPELPAAVDLSSTGEPSSG 1558 RALDPAAAAYLFQRQLSP-----TPG---YPSQYQLYAMENTRQTILNDYITSQQMQ 1624 ------PSALVSTPVRTKTSNRYSPESQAQSVHHQR 2114 -----QAAATLTEVANGIESLGVKPDLPPPPSKAPMKKENQWFDVGVI 1818 920 SSQVINP-TAITVSAAQTTLTAAGGLTT-PTITMQPVSQPTQVTLITA-PSGVEAQPVHD 976 : || | :: | :: : HETGTINTATISNAGSAQRVCSNPPCETHEIGITHTATIATSNGGTGQPEGGQQPPAGRP CETHQTTSTGTTMSVSVGALLPDATSSHRTVESGLEVAAAPSVTPQA-------1839 TKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSV 1899 VYSEAGKDKGPPPKSRYEEELRTRGKTTI--TAANFIDVIITRQIASDKDARERGSQSSD 1957 SSSSLSSHRYETPSDAIEVISPASSPAPPQEKL-QTYQPEVVKANQAENDPTRQYEGPLH 2016 HYRPQQESPSPQQQLPPSSQAEGMGQVPRTHRLITLADHICQIITQDFARNQVSSQTPQQ ------LIPEELAVTAAAEAAAQAAATEEAQALA---IQAVLQ--AAQQAVMGTGEP MDTSEAAATVTQAELGHLSAEGQEGQATTIPIVLTQQELAALVQQQQLQEAQAQQQHHHL PGSRVSP-----ENLVDKSRGSRPGK-----SPERSHVSSEPYEPISP 2199 ENTSPMV------KLNSSGGD-S LPVSILASPTTEQPTATVTIADSGQGDVQPGTVTLVCSNPPCETHETGTTNTAT ---TTV -AREPGGRSPAFV-OLAPLSSKVRLSSPSIKDLPAGRHSHAVSTAAMT------1559 QESAGSA-----VVATVVVQP---PPPTQSEVDQLSLPQELMAEAQAGTTTLMVTG---TTATSNMAGQHGCSN--PPCE------THET----PQVPVVHEKQDSLLLLSQRGAEPAEQRNDARSPGSISYLPSFFTK--2076 PPTSTFQNS-----1773 AKL-----1286 1344 1034 1092 1115 1516 1576 1198 1625 1357 1779 1449 1401 1297 1724 1713 977 1461 1653 2115 2153 1607 g 셤 ď g à 셤 δ οy à 셤 ŏ g ò QQ δ g ò g δ 8 à g qq Ω δ a 셤 셤 ò ò g QΥ ŏ 셤 οy ÓΥ

Db 105HSTMSSKSPRDWEQFEYKIOAELAVILKFVLDHEDGLNLNEDLENFLQKAPVPST 159  Qy 143AKKDPAFGGKHEAPSSPISGQPCGD	QY         33.2 KAKESKTREYZEKQFPEIRKQREQGERFQ-RVGQRGAGLSATIARSEHEISEIIDGLSEQ         390           b         369 ALQDKKCLEEKNEILQGKLSQLEEHLSQLQDNPPQEKGEVLGDVLQL         415           QY         391 ENNEKQMRQLSV		DD 902ECEQLVKEVAAWRDGYEDSQOEEAQYGAMFQEQLMTLKEECEKARQELQ 850  QY 878 DSSATGSADEDVDGEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVI 937  B51EAKEKVAGIESHSELQISRQONKLAEL 877  QY 938 PPMVSCTPCNIPIGTPVSGYALYQRHIKAAMHESALLEEQRQRQEQIDLECRSSTSPCGTS 997  ::
QY         2225 DWAAAQPGTEIFNLPAVTTSGSVSRCHSFADPASNLGLEDIIRKALMGSFDDK         2278           B         1879 EISAFKTCLPGFPGAPCAIKISKSPDGAHLTWEPPSVTSG	RESULT 28 US-08-195-487-4   Sequence 4, Application US/08195487     Sequence 4, Application US/08195487     Patent No. 5783403     GENERAL INFORMATION:	HENCERPORTS OF HERE	TYPE: anino acids   TYPE: anino acid

a a	995			
O.Y	1178 1031	PTEALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIKNAREGTRSPRT 1237   ::::::::::::::::::::::::::::::::::::		
oy Dp	1238	AHEISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIM 1297   1:		
Qy Dp	1298	QGTPRATTESFEDGLKYPKQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHEIPRQ 1357		
Oy Dp	1358 1132	DILTQESRKTPEVVOSTRPIIEGSISQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSR 1415     :       :       :		
Oy Dp	1416 1186	GMPPLEIVPENIKVVERGKYEDVRAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQ 1470		
O.y D.b	1471	LSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTSDVTIPPNKSTNHERKSTLTPTQRESIP 1530 :::		
Oy Db	1531 1263	AKSPVPGVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAA 1584 : :		
Oy Db	1585 1288	YLFQRQLSPTPGYPSQYQLXAMENTRQTILNDYITSQQMQVNLRPDVARGLSPREQPLGL 1644		
oy Op	1645	PYPATRGIIDLINNMPPTILVPHPGGTSTPPMDRITYIPGTGIIFPPRPYNSASMSPGHPT 1704   1		
Oy Dp	1705 1365	HLAAAASAERERERERERERERERIAAASSDLYLRPGSEQPGRPGS 1750 		
oy Op	1751	HGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMPLPAGGPSISQGLP 1810 :1:   :1  :   :1    :1		
Oy Dp	1811	ASRXNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLKSRSAAVSEQQQLEQKT 1870		
oy Ob	1871	LEVEKRSVQCLYTSSAFPSGKPQPHSSVYSEAGKDKGPPPKSRYEEELRTRGKTTITAA 1930 		
oy.	1931 1539	NFIDVIITRQIASDKDARERGSQSSDSSSLSSHRYETPSDAIEVISPASSPAP 1984		
Oy Dp	1985 1576	PQEKLQIYQPEVVKANQAENDPTRQYEGFLHHY-RPQQESPSPQQQLPPSSQ 2035		
Oy Dp	2036	AEGMGQVPRTHRLITL-ADHICQIITQDFARNQVSSQTPQQPPTSTFQNSPSALV 2089	,	
Q Op	2090	STPVRTKTSNRYSPESQAQSVHHQRPGSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEP 2149		

OY 2181DARSPGSISY Db 1805 MTKKLDVEEPDSAN- QY 2232 GTEIFNLPAYTSGSAR QY 2232 GTEIFNLPAYTSGSAR QY 2286 MSQPMGVVPGTANT- Db 1861 GYRPTTRSSAR QY 2286 MSQPMGVVPGTANT- Db 1909 LQQRNRYCPPHLKTC QY 2336 KSPIPGGGYLGT Db 1956 MQPLQIAGGTTRAQK QY 2392MLSSTPPTPI Db 2004 DRHEGRKQSTTEAQK RESULT 29 CFT-US93-06160-4 SGQUENCE 4, APPLICATION: APPLICANT: APPLICANT: TITLE OF INVENTION: TITL	LESEFTKLENTSPWYKSKKQEIFEKLNSSGG -SEFYSTRSAPASQASLRATSSTQSLAR-LGSPDY -SERG-HSFADPASNLGLEDITKALMGSFDDKVE		1804 1860 2285 1908 1955 2331 2003
2181  1805  2232  2236  1861  1909  2336  2392  2004  2004  2004  2004  2004  2007  2007  2007  2007  2007  2007  2007  2007	SPGSISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSGG      :     :     :		2231 1860 2285 1908 2335 2391 2003
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1956 MQPI 2392 2004 DRHE 2017 29 T-US93-06160 SEQUENCE 4, GENERAL INF APPLICANT TITLE OF TITLE 2415 2032 2032 EAR MATRIX		2003	
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ADDRESSEE: STREET: 53 CITY: BOST STATE: MA COUNTRY: US ZIP: 02109 COMPUTER READI	HURWITZ &		
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; COMPUTER READA			
1	ABLE FORM: :- Floppy disk		
COMPOTER	IBM PC compatible		
SOFTWARE	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0. Version #1.25		
CURRENT APPLIC			
; APPLICATION NUMBER: ; FILING DATE: 199306	NOMBER: PCT/US93/U016U :: 19930621		
CLASSIFICATION	ION:		
, NAME: PITCI	; ⊡		
REGISTRATION NUMBER:	REGISTRATION NUMBER: 27,829		
; TELECOMMUNICAS	ION:		
; TELEPHONE:	IONE: 617/248-7000		
; INFORMATION FOR	SEQ ID NO: 4:		
; SEQUENCE CHAR	CTERISTICS:		
; LENGTH: 21(	2101 amino acids		
ဝို မ	oriu linear : protein		
0-4			
tch	2.3%; Scc	2101;	
Best Local Similarity Matches 480; Conser	18.4%; vative 330	869; Gaps	ps 110
OV 52 QASQLLQQQQQQQL	OOOOOLRRRPSLLSEFHPGSDRPQERRISYEPFHPG		95

143	96	PSPVDHDSLESKRPRLEQVSDSHFQRVSAAVLPLVHPLPEGLRASAD 142 
HEKNOLADERSKLÖKE ELIGSMORVDRETARVBOOLIKLKKKOOOLEEBAAKDED	14.	CSSTFPEELSPPSHQAKREIRFLELQKVASSSSGNNFLSGSPASPMGDILQTPQFQMR
PEKPYSPPPVECKHRSIVOIIYDENEKKAEEAHKIFEGLGPRVELPLYNOPSDTKYYHEN  :::   :   :	168 218	DQNASPSKLSKEELJQSMDRVDREIAKVEQQILKLKKKQQQLEEEAAKPPE
1. FYNOVMEKKILLEFERENDARORE——OKICORNOQUAEMEKKVDRIENBPRR I—KTNOVMEKKILLEFERENDARORE——OKICORNOQUAEMEKKVDRIENBPRR MDRKINGLSEENGDLSFKLREFASHLOGLQDALNEITEEHSKATGEMEKGAGLEKELSA KAESKTREYYEKOPPEIRKOPEGOERRO—VRGGRGAGLSATJARSEHEISEIJDGLSEG  ALODKKCLE——EKNETJARKEREDGRAVEFINBNGIAERGPEKGALGOVODNYDD  ETT. S.	215	PEKPVSPPVEQKHRSIVQIIYDENRKKAEEAHKIFEGLGPKVELPLYNQPSDTKVYHEN
MDRKINGLSEENGDLSFKIREFASHLOOLODALNELTEEHSKATGEWLEKQAGLEKELSA KARESKTREYYEKOFPEIRKOREQOERPQ-RVGORGAGLSATIARSEHEISEIIDGLSEG ALGÖKKCLE	279	FRECQDEKTEKSQ  IKTNOVMRKKLILFFKRRNHARKQREQKICQRYDQLMEAWEKKVDRIENNPRR  :
KARESKTREYYEKOFPEIRKOREOGENPO-RYGORGAGISATIARSEHEISEIIDGISEG  ALQDKKCLE	305	MDRKINQLSEENGDLSFKLREFASHLQQLQDALNELTEEHSKATQEWLEKQAQLEKELSA
ENNEKQMROLSVIPPWAFDAEORRYKEINANGLMEDPMKVYKDROFMNWWTD    : :   : :   :   :   :	337	KAKESKTREYYEKQFPEIRKQREQQERFQ-RVGQRGAGLSATIARSEHEISEIIDGLSEQ ::
HEKEIFKDKFIQHPRNFGLIASYLERKSVPDCVLYYYLTKKNENYRALVR    1	391	ENNEKOMROLSVIPPMMFDAEQRRVKFINMNGLMEDPMKVYKDROFMNVWTD   ::
LÓSSISNLSOAKEELEQASGAHGARLTAQVAS	443	HEKEIFKDKFIQHPKNFGLIASYLERKSVPDCVLYYYLTKNENYKALVR
RNYGKRRGRNOOIARPSQEEKVEEKEEDKAEKTEKKEEEKKDEEE  ::::::::::::::::::::::::::::::::	47]	
KDEKEDSKENTKEKDKIDGTAEETEEREQATPRGRKTANSGGRRKGRITRSMTNEAAAAS    :	493 516	RNYGKRRGRNQQIARPSQEEKVEEKEEDKAEKTEKKEEF
AAAAATEEPPPPLPPPPEDISTEPVETSRWTEEEMEVAKKGIVEHGRNWAAIAKWGTK  AAAAATEEPPPPLPPPPPPISTEPVETSRWTEEEMEVAKKGIVEHGRNWAAIAKWGTK  KEKAAKLEILQQQLQVANEARDSAGTSVTQAQREKAELSRKVEELQACVETARQEQHE SEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRRPFEERDVSQCESVASTVSAQ  SIGIN	538	KDEKEDSKENTREKDKIDGTAEETEEREQATPRGRKTANSGGRRKGRITRSMTNEAAAS
KEKAAKLEILQOQLQVANEARDSAQTSVTQAQREKAELSRKVEELQACVETAAQEQHE SEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRKPREERDVSQCESVASTVSAQ	598	LKEVAEKQEATRQ-DHAQQLATAAEERE-ASLRERDAALKQ
SEAQCKNFYENYKRRHNLDNLLQQHKQKTSRKPREERDVSQCESVASTVSAQ  ::     :	611	
EDEDIEASN EEENPEDSEVEAVKPSEDSPENATSRGNTEPAVELEPTT	65£	SEAQCKNFYENYKRRHNLDNLLQQHKQKTSRKPREERDVSQCESVASTVSAQ ::
EEEKRRAADALEEQGRCISELKAETRSLVEGHKRERKELEEERAGRKGLEARLLQL ETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDVDQQEHSAEGSVCDPPPAT	710	EDEDIEASNEEENPEDSEVEAVKPSEDSPENAISRGNIEPAVELEPTI
ETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDVDQOEHSAEGGSVCDPPPAT	715	EEEKRRAADALEEQQRCISELKAETRSLVEQHKRERKELEEERAGRKGLEARLLQL
KADSVDVEVRYPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQOINAQREPQSDN	758	ETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDVDQQEHSAEEGSVCDPPPAT
EGEQLVKEVAAMR	818	KADSVDVEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDN
DSSATCSADEDVDGEPERQRMFPMDSK PSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVI          :   :   :     :	803	:
PPWVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEQRQRQEQIDLECRSSTSPCGTS ::	878	DSSATCSADEDVDGEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVI
PPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEQRQRQEQIDLECRSSTSPCGTS ::     :     :     :	851	EAKEKVAGIESHSELQISRQONKLAEL
KSPNREWEVLQPAPHQLITNLPEGVRLPTRPTRPPPPLIPSSKTTVASEKPSFIMGGSI	936 878	PPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEQRQRQEQIDLECRSSTSPCGTS ::
	966	KSPNREWEVLQPAPHQLITNLPEGVRLPTTRPTRPPPPLLPSSKTTVASEKPSFIMGGSI
SQGTPGTYLTSHNQASYTQETPKPSVGSISLGLPRQQESAKSATLPYIKQEEFSPRSQNS	914	:::
	058	SQGTPGTYLTSHNQASYTQETPKPSVGSISLGLPRQQESAKSATLPYIKQEEFSPRSQNS

QQ	
0y	1118 QPEGLLVRAQHEGVVRGTAGAIQEGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGI 1177
qq	995 QOEERGQQEREVARLTQERGRAQADLALEKAARAEL 1030
δ	<u>o</u>
q	1031EMRLONALNEQRVEFAT~LQEALAHALTEKEGKD 1063
QY	B AHEISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIM
qq	1064 -QELAKLRGLEAAQIKELEELRQT-VKQLKEQLAKKEKEHASGSGA 1107
δλ	QGTPRATTESFEDGLKYPKQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHEIPRQ 13 
<b>q</b>	1108 QSEAAGRIEPTGPKLEALRAEVSK1131
δо .	1358 DILTQESRKTPEVVQSTRPIIEGSISQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSR 1415
ф	1132LEQQCQKQQEQADSLERSLEAERASRAERDSALETLQGQLEEKAQELGHSQSAL 1185
Οy	1416 GMPPLEIVPENIKVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQ 1470
QQ	1186 ASAQRELAAFRIKVQDHSKAEDEWKAQVARGRQEAERKNSLISS 1229
Oy	1471 LSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTSDVTIPPNKSTNHERKSTLTPTQRESIP 1530
qq	1230LEEEVSILNRQVLEKEGESKELKRLVMAESEKS 1262
Οy	1531 AKSPVPGVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAA 1584
qq	1263
Qy	1585 YLFORQLSPTPGYPSQYQLYAMENTRQTILNDYITSQQMQVNLRPDVARGLSPREQPLGL 1644
qq	1288 LLCGRRCRAS-GREAEKÇRVASENLRQELTSQAERAELGGELKAWGEK-FFQKEQALS- 1344
. Оу	1645 PYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRITYIPGTQITFPPRPYNSASMSPGHPT 1704
đ	1345VSELLPAK 1364
οy	1705 HLAAAASAEREREREREKERERERIAAASSDLYLRPGSEQPGRPGS 1750
q	1365 HLCQQLQAEQAAAEKRHREELEQSKQAAGGLRAELLRAQRELGELIPLRQKVAEQDRTAQ 1424
Qγ	1751 HGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMPLPAGGPSISQGLP 1810
đ	1425 QLRAEKASYAEQLSMLKKAHGLLAEEN
QY	1811 ASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQKT 1870
QQ	1455 GERANLGRQFLEVELDQAREKYVQELAAVRADAETRLAEVQREAQSTARE 1504
οy	1871 LEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRGKTTITAA 1930
q	1505 LEV
οy	1931 NFIDVIITRQIASDKDARERGSQSSDSSSSLSSHRYETPSDAIEVISPASSPAP 1984
qq	1539 ELSKKLADSDQASKVQQQKLKAVQAQGGESQQEAQRF158KKLADSDQASKVQQQKLKAVQAQGGESQQEAQRF
δy	1985 PQEKLQTYQPEVVKANQAENDPTRQYEGPLHHY-RPQQESPSPQQQLPPSSQ 2035
qq	1576 -QAQLNELQAQLSQKEQAAEHYKLQMEKAKTHYDAKKQQNQELQEQLRSLEQLQKENKEL 1634
Οy	2036AEGMGQVPRTHRLITL-ADHICQIITQDFARNQVSSQTPQQPPTSTFQNSPSALV 2089
q	1635 RAEAERICHELQQAGLKTKEAEQTCRHLTAQVRSLEAQVAHADQQLRDLGKEQVATDALK 1694
ΟŊ	2090 STPVRTKTSNRXSPESQAQSVHHQRPGSRVSPENLVDKSRGSRPGKSPERSHVSSEPXEP 2149

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QY 52 QASQLLQQQQQQQLRRRPSLLSEFHPGSDRPQERRTSYEPFHPG 95 :  : :  :  :  :  :  :  .  .  .  .  .  .  .  .  .  .  .  .  .	96 PSPVDHDSLESKRPRLEQVSDSHFQRVSAAVLPLVHPLPEGLRASAD	DD 105HSTMSSKSPRDWEQFEYKIQAELAVILKFVLDHEDGLNLNEDLENFLQKAFVPST 159 QY 143AKKDPAFGCKHEAPSSPISGQPCGD 167	Db 160 CSSTFPEELSPPSHQAKREIRFLELQKVASSSSGNNFLSGSPASPMGDILQTPQFQMR 217 Qy 168DQNASPSKLSKEELIQSMDRVDREIAKVEQQILKKKKQQQLEEEAAKPPE 218	218 RLKKQ	QY 219 PEKPVSPPPVEQKHRSIVQIIYDENRKKAEEAHKIFEGLGPKVELPLYNQPSDTKVYHEN 278	279 IKTNQVMRKKLILFFKRRHHARKQREQKICQRYDQLMEAWEKKVDRIENNPRR	OY 332 KAKESKITEYYEKQFPEIRKQREQQERFQ-RVGQRGAGLSATIARSEHEISEIIDGLSEQ 390	Db 369 ALQDKKCLEEKNEILQGKLSQLEEHLSQLQDNPPQEKCEVLGDVLQL 415 Qy 391 ENNEKQMRQLSVIPPMMFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTD 442	443 HEKEIFKDKFIGHPRNEGLIASYLERKSVPDCVLYYYLTKKNENYKALVR	493 RNYGKRRGRNOOLARPSQEEKVEEKBEKREEFT	OY 538 KDEKEDSKENTKEKDKIDGTAEETEEREQATPRGRKTANSQGRRKGRITRSMTNEAAAAS 597	QY 598 AAAAAATEEPPPLPPPEPISTEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAKWGTK 657	QY 658 SEAQCKNFYENYKRRHNLDNLLQQHKQKTSRKPREERDVSQCESVASTVSAQ 709 ::	QY 710 EDEDIEASNEEENPEDSEVEAVKPSEDSPENATSRGNTEPAVELEPTT 757   1:1   :  :  :  ::    ::    ::    Db 719 EEEKRRAADALEEQQRCISELKAETRSLVEQHKRERKELEEERAGRKGLEARLLQL 774	QY 758 ETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDVDQQEHSAEEGSVCDPPPAT 817	QY 818 KADSVDVEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDN 877 :	QY 878 DSSATCSADEDVDGEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVI 937	QY 938 PPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEQRQRQEQIDLECRSSTSPCGTS 997 ::
SREPQAKPQLDLSIDSLDLSCEEGTPLSITSKLPRTQPDGTSVPGEPASP 1744 ISPPQVPVVHEKQDSLLLLSQRGAEPAEQRN 2180		DAKSPGSISILKSFFTRLENISFMVKSKKQEIFRKLNSSGGGDSDMAAARP 2231 	GTEIFNLPAVTTSGSVSSRG-HSFADPASNLGLEDIIRKALMGSFDDKVEDHGVV 2285	SPHSGGVCKPKLISKSNSRKS	CO-FPYNP	MQPIQIAEGTGTTTRQQRKRVSLEPHQGPGTPESKKATSCFP-RPMTPR 2003	2004 DRHEGERQSTERAQREARDARRQ 2032	SULT 30 08-466-390-4 Sequence 4, Application US/08466390	ATION: TOUKATLY, GARY LIDGARD, GRAHAM P EENTION: NOVEL, MALIGNANT CELL, TVPE MARKERS OF THE	INTERIOR NUCLEAR MATRIX i of 55S: HURWITZ & THIBEAULT	125 HIGH STREET 0STON MA USA	ZIF: 02110 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/466,390	TILING DAILS: 00-00N-1995 CLASSIFICATION: 455 ATTORNEY/AGENT INFORMATION: NAME: PITCHER ESQ, EDWUND R	REGISTRATION NUMBER: 27,829 REFERENCE/DOCKET NUMBER: MTP-013 TELECOMUNICATION INFORMATION: TELEPHONE: (617) 248-7000	TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 2101 amino acids	amino acid yy: linear TYPE: protein 4	Query Match 2.3%; Score 285.5; DB 1; Length 2101; Best Local Similarity 18.4%; Pred. No. 3.7e-09; Table 6.00. Construction 18.4%; Pred. No. 3.7e-09;

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SREPQAKPQLDLSIDSLDLSCEEGTPLSITS------KLPRTQPDGTSVPGEPASP 1744
                                                                                                                                                                                                                                                                                                              3YR----PITRSSARRSQAGVSSGAPPGRN-----SFYMGTCQDEPEQLDDWNRIAE 1908
                                                    STPVRTKTSNRYSPESQAQSVHHQRPGSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEP 2149
                                                                                                                                                               IS---PPQV------PVVHEKQ------DSL---LLLSQRGAEPAEQRN----- 2180
                                                                                                                                                                                                     STEIFNLPAVTTSGSVSSRG-HSFADPASNLGLEDIIRKALMGSFDDKVE----DHGVV 2285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #SQPMGVVPCTANT----SVVTSGETRREEGDPSPHSGGVCKPKLISKSNSRKS 2335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAEAERLGHELQQAGLKTKEAEQTCRHLTAQVRSLEAQVAHADQQLRDLGKFQVATDALK 1694
                                                                                                                                                                                                                                                                              ----DARSPGSISYLPSFFT----KLENTSPMVKSKKQEIFRKLNSSGGGDSDMAAAQP 2231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSPI---PGQGYLGTERPSSVSSVHSEGDYHRQTPGWAWEDRPSSTGSTQ-FPYNPLTMR 2391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CANT: TOUKATLY, GARY
CANT: LIDGARD, GRAHAM P
CANT: LIDGARD, GRAHAM P
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SISPONDENCE ADDRESS:
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Y: BOSTON
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MEDUTER READABLE FORM:
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MEDUTER: IBM PC compatible
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SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin NUMBER: US/08/470,950
CLASSIFICATION NUMBER: 06-JUN-1995
CORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-013
FELECOMMUNICATION INFORMATION:
FELECOMMUNICATION 1248-7100
SOUTH SECOND NO: 4:
GUENCE CHARACTERISTICS:
CENGTH: 2101 amino acids
TOPOLOGY: Linear
INFOLOGY: Linear
TOPOLOGY: Linear
TOPOLOGY: Linear
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	CSSTFPEELSPPSHQAKREIRFLELQKVASSSSGNNFLSGSPASPMGDILQTPQFQMR	δλ	1178 PTEAL
0 رو د	168DONASPSKLSKEELIQSMDRYDREIAKVEQQILKLKKKQQQLEEEBAAKPPE 218	qa	1031 EMR
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qq	878	::
δλ	866	KSPNREWEVLOPAPHOLITNLPEGVRLPTTRPTRPPPPLIPSSKTTVASEKPSFIMGGSI 1057
q	914	KEVARLETLYRKAGEQOETASRELYKEPARAGDROPEWL952
oy 4	1058	PYIKQEEFSPRSQNS
2	808	- EEQQGGRQFCSTQAALQAMEREAEQMGNELERRIRAALMESQGGRQFCSTQAA
Oy Dp	1118	QPEGLLVRAQHEGVVRGTAGAIQEGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGI 1177
δλ	1178	PTEALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIKNAREGTRSPRT 1237
QQ	1031	EMRLQNALNEQRYVEFATLQEALAHALTEKEGKD
δ	1238	AHEISLKRSYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIM 1297
QQ	1064	-OELAKLRGLEAAQIKELEELROT-VKOLKEQLAKKEKEHASGSGA 1107
οy	1298	OGTPRATTESFEDGLKYPKQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHEIPRQ 1357 
qq	1108	QSEAAGRTEPTGPKLEALRAEVSK131
δŏ	1358	TRPILEGSISQGTPIKEDNNSGQSAIKHNVKSLITGPSKLSR 141 :: :   ::   ::     ::
QQ	1132	LEQQCQKQQEQADSLERSLEAERASRAERDSALETLQGQLEEKAQELGHSQSAL 1185
δλ	1416	GMPPLEIVPENIKVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQ 1470
ති <sub>.</sub>	1186	ASAQRELAAFRTKVQDHSKAEDEWKAQVARGRQEAERKNSLISS 1229
Qy	1471	LSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTSDVTIPPNKSTNHERKSTLTPTQRESIP 1530
QQ	1230	LEEEVSILNRQVLEKEGESKELKLVMAESEKS 1262
ΟŊ	1531	AKSPVPGVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAA 1584
QQ	1263	QKLEESCACCRQRQPATVPELQNAA 1287
οy	1585	YLFQRQLSPTPGYPSQYQLYAMBNTRQTILNDYITSQQMQVNLRPDVARGLSPREQPLGL 1644
ΩD	1288	LICGRRCRAS-GREAEKQRVASENLRQELTSQAERAEELGQELKAWQEK-FFQKEQALS- 1344
Qy	1645	PYPATRGIIDLINMPPTILVPHPGGTSTPPMDRITYIPGTQITFPPRPYNSASMSPGHPT 1704
QQ	1345	TLQLEH TSTQAL TSTQAL VSELLPA K 1364
Qy	1705	HLAAAASAEREREREREKERERERIAAASSDLYLRPGSEQPGRPGS 1750
qq	1365	HLCQQLQAEQAAAERRHREELEGSKQAAGGLRAELLRAQRELGELIPLRQKVAEQERTAQ 1424
QY	1751	HGYVRSPSPSVRIQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMPLPAGGPSISQGLP 1810
QQ	1425	QLRAEKASYAEQLSMIKKAHGLLAEEN
οy	1811	ASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQKT 1870
qq	1455	GERANIGRQFLEVELDQAREKYVQELAAVRADAETRLAEVQREAQSTARE 1504
δλ	1871	LEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRIRGKTTITAA 1930
qq	1505	LEVROKLTAQVE 1538
δ	1931	NFIDVIITRQIASDKDARERGSQSSDSSSSLSSHRYETPSDAIEVISPASSPAP 1984
qq	1539	ELSKKLADSDQASKVQQQKLKAVQAQGGESQQEAQRFLSKKLADSDQASKVQQQKLKAVQAQGGESQQEAQRF
οy	1985	PQEKLQTYQPEVVKANQAENDPTRQYEGPLHHY-RPQQESPSPQQQLPPSSQ 2035

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219 PEKPVSPPPVEQKHRSIVQIIYDENRKKAEEAHKIFEGLGPKVELPLYNQPSDTKVYHEN 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : | ||: : | || | : : : : : : : | :| 309 MDRKINQLSEENGDLSFKLREFASHLQQLQDALNELTEEHSKATQEWLEKQAQLEKELSA 368
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                                                                          Query Match 2.3%; Score 285.5; DB 1; Length 2101; Best Local Similarity 18.4%; Pred. No. 3.7e-09; Matches 480; Conservative 336; Mismatches 924; Indels 869; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         279 I--KTNQVMRKKLILFFKRRNHARKQRE-----QKICQRYDQLMEAWEKKVDRIENNPRR 331
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  protein
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2090 STRVERTSNRYSPESOAOSVHHORPGSRVSPENLYDKSRGSRPGKSPERSHYSEPEPP 1695 SREGOADALDLSIDSJCEGEGTPLSITS	Qy Db	2036ABGMGQVPRTHRLITL-ADHICQIITQDFARNQVSSQTPQQPPTSTFQNSPSALV	989
2150 ISPPDVYPVHERQDSLLLLGGRGAEPAEGRN	QY Dp	2090 STPVRTKTSNRYSPESQAQSVHHQRPGSRVSPENLVDKSRGSRPCKSPERSHVSSEPYEP 21	4 4
1181DARSPGSISYLPSFFTKLENTSPHVKSKKOEIFRKINASGGGGDSDMAAAQP 11805 WTKKLDVEEDDSANSSFYSTRSAPASOASLRATSSTOSLAF [15] [1] [1] [1] [1] [1] [1] [1] [1] [1] [1	Q D	2150 ISPPQVPVVHEKQDSLLLLSQRGAEPABQRN	180
2232 GTEIFNLPAVTTSGSVSRG-HSFADPASNIGLEDIIRKALMGSFDDKVEDHGVV 1861 GYRPTRESSARRSQAGVSGAPPGRNSPYMGTCODEPEQLDDWNRIABE 2286 MSQPMGVVPGTANTSVYNGSERREEGDPSPHSGGCVCKPLIJSKSNSRKS 2386 MSQPMGVVPGTANT	Qy	2181DARSPGSISYLPSFFTKLENTSPWYKSKRQEIFRKINSSGGGDSDMAAAQP	231
2286 MSQPMGVVPGTANTSVYTSGETRREEGDPSPHSGGVCRPKLISKSNSRKS	Qy	2232 GTEIFNLPAVTTSGSVSSRG-HSFADPASNLGLEDIIRKALMGSFDDKVEDHGVV	285
2336 KSPIPGGGYLGTERPSSYSSVHSEGDYHRQTPGWAWEDRPSSTGSTQ-PPTNPLTMR  1956 MOPIQIAEGTGITTRQORKRVSLEPHQGPGTPESKKATSCFP-RPWTPR  2392MLSSTPPTPIACAPSAVNQAAPHQ 2415  2004 DRHEGRKQSTTEAGKKAAPASTKQADRRQ 2032  SULT 33  SULT 33  SULT 34  STAPLICAMT: LIGGARLA MALIGNART CELL TYPE MARKERS OF THE TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX  APPLICAMT: LIGGARLA MALIGNART CELL TYPE MARKERS OF THE TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX  APPLICAMT: LIGGARLA MALIGNART CELL TYPE MARKERS OF THE TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX  APPLICAMT: LIGGARLA MALIGNART & THIBEAULT  STREET: 125 HIGH STREET  CITY: BOSTON  STREET: 125 HIGH STREET  CITY: BOSTON  STREET: 125 HIGH STREET  COUWIRK: NA  COUWIRK: PLOPOS/MS-DOS  SOFTWARE: PLOPDY disk  COUWIRK: PLOPOS/MS-DOS  SOFTWARE: PLOPOS/MS-DOS  SOFTWARE: PLOPOS/MS-DOS  SOFTWARE: PLOPOS/MS-DOS  CURRESTONION NUMBER: US/08/483,924  FILLGAILCATION NUMBER: US/08/483,924  FILLGAILCATION NUMBER: US/08/483,924  FILLGASIFICATION: 435  ATTORNEY/AGENT INFORMATION:  REGISTRATION NUMBER: 27,829  RESTSPRENCE/COCKET NUMBER: 27,829  RESTSPRANION NUMBER: 27,829  RESTSPRANION NUMBER: 27,829  RESTSPRANION NUMBER: 27,829  TELECOMMUNICATION INFORMATION:  TELEPHONE: (617) 248-700  TELEFAN: (617) 248-700  TELEFAN: (617) 248-700	Qy	2286 MSQPMGVVPGTANTSVVTSGETRREEGDPSPHSGGVCRPKLISKSNSRKS   1   1   1   1   1   1   1   1   1	335
2392MLSSTPPTPIACAPSAVNQAAPHQ 2415 2004 DRHEGRKQSTTEAQKKAAPASTKQADRRQ 2032 50LT 33 -08-433-924-4 Sequence 4, Application US/08483924 FABLICANT: TOUKATLY, GARY APPLICANT: LIDGARD, GRAHAM P TITLE OF INVENTION: APPLICANT: LIDGARD, GRAHAM P TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX CORRESPONDENCE S: ADDRESSEE: TESTA, HURMITZ & THIBEAULT STREET: 125 HIGH STREET CITY: BOSTON STATE: MA COUNTRY: USA ZIP: O2110 COMPUTER: EADABLE FORM: MEDION TYPE: PLOPPY disk COMPUTER: IBM PC Compatible COMPUTER: IBM PC Compatible COMPUTER: IBM PC COMPATION: MEDION TYPE: RICHORY O38 ZIP: ADDRESSEE: TOOPPY disk COMPUTER: IBM PC COMPATION: MEDION TYPE: RICHORY O38 ZIP: ADDRESSEE: TOOPPY disk COMPUTER: STATE: MA CONFUTER: STATE: MA TOORET STEATION NUMBER: 27,829 REGISTRATION NUMBER: 27,829 REGISTRATION NUMBER: 27,829 REGISTRATION NUMBER: MTP-013 TELEPHONE: (617) 248-7000 TELEPHONE: (617) 248-7000 TELEPHONE: (617) 248-7000 TELEPHONE: (617) 248-7000 TELEPHONE: (617) 248-7000 INFORMATION FOR SEQ ID NO: 4:	Qy	2336 KSPIPGQGYLGTERPSSVSSVHSEGDYHRQTPGWAWEDRPSSTGSTQ-FPYNPLTMR	391 303
SULT 33 -08-483-924-4  Sequence 4, Application US/08483924  Patent No. 5882876 GENERAL INFORATION: APPLICANT: TORKATLY, GARY APPLICANT: TORKATLY, GARY APPLICANT: LIDGARD, GRAHAM P TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF TITLE OF INVENTION: NOVEL MALIGNANT & THIBEAULT STREET: 125 HIGH STREET COUNTY: BOSTON STATE: MA COUNTY: USA ZIP: 03110 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: 107-108/MS-DOS SOFWWARE: PATENTION DATA: APPLICATION NUMBER: US-09/08/483,924 FILING DATE: 07-JUN-1995 ATTONNEY, AGENT INFORMATION: NAME: PITCHER ESQ. EDMUND R REGISTRATION NUMBER: 77,829 REGISTRATION NUMBER: MTP-013 TELECHONE: (617) 248-7000 TELECHONUMICATION FOR SEQ ID NO: 4:	2	2392MLSSTPPTPIACAPSAVNQAAPHQ 2415 2004 DRHEGRKQSTTEAQKKAAPASTKQADRRQ 2032	
CCATION: 435 GENT INFORMATION: STITCHER ESQ, EDMUND R WION NUMBER: 27,829 TEADCOKET NUMBER: MTP-01 MICATION INFORMATION: RE: (617) 248-700 FOR SEQ ID NO: 4:	8 B D C C C C C C C C C C C C C C C C C C	SULT 33 -08-483-924-4 -08-483-924-4 -08-483-924-4 -08-483-924-4 -08-483-924-6 -08-882876 -08-882876 -08-882876 -08-882876 -08-882876 -08-882876 -08-882876 -08-882876 -08-882876 -08-882876 -08-88288888888888888888888888888888888	
		AGENT 10-20M-1993 AGENT INFORMATION: 17CHER ESO, EDMUND R ATION NUMBER: 27,829 MICATION INFORMATION: EE, C617) 248-7000 EE, (617) 248-7100 EOR SEO ID NO: 4:	

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                                                                                                                                                Length 2101;
                                                                                                                                              Query Match 2.3%; Score 285.5; DB 2; Length 3 Best Local Similarity 18.4%; Pred. No. 3.7e-09; Matches 480; Conservative 336; Mismatches 924; Indels
                                                                                                                                                                                                                                                                                               PSPVDHDSLESKRPRLEQVSDSHFQRVSAAVLPLVHPLPEGLRASAD----
               LENGTH: 2101 amino acids
TYPE: amino acid
TOPOLGGY: linear
MOLECULE TYPE: protein
US-08-483-924-4
SEQUENCE CHARACTERISTICS
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QQ	851EAKEKVAG	
δλ	938 PPMVSCTPCNIPIG	PPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEQRQRQEQIDLECRSSTSPCGTS 997
qq	878 HANLA	RALQOVQEKEVRAQKLADDLSTLQEKMAATS 913
QY Dp	998 KSPNREWEVLQPAP     :::  914 KEVARLETLVRKAG	KSPNREWEVLQPAPHQLITNLPEGVRLPTTRPPPPLIPSSKTTVASEKPSFIMGGSI 1057 
QY	1058 SOGTPGTYLTSHNO	SQGTPGTYLJSHNQASYTQETPKPSVGSISLGLPRQQESAKSATLPYIKQEEFSPRSQNS 1117
QQ	:     953 -EEQQGRQFCSTQA	:
οy	1118 QPEGLLVRAQHEGV	QPEGLLVRAQHEGVVRGTAGAIQEGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGI 1177
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ογ	1531 AKSPVPGVDPVVSH	AKSPVPGVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAA 1584
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QY	1585 YLFQRQLSPTPGYP	YLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITSQQMQVNLRPDVARGLSPREQPLGL 1644
q	1288 LLCGRRCRAS-GRE	LLCGRRCRAS-GREAEKQRVASENLRQELTSQAERAEELGQELKAWQEK-FFQKEQALS- 1344
Οy	1645 PYPATRGIIDLTNM	PYPATRGIIDLINMPPILLVPHPGGTSTPPMDRITYIPGTQITFPPRPYNSASMSPGHPT 1704
qq	1345	TLQLEHTSTQALVSELLPAK 1364
Qy	1705 HLAAAASAE	AAAASAERERERERERERERERERIAAASSDLYLRPGSEQPGRPGS 1750
Dp	1365 HLCQQLQAEQAAAE	
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qq	1425 QLRAEKASYAEQ	-LRAEKASYAEQLSMLKKAHGLLAEEN
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                                                                                                                                                                                                   SREPQAKPQLDLSIDSLDLSCEEGTPLSITS-----KLPRTQPDGTSVPGEPASP 1744
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                                                                                                                                                                                                                                                                                                                                                                                                                          1805 MTKKLDVEEPDSAN--SSFYSTRSAPASQASLRATSSTQSLAR-LGSPDYGNSALLSL-P 1860
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTEIFNLPAVTTSGSVSSRG-HSFADPASNLGLEDIIRKALMGSFDDKVE-----DHGVV 2285
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                                                                                                                                                                                                                                                 STPVRTKTSNRYSPESQAQSVHHQRPGSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEP
                                                                                                                                                                                                                                                                                                                       2150 IS---PPQV-----PVVHEKQ-----DSL---LLLSQRGAEPAEQRN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2286 MSQPMGVVPGTANT-----SVVTSGETRREEGDPSPHSGGVCKPKLISKSNSRKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSPI----PGQGYLGTERPSSVSSVHSEGDYHRQTPGWAWEDRPSSTGSTQ-FPYNPLTMR
                                                                                                     PQEKLQTYQPEVVKANQAENDPTRQYEGPLHHY-RPQQESPSPQQQLPPSSQ-----
                                                                                                                                                                           ---AEGMGQVPRTHRLITL-ADHICQIITQDF--ARNQVSSQTPQQPPTSTFQNSPSALV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Trichohyalın and Transglutaminase-3 and TITLE OF INVENTION: Mehods of Using Same NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear STREET: 620 Newport Center Drive, Sixteenth Floor
                                                                    1539 E----LSKKLADSDQASKVQQQKLKAVQAQGGESQQEAQRF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk .
COMPUTER: IBM PC COMPATIBLE
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: US/08/056,200
FILING DATE: 30-APR-1993
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Patent No. 5616500
GENERALINEORAMYION:
APPLICANT: Steinert, Peter M.
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Lee, Seung-Chul
Kim, In-Gyu
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APPLICANT: Chung, SOO-Il
APPLICANT: Park, Sang-Chul
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
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US-08-056-200-94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 LKKKQQQLEEEAAKPPEPEKPVSPPVEQKHRSIVQIIYDENRKKAEEAHKIFEGLGPKV 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 RHQQEFAVPDYRSSHLEVSQASQLLQQQQ----QQQLRRRPSLLSEFHPGSDRPQERRTSY 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  319 EKKVDRIENNPRR----KAKES-----KTREYYEKQFPEIRKQREQQER-----
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NAME: Fedrick, Michael F.
REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: 114054.001A
TELECOMMUNICATION INFORMATION:
                                                                                                               TELEPHONE: (714) 760-0404
TELEFAX: (714) 760-9502
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 1898 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-056-200-94
                                                                                                                                                                                                                                                                                                            linear
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                                                           1085 RETRRAGELERQYRKEEELQQE----EEQLLREEPEKRRRGERERQCREEEELQQEEEQL 1140
1032 EWERQYRKKDELQQEE-----EQLLREEREKRRLQERERQYREEEELQQEEEQLLGEE 1084
                                                                                                                  1141 LREEREKRRRQELERQYREEEELQRQKRKQRYRDED------QRSDLKWQWEPEKEN 1191
                                                                                                                                                                                           1192 AVRDNKVYCKGRENEQFRQLEDSQVRDRQSQQDLQHLLGEQQERDREQERRRWQQANRHF 1251
                                                                                                                                                                                                                           PMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTPVSGYAL 959
                                                                                                                                                                                                                                                                                        960 YORHIKAMHESALL----EEQRQRQEQIDLECRSSTSPCGTSKSPNREWEVLQPAPHQ 1013
                                                                                                                                                                                                                                                                                                              -----NHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRP-----EPQSDN
                                                                                                                                                              APPLICANT: Lee, Seung-Chul
APPLICANT: Kim, In-Gyu
APPLICANT: Chung, Soo-11
APPLICANT: Park, Sang-Chul
TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and
TITLE OF INVENTION: Mehods of Using Same
                              -ETQVNDSISAETAEQMDVDQQEHSAEEGSVCDPPPATKADSVDVEVRVPE-
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P: 620 Newport Center Drive, Sixteenth Floor
Newport Beach
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APPLICATION NUMBER: US/08/800,644
FILING DATE: 14-FEB-1997
CLASSIFICATION 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/056,200
FILING DATE: 30-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentrn PATENT
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 94, Application US/08800644 Patent No. 5958752 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Fedrick, Michael F.
REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NII
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Steinert, Peter M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (714) 760-0404
TELEFAX: (714) 760-9502
INFORMATION FOR SEQ ID NO: 94
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Length 1898;

DB 2;

Score 284; DB 2 Pred. No. 4e-09;

Query Match 2.2%; Best Local Similarity 18.5%;

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                                                                                                                                                                                                                                                                                               EPFHPGPSPVDHDSLESKRP-----RLEQVSDSHFQRVSAAVLPLVHPLPEGLRASA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DAKKDPAFGGKHEAPSSPISGQPCGDDQNASPSKLSKEELIQSMDRVDREIAKVEQQILK 201
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Conservative 170; Mismatches 376; Indels 382; Gaps
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                               TVSQIDPS--SIERAYAALGLPYQVNQMPTQPQVQAKNQQNQQPGQSPQGMRPMSNMSAS
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                                                                                                          Sequence 2, Application US/08227536
Patent No. 5658784
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Exen, Mark
APPLICANT: Livingston, David
TITLE OF INVENTION: NUCLEIC ACID, ENCODING TRANSCRIPTION
TITLE OF INVENTION: FACTOR P300 AND USES OF P300
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARCHAUGHIN, Gagnebin & Hayes
STREET: Ten Post Office Square
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                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                             ATTORNEY AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen A.
REGISTRATION NUMBER: 34,380
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/227,536 FILING DATE: 14-APR-1994
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TELECOMMUNICATION INFORMATION:
TELEFAHONE: (617) 542-2290
TELEFAX: (617) 451-0313
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                           Floppy disk
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC COM
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1084 LGIPDYFDIVKSPMDLSTIKRKLDTGQYQEPWQYVD------DIWLMFNNAWLYNR 1133
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672 GPNMGQPQPGMTSNGPLPDPSMIRGSVPNQMMPRITPQSGLNQFGQMSMAQPPIVPRQTP 731
                                                                                                                                                                     732 PLQHHGQ-----LAQPGALNPPMG-YGPR---------MQQPSNQG---Q 763
                                                                                                                                                                                                                                                                                                                                                                                                 522 AEKTEKKEEEKKDEEEKDEKEDSKENTKEKDKIDGTAEETEEREQATPRGRKTANSQGRR 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               582 KGRITRSMINEAAAAAAAAATEEPPPPLPPP-------PEPISTEPVETSRWT 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  630 EEEMEVAKKGLVEHGRNWAAIAKMVGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRK 689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                941 --SQPAVSIEGOVSNPPSTSSTEVNSQAIAEKQPSQEVKMEA------KMEVDQ 986
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                                                                                                405 PMMFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNFGLIAS 464
                                                                                                                                                                                                                                                  YLERKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGRNQ---QIARPSQEEKVEEKEEDK 521
                                                                                                                                                                                                                                                                                                                    -----QGMNVTNIPLAPSSGQAPVSQAQM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SSSSCPVNSPIMPPG-----SQGSH
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NUCLEIC ACID ENCODING TRANSCRIPTION FACTOR P300 AND USES OF P300

TITLE OF INVENTION: NUCLEIC ACID ENCODING TRAN
TITLE OF INVENTION: FACTOR P300 AND USES OF P3
NUMBER OF SEQUENCES: 13
CARRESPONDENCE ADDRESS:
CARDRESSEE: Weingarten, Schurgin, Gagnebin &

Ten Post Office Square

Boston

OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/04682

COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-PORTING

COMPUTER READABLE FORM:

02109

COUNTRY:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,536
FILING DATE: 14-APril-1994

FILING DATE: CLASSIFICATION:

ATTORNEY/AGENT INFORMATION: NAME: Holliday C. Heine, REGISTRATION NUMBER: 34,

CLASSIFICATION:

REGISTRATION NUMBER: 34,346
REFERENCE/DOCKET NUMBER: DFCI-308Xq9999
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-2290
TELEFAX: (617) 451-0313
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

: 2414 amino acids amino acid

LENGTH:

; MOLECULE TYPE: protein PCT-US95-04682-2

TOPOLOGY:

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FORQLSPTPGYPSQYQLYAMENTRQTILNDYITSQQMQVNLRPDVA----RGLSPREQPL 1642
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                                                                                                                                                                                                                                                                                                                                                                                                                               -AKSPVPG----VDPVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAAYL 1586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NANCSLPSCQXMKRVVQHT-----KGCKRKTNGGCPICKQLIALCCYH-----AKH 1795
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                                                                                                                                                                                                KLYATME-----KHKEVF----FVIR--LIAGPAANSLPPIVDPDPLIPCDLMDGRDA
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                                                               1373 STRPIIEGSISQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVER
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PRMQPQPSPHHVSPQTSSPHPGLVAAQANPMEQGHFASPDQNSMLSQLASNP 2380
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                                                                                                                                                                                                                                                                                                                                          ----STLTP--TQRESIP---
                                                                                                                                                      1433 GKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDD-
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118;
                                                                                                              401 SHWKNCTRHDCPVCLPLK---NAGDKRNQQPILTGAPVGLGNPSS---LGVGQQSAPNLS 454
                                                                                                                                                                 177 SKEELIQSMDRVDREIAKV------EQQILKLKKKQQQLEEEAAKPPEPEKPVSPP 226
                                                                                                                                                                                                       TVSQIDPS--SIERAYAALGLPYQVNQMPTQPQVQAKNQQNQQPGQSPQGMRPMSNMSAS 512
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                                                                                                                                                                                                                                                                           -QRVGQRGAGLSATIARSEHEI----SEIIDGLSEQEN----NEKQMRQLSVI----P
Query Match 2.2%; Score 284; DB 5; Length 2414; Best Local Similarity 19.0%; Pred. No. 5.6e-09; Matches 454; Conservative 300; Mismatches 864; Indels 774;
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Sequence 2, Application PC/TUS9504682 GENERAL INFORMATION: APPLICANT:

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764 FLPOTOFPS796	RR 5	797	582 KGRITRSMTNBAAAAAAAAAATEEPPPPLPPPPEPISTEPVETSRWT 629	817 IHCPQLPQPALHQNSPSPVPSRTPTPHHTPPSIGAQQPPATTIPAPVPTPP 867	630 EEEMEVAKKGLVEHGRNWAAIAKMVGTKSEAQCKNFYFNYKRHNLDNILQQHKQKTSRK 689	868AMPPGP	690 PREERDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVK-PSEDSPENAITSR 744      :     :       :	745 GNTEPAVELEPITETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDVDQ	::    :  941SQPAVSIEGQVSNPPSTSST	801 QEHSAEEGSVCDPPPATKADSVDVEVRYPENHASKVEGDNTKERDLDRASEKVEPRDEDL 860	861 VVAQQINAQRPEPQSDNDSSATCSADEDVDGEPERQRWFPNDSKPSL 907	1032 TSATQSSPAPGQSKKKIFKPEELRQALMPTLEALYRQDPESLPFRQPVDPQL 1083	908 LN-PTGSILVSSPLKPNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTPVSGYALYQR 962	963 HIKAMHESALLEEQRQRQEQIDLECRSSTSPCGTSKSPNREWEVLQPAPHQLITNLPE 1020	1134 KTSRVYKYCSKLSEVFEQEIDPVMQSLGYCGRKLEFSPQTLCCY 1178	1021 GVRLPTTRPTRPPPPLIPSSKTTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQETPK 1080   1   1   1   1   1   1   1   1   1	1081 PSVG-SISLG-LPRQQESAKSATLPYIKQEEFSPRSQNSQPEGLLVRA 1126	1207 EIQGESVSLGDDPSQPQTTIN	1127 -QHEGVVRGTAGAIQEGSITRGTPTSKISVESIPSLR-GSITQGTPALPQ 1174	1175 TGIPTEALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIK 1226 11		1378 VQEYGSDCPPPNQRRVYISYLDSVHFFRPKCLRTAVYHEILI-GYLEYVKKLGYTTG 1433	1262 ESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYP 1315	1316 KQIKRESPPIRAFEGAITKGKPY-DGITTIKEMGRSIHEIPRODILTOESRKTPEVVQ 1372 14   1   1   1   1   1   1   1   1   1	1373 STRPIIEGSISQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSRCMPPLEIVPENIKVVER	: : :   : :	1433 GKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDD 1478    :
qq	ò	qq	٥y	g	Qy	Q	δ δ	δŏ	QQ	Oy Dp	οy	q	Qy Dp	Οy	g	Oy Dp	Qy	g	Qy	QY	δλ	QC	QY Dp	Qy	οχ	qq	Oy Db

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1531 -AKSPVPG---VDPVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAYL 1586
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                                                                                                         1630 FLTLARDKHLEFSSLRRAQWSTMCMLVELHTQSQDRFVYTCNECKHHVETRWHCTVCEDY 1689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1745 PGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITP-LDPTAQLRIMPLPAGGP 1803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1933 IDVIITRQIASDKDARERGSQSSDSSSSLSSHRYETPSDAIEVISPASSPAPPQEKLQTY 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1686 ITFPPRPYNSASMSPG-HPTHLAAAASAERERERERERERERERIAAASSDLYLRPGSEQ 1744
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                                                                                                                                                                                                                                     1504 DVTIPPNKSINHERK------STLTP--TQRESIP-----
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1479 --TSARRTPVSYQ-----NTM-----
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CITY: Lexington
STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----SLESKRPRLE-QVSDSHFQRVSAAVLPLVHP--LP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGLRASADAKKDPAFGGKHE-----APSSPISGQPCGDDQNASPSKLSKEELIQSMD 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPLPATLETPV-PAFLKNQEFLQARTPTLASTPIPPTP----QAPSPA----- 399
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                                                                                                  SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLLSEFHPGSDRPQERRTSYEPFHPGPSPVDHD-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4641AAAA
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-861-6240.
                                                                                                                                                                                                                                                                                                                          FILING DATE: 25-CCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,762
FILING DATE: 02-UN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/180,548
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/660,412
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,803
FILING DATE: 25-CCT-1990
                                                                                                                                                        APPLICATION NUMBER: US/07/853,913
FILING DATE: 19920319
CLASSIFICATION: 435
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                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1618 amino acids
                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein US-07-853-913-4
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U.S.A.
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EEGEESREESEEDELGETLPDSTPLGFYLRSPTSPRWTPLESRGHPLKETGKEGW---- 1330 : :: : : | :|:| :: : : EVMEPPLEEESLEAKRVQGLEGPRKDLEEAGGLGTEFSE--LPGKSRDPWEPPREGREES 1175 | :|| :| || PULVSPSPTYTPILEDAPGLQPQAEGSQEASWGVQGRAEAGKVESEQEELGSGEIPEGLQ 1275 1028 RPTRPPPPLIPSSKTTVASEKPSFIMG-----GSISQ-----GTPGTYLTSHNQASYT 1075 GVVR----GTAGAIQE-GSITRGTPTSKISVE-SIP---SLRGSITQGTPALPQTGIPTE 1180 948 VQRWED----TVEKDQELAQESPPGMAGVENKDEAELNLREQDGFTGKEEVVEQGELNA 1002 EEQRQRQEQIDLECRSSTSPCGTS----KSP-NREWEVLQPAPHQLITNLPEGVRLPTT 1027 1076 QETPKPSVGSISLGL-----PRQQESAKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHE 1129 1430 GAGRWGPGSSVGSLQALSSSQRGEFLESDSVSVPWDDSLRGAVA----GAPKTALETE 1485 ----ALVKGSISRM-PI----EDSSP-----EKGREEAASKGHVI-----YEGKSGH 1218 1486 SQDSAEPSGSEEESDPVSLEREDKVPGPLEIPSGMEDAGPGADIIGVNGQGPNLEGKSQH 1545 775 AEDESVETQVNDSISA---ETAEQMDVDQQEHSAEE------GSVCDPPPATKA 819 PPMVSCTPCNIPI-----ALL 973 -EKENQE------DLRSPEVGDEEALR----PLTKENQEPLRSLE------DENKEA 709 FKDKFIQHPKNFGLIASYLERKSVPDCVLYYYLTKKN-ENYKALVRNYGKRRGRNQQIA 506 ---LETLKSPETQAPLWTPEEINKSGGNESSRKGNSRTTGVCGSEPRDIQTPGRGESGII 892 731 VK----PSEDSPEN-----ATSRGNTEPAVELEPTTETAPSTSPSLAVPSTKP 774 DSVDVEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRP -- EPQSDN 877 K-----TREYYEKQFPEIRKQRE-QQERFQRVGQRGAGLSATIARSEHEISEIIDGL 387 SEQENNEKQMRQLSVIPPMMFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHEKEI 447 ----LEKENQEPLKTL-----EEEDQSIV 732 RPSQEE-----KVEEKEEDKAEKTEKKEEEKKDEEEKDEKEDSKENTKEKDKIDGTAEE 560 TEEREQATPRGRKTANSQGRRKGRITRSMTNEAAAA-----SAAAAAATEEPPPPL 611 787 LKSLDQEIARPLENENQE-----FLKSLKEESVEAVKSLETEILESLKSAGQEN---- 835 PPPPEPISTEPVETSRWTEEEM-----EVAKKG------LVEHGRNWAAIA 651 652 KMVGTKSEAQCKNFYFNYKR-----RHNL---DNLLQQHKQKTSRKPREE-----RD 695 DSSATCSADEDVDGEPERQRMFPMDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVI 937 614 KPTGKEDTQTLQSLQKENQELMKSLEGNLETFLFPGTENQELVSSLQENLESLTAL--------DPAVLASEGLEEPSEKEEGEEGEECGRDSDLSEEFEDLGTEAPFL----PGVP 893 1061 1118 1176 1216 1276 1130 337 388 448 710 507 733 561 836 969 820 1181 974 g ò ò g ò 셤 9 ò QQ à 셤 g δά q δŽ g δλ g q ġ ò ò g ð ò à ð g ŏ ŏ g ò

us-09-522-753-11.rai

219	ILSYDNIKNAREGTR-SPRTAHEIS-LKRSYESVEGNIKQGMSMR 1261 :	% d %	1238 AHEISLKR  - 987 V-PTSVHI. 1294 GSIMQGTP
RESULT 39 5180808-2 ; Patent No. APPLICA TITLE ( ; SEQUENCES 1	1180808-2 1180808-2 Patent No. 5180808 APPLICANT: RUOSLAHII, ERKKI I. TITLE OF INVENTION: VERSICAN CORE PROPEIN, NUCLEIC ACID SEQUENCES ENCODING THE SAME, NUCLEIC ACID PROPES, ANTI-VERSICAN ANTIBODIES, AND METHODS OF DETECTING THE SAME	6 6 6	
NUMBI CURRE APE	NUMBER OF SEQUENCES: 4 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/441,179 FITING NAME: 72-MAY-1890	y d	1403 VKSLITGP: ::    1123 IESETTSE
; SEQ ID NO:2; ; LENGT; 5180808-2	;SEQ_ID_NOILS: ;SEQ_ID_NOILS: ; LENGTH: 2409 5180808-2	DP 63	1462 TLHEAPKA(      174KK
Query Match Best Local Matches 42	y Match 2.2%; Score 275; DB 6; Length 2409; Local Similarity 20.0%; Pred. No. 2e-08; Indels 602; Gaps 100; hes 420; Conservative 259; Mismatches 823; Indels 602; Gaps 100;	Qy	1521 LTPTQRES           1223 ALVTES
Qy 604	TEEPPPPLPPPPEPISTEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAKWYGT 656 :	S &	1566 TQLDPAMP1  :  1281 TE
	KSEAQCKNFYFNYKRHNLDNLLQQHKQKTSRKPREERDVSQCESVASTVSAQEDEDI	Qy	1626 NLRPDVAR(   :1 :   1315 NRMENVAK)
Oy 715	EASNEEENPEDSEVE	QY	1686 ITFPPRPY       :  1357 PTVAPLPF
		Oy Db	1721  1414 FLARAYGF
824		Qy Dp	1773 SVFQGTNG:   ::  1469 STTFVSDG
963 863 628		δλ	1830 SAPQMDVS 
Qy 918 Db 688		Qy Dp	1879 QCLYTSSA) 1 1585 SDKNTIID:
978	GTSKSPNREW          GTRKSFMSLTTPTOSER	Oy Ob	1921 TRGKTTITI ::  . 1638 AAVNLSLT
1005		Qy	1971 -DAIEVISI :: : 1693 ETELDVLLI
1	QNSQPEGLLV ::    ::	Qy	2007 T-RQYEGP)   1:1 1753 TLGQFERT(
Oy 1125 Db 901	RAQHEGVVRGTAGAIQEGSITRGTPTSKISVESIPSLRGSITQGTPALPQTGIPT-EALV 1183 :	QY Dp	
Oy 1184 Db 935	KGSISRMPIEDSSPEKGREEAASKCHVIYEGKSGHILSYDNIKNAREGTRSPRT 1237 	Qy G	2094 RTKTSNRYS 1: 1868GSSVM
	•	δλ	2154 QVPVVHEK

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ISH------ISDSEGPSSTMVS---TSAFPWEEFTSSAEGSGEQLVTVS 1032
                                                                                                                   PRATTESFEDGLKYPKQIKRESPPIRAFEGA----ITKGKPYDGITTIKEMGR 1349
                                                                                                                                                         QDIL--TQESRKTPEVVQSTRPIIEGSISQG-----TPIKFDNNSGQSAIKHN 1402
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1909 TKLEPSEDDGKPELLEEMEASPTELIAVEGTEILQDFQNKTDGQVSGEAIKMFPTIKTPE 1968
                                                                                                                                                                                                  2025 PETQAALIRGODSTIAAS----EQOVAARILDSNDQATVNPVEFNTEVATPPFSLLETSN 2080
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                                                                                                 1969 AGT---VITTADEIELE-GATQWPHSTSASATYGVEAGVVPWLSPQTSERPTLSSSPEIN 2024
                                                                                                                                                      2249 S-----RGHSFADPASNLGLEDIIRKALMGSFD----DKVEDHGVVMSQPMGVVPGTA 2297
                                                                                                                                                                                                                                                                                                                                 GTERPSSVSSVHSEGDYHRQTPGWAWEDRPSSTGSTQFP-YNPLTMRMLSSTPPTPIACA 2404
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                                                                2199 ENTSPMVKSKKQEIFRKLNSSGGDSDMAAAQPGTE-----IFNLPAVTTSGSVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08459568
Patent No. 5811304
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.2%; Score 274.5; Best Local Similarity 18.0%; Pred. No. 1.3e Matches 365; Conservative 224; Mismatches
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REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1264
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/459,568
FILING DATE: 02-JUN-1995
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TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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: California
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STATE: Ca
COUNTRY:
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US-08-459-568-2
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---NODAVPOV 238
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Patent No. 5831008
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             562 EEREQATPRGRKTANSQGRRKGRITRSMTNEAAAASAAAAATEEPPPPLPPPPEPISTE 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    622 PVETSRWTEEEMEVAKKGLVEHGRNWAAIAKMVGTKSEAQCKNFYFNYKRRHNLDNLLQQ 681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NQOIARPSQEEKVEEKEEDKAEKTEKKEEEKKDEEEKDEKEDSKENTKEKDKIDGTAEET 561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1706;
                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/399,411
FILING DATE: 06-MAR-1995
E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.2%; Score 274.5; I
Best Local Similarity 18.0%; Pred. No. 1.3e-
Matches 365; Conservative 224; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LJ 1264
                                                                                                                                                                                                                                                                                                                                         FILING DATE: 06-MAR-1995
CLASSIFICATION: 530
ATORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 1706 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS LENGTH: 1706 amino ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                          STATE: California COUNTRY: USA
                                                                                                                                                                                                               COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                    : San Diego
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-399-411-2
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81;

g	554	SNISENLNYYIDGKIQTNSSTSNCDVIEMESNSAHLYGIDCLLTPVTVEITQ 605		
δ	1070	NQASYTQETPKPSVGSISLGLPRQQESAKSATLPYIKQEEFSPRSQNSQPEGLLVR 1125	δŏ	2054
QQ	909		අු ,	1339
δ	1126	AQHEGVVRGTAGAIQEGSIT	Š a	1395
e G	654		ò	2144
oy Db	1186	SISRMPIEDSSPEKGREEAASKGHVIYEGKSGHILSYDNIKNAREGTRSPRTAHEISLKR 1245     :     :     :     SISTAEVVSFHKEKGVYLSSKLKQLLQTQDKLTLPA 699	qq	1455
δ	1246	SYESVEGNIKQGMSMRESPVSAPLEGLICRALPRGSPHSDLKERTVLSGSIMQGTPRATT ::     :     :     :	Oy Dp	2194
a	200	GFSAAEVTS 725	ò	2253
ç q	1306	ESFEDGLKYPRQIKRESPPIRAFEGAITKGKPYDGITTIKEMGRSIHEIPRQDILTQESR 1365  :   :	g 6	1546
ογ	1366	KTPEVVQSTRPIIEGSISQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSRGMPPLEIVPE	QY	2313
e e	758	WTDTVLTSKKP KLESRSDSPAWSLSGRDERETGSPPC 794		
g g	1426 795	NIKVVERGKYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARR 1483 :::   :   :   :   :	RESULT US-08-5	ESULT 4 S-08-516 Sequenc
ογ	1484	TPVSYQNTMSRGSPMMNRTSDVTIPPNKSTNHERKST	 B	Patent GENERA APPL
q	826	KQKSEGTGKTPVPWESVLDL 845		TITL
P &	1541	1541 VVSHSPEDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPAAAXLEQRQLSPTPGYPSQ 1600		NUMB CORR
ογ	1601	YQLYAMENTRQTILNDYITSQQMQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPP 1660		SU
q	879	LQKVLLNEY-NGVSLPTETTPEVTRSPSPCKSPDTQPDFEL-GPDSSCSVPT 928		SS
ç, q	1661 929	TILVPHPGGTSTPPMDRITYIPGTQITFPPRPYNGASMSPGHPTHLAAAASAERERER 1718		COMP
9 6	1719 978	EREKERERERIAAASSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQETWLQQRPSVFGGT 1778		SO CURR
yo 4	1779	NGTSVITPLDPTAQLRIMPLPAGGP		FI CL PRIO
\ \delta \delta \ \delta \ \delta \ \delta \ \delta \ \delta \ \delta \ \delta \ \delta \ \delta \ \delta \ \delta \ \delta \ \delta \ \de	1821	-LAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEV		FI PRIO AP
δ .	1874			ATTO NA
Op	1120	-SKNFICNVCESPFLSIKDLTKHLSV		TELE
P Q	1934	DVIITRQIASDKDARERGSQSSDSSSLSSHRYETPSDAIEV 1975 ::::	н	TE TE INFORM
· λο	1976	ISPASSPAPPGEKLQTYQPEVVKANQAE		SEQU
q G	1230	-NVEHMPSLPEEPLETSREEELNDSSEELYTTIKIMASGIKTKDPDVRLGLNQHYPSFKP 1288		TO
Q.	2006	PTRQYEGPLHHYRPQQESPSPQQQLPPSSQAEGMGQVPRTHRLITLAD 2053	0-Sn	US-08-516

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HICQIITQDFARNQVSSQTPQQPPTSTFQNSPSALVSTPVRTKTSNRYSPESQAQSVHHQ 2113
                                              9 HILACASASDKKRYTPKKNP-VPLKQTVQPKNGVVV---LDNSGKNAFRRMGQPKRLSFN 1394
                                                                                                  4 RPGSRVSPENL------ 2143
                                                                                                                                           5 VELGKMSPNKLKLSALKKKNQLVQKAILQKNRAAKQKADLRDTSEASSHICPYCDREFTY 1454
                                                                                                                                                                                                       ....SEPYEPISPPQVPVVHEKQDSLLLLSQRGAEPAEQRNDARSPGSISYLPS 2193
                                                                                                                                                                                                                                      5 IGSLNKHAAFSCPKKPLSPSKRKVSHS-----SKKGGHASSSSSDRNS----- 1497
                                                                                                                                                                                                                                                                                                                4 FFTKLENTSPMVKSKKQEIFRKLNSSGGDSDMAAAQPGTEIFNLPAVTTSGSVSSRGH- 2252
                                                                                                                                                                                                                                                                                                                                                                                                                     3 SFADPASNLGLEDIIRKALMGSFDDKVEDHGVVMSQPMGVVPGTANTSVVTSGETRREEG 2312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----RNSSPIRMAKITHVEG 1577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------RKSKSPIPGQGYLGTER 2349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hungo, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
TOTHE OF SEQUENCE: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: A170 La Jolla Village Drive, Suite 700
STREET: San Diego.
STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CALLY: 9412.

CALT: 9412.

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COFFACING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Partentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/516,859A
FILING DATE: 18-AUG-1995
CLASSIFICATION NUMBER: US/08/399,411
FILING DATE: 06-MAR-1995
PRIOR APPLICATION NUMBER: US 08/399,411
FILING DATE: 18-AUG-1994
ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1776
TELEPHONE: (619) 535-901
TELEPHONE: (619) 535-901
TELEPHONE: (619) 535-901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KFAASVKS-----KKASSSSL-----
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: No. 6069231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 DPSPHSGGVCKPKLISKSNS----
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SNGTH: 1706 amino acids
FPE: amino acid
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845	1600 878	1660 928	1718 977	1778	1820 1066	1873	1933 1172	1975 1229	2005	2053	2113 1394	2143 1454	2193 1497	2252 1545	2312 1577	
:	1 VVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRALDPRAAAYLFORQLSPTPGYPSQ	1 YOLYAMENTRQTILLNDYITSQOMQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPP ::	1 TILVPHPGGTSTPPMDRITYIPGTQITFPPRPYNSASMSPGHPTHLAAAASAERERER	BERKERERERIAAASSDLYLRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFGGT	9 NGTSVITPLDPTAQLRIMPLPAGGPSISQGLPASRYNTAADASISQGLPASRYNTAADA	- LAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAVSEQQQLEQKTLEV	1 EKRSVQCLTTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELRTRGKTTITAANFI ::	1DVIITRQIASDKDARERGSGSSDSSSLSSHRYETPSDAIEV :::	6 ISPASSPAPPQEKLQTYQPEVVKANQAEND :  :  :   :   :   :   0 -NVEHMPSLPEEPLETSREEELNDSSEELYTTIKIMASGIKTKDPDVRLGLNOHYPSFKP	FOR THE PROPERTY PROPERTY PROPERTY PROPERTY PRINTED PROPERTY PROPE	4 HICQIITQDFARNQVSSQTPQQPPTSTFQNSPSALVSTPVRTKTSNRYSPESOAGSVHHQ	RPGSRVSPENLVDKSRGSRPGKSPERSHVS	1SEPYEPISPPQVPVVHEKQDSLLLLSQRGAEPAEQRNDARSPGSISYLPS	FFTKLENTSPMVKSKKQEIFRKLNSSGGGDSDMAAAQPGTEIFNLPAVTTSGSVSSRGH-	3 SFADPASNLGLEDIIKKALMGSFDDKVEDHGVVMSQPMGVVPGTANTSVVTSGETRREEG	3 DPSPHSGGVCKPKLISKSNS
826	1541	1601 879	1661 929	1719 978	1779	1821	1874	1934	1976 1230	2006	2054	2114	2144	2194	2253	2313
Db	O.Y Db	Q Dp	Qy	Qy Db	Qy Db	Qy	Qy Db	Oy Dp	Qy Db	Qy Db	Qy Dp	Qy Db	Qy Dp	Oy Dp	Qy Db	Qy

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1184 KGSISRMP--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 LPLVHPLPEGLRASADAKKDPAFGGKHEAPSSPISGQPCGDDQNASPSKLSKEELIQSMD 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 492 WELV------EKEADIEVKVENSSA------QKTQESGLDTEETQDSQG ·528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------PEPEKPVSPPPVE 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ::| | | :::|| | :::|
529 PLQKETLKALGEEPLMSLK---IQNYETAGKENCNSSTEGHLGTLEGPEKEKQIPLKSLE 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QKHRSIVQIIYDENRKKAEEAHKIFEGLGPKVELPLYNQPSDTKVYHENIKTNQVMRKKL 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             290 ILFFKRRNHARKQREQKICQRYDQLMEAWEKKVDRIENNPRRKAKESKTREYY----EKQ 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       392 PPISEAPCPPNA------EVRAQEVPLS----LLQTQAPEPLWLKATVPSSSAILPE 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              439 LEEPGGKQQGHFPDDLTSLATNLNPHHPTLEAKDGESSESR-----VSSIFQEDEGQI 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 PPHSVQYTFPNTRHQQEFAVPDYRSSHLEVSQASQLLQQQQQQLRRR---PS---LLSE 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.1%; Score 270.5; DB 1; Length 1805; Best Local Similarity 19.7%; Pred. No. 2.6e-08; Matches 308; Conservative 215; Mismatches 565; Indels 479;
                                    Nestin Expression As An Indicator of Neuroepithelial Tumors
                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                         ADDRESSEE: Hamilton, Brook, Smith & Reynolds, STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,762
FILING DATE: 02-70N-1988
FILING DATE: 02-70N-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/180,548
ATTORNEY/ABOTT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REGISTRATION NUMBER: 32,227
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/660,412
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,803
FILING DATE: 25-CCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 RVDREIAKV -- EQQILKLKKKQQQLEEEAAKP-
                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/853,913
FILING DATE: 19920319
                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
APPLICANT: MCKay, Ronald D.G. APPLICANT: Lendahl, Urban
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 1805 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-07-853-913-2
                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                               Lexington
Massachusetts
                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                    TITLE OF INVENTION:
                                                                                                                                                                                    COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POPOLOGY:
                                                                                                                                                                STATE:
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966 SQETF-GPLEKENAESLRSLAG--ODQEEQKLEQETQQTLRAVGNEQMAVSPPEKVDPEL 1022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1262 SMPEVTERDEDRAQAGEQDSIEVTLGLEAARTGLELEQEVVGLEDPRHFAREEAIPPSLG 1321
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624 TL--KRFSSLGKESQEVVRPSKEGNLESWTAFKEESQHPLGFPGAEDQMLERLVEKEDQS 681
                                                                                                                     346 FPEIRKQREQQ--ERFQRVGQRGAGLSATIARSEHEISEIIDGLSEQENNEKQMRQLSVI 403
                                                                                                                                                                                                FPRSPEEEDQEACRPLOKENQEPLGY-----EEAEGQILERLIEKESQE-----SLR 728
                                                                                                                                                                                                                                                                           404 PPMMFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNFGLIA 463
                                                                                                                                                                                                                                                                                                                                      464 SYLERKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEKVEEKEEDKAE 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             524 KTEKKEEEKKDEEEKD------EKEDSKENTKEKDKIDGTAEETEEREQATPRGRKTA 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    576 NSQGRRKGRITRSMTNEAAAASAAAAATEEPPPPLPPPPEP-----ISTEPVETSRW 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               629 TEEEMEVAKKGLVEHGRNWAAIA-----KMVGTKSEAQCKNFYFNYKRRHNLDNLLQQH 682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------PLKPNPLDLPQLQH--RAAVIPPMVS 942
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994 CGISKSPNREWEVLQPAPHQLITNLPEGVRLPTTRPTRPPPPL-IPSSKTTVASEKPSFI 1052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1282 PHSDLKERTVLSGSIMQGTPRATTESFEDGLKY-----PKQIKRESPPIRAFEGAITKG- 1335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1674 PMDRITYIPGTQITFPPRPYNSASMSPGHPTHLAAAASAERE-----REREREKERERER 1728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1113 RSQNSQPEGLLVRAQ--HEGVVRGTAGAIQEGSITRGTPTS-----KISVESIPSLRGS 1164
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                                                                                                                                          203 SRMFQAPPGAPPH---------PQLYPGGTGGVLSGPPMGPKGGGA 240
                                                                                                                                                                                                                                                                                                                                                             ----GASGAP-----PTKPPTTPVGGGNLPSAPPPANFPHVTPNLPPPALRPLNN 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               344 PGPEKGP-----TLAPSPHS------LPPASSSAPAPPWRFPYSSSSSAAAASSS 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389 SSSSSSSASP--FPASQALPSYPHSFPPPT----SLSVSNQPPKYTQPSLP--SQAVWSQ 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          497 QHHGNSGPPPPGAFPHPLEGGSSHHAHPYAMSPSLGSLRP-----YPPGPAHLPPPHS 549
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       EDEDIEASNEEENPEDSEVEAVKPSEDSPENATSR---GNTEPAVELEPTTETAPSTSPS 766
                                               143 NDSDSSSGLSQGPARPYHPPPLFPPSPQPPDSTPRQPEASFEPHPSVTPTGYHAPMEPPT 202
                                                                                                                                                                                                                                                                                                             883 CSADEDVDGEPERQRMFPMDSKPSLLNPTGSILVSSP-----LKPNPLDLPQLQ--HR 933
                                                                                                                                                                                                                                                                                                                                                                                                               934 AAVĮPPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEQRQRQRQEQIDLECRSSTSP 993
                                                                                                       ----LAVPSTKPAEDESVETQVNDSISAETAEQMDVDQQEHSAEEGSVCDPPPATKADSV
                                                                                                                                                                                                          823 DVEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSAT
                                                                                                                                                                                                                                                          ---GKOHPPPTTPISVSSS
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1577 ADHVGQVPPVLQPACWDQGGESDGFADEEESGEEGEEEDADEEGAESGAQWWGSGASGGG 1636
                                                       ----REGTRSPRTAHEISLKRS 1246
                                                                                                                                                       1247 YESVEGNIKQCMSMRESPVSAPLEGLICRALPRG--SPHSDLKERTVLSGSIMQGTPRAT 1304
                                                                                                                                                                                  GTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRKPREERDVSQ-----CESVASTVSAQ 709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Proapoptotic Peptides, Dependence TITLE OF INVENTION: Polypeptides and Methods of Use NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite
                                                     -----AASKGHVIYE--GKSGHILSYDNIKNA-
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23, Application US/09041886 Patent No. 6235872
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ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Carbryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECHONICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-8049
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bredesen, Dale E. APPLICANT: Rabizadeh, Sharro
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 297; Conserva
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US-09-041-886-23
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qq	976 PGPPGLH-PPPFHPSIGPLERPRIALAGEDER BENGGEREN SYRENGER 1036	q <sub>Q</sub>	434 DE
ô	IAAASSDLYLRPGSEOPGRPGSHGYVRSPSPSPSVPTOFTMI OODDSVTDGTMGT	Qy.	SE 696
		qa	479 ET
λo	SISOGLPASRYNTAADALAALWAAAAAAAAA	Qy	1017 NI
		qa	539 DI
νδ	KRSVOCLYTSSAFPSGKPOPHSS	Qy	1035 PI
		qa	599 LA
'n		Qy	1077 ET
		qa	659 RT
		QY	6011
RESUL US-09	RESULT 45 US-09-157-420-1	qa	719 TL
Seq:	Sequence 1, Application US/09157420 Patent No. 6180760	οy	1141 EG
GEN:	SRAL INFORMATION: PLICANT: TAKAI, YOShimi	qa	778 -S
; API	APPLICANT: NAKANISHI, Hiroyuki APPLICANT: MANDAI, Kenji	ò	1189 RM
; API	PLICANT: WADA, Manabu PLICANT: OBAISHI, Hiroshi	qq	832 HI
FI	TITLE OF INVENTION: ACTIN FILAMENT-BINDING PROTEIN "L-AFADIN" FILE REFERENCE: 98-1042*/LC(WMC)/653	QY	1244 KR
55	CURRENT APPLICATION NUMBER: US/09/157,420 CURRENT FILING DATE: 1998-09-21	qq	OI 688
SOL	NUMBER OF SEQ ID NOS: 1 SOFTWARE: PatentIn Ver. 2.0	Qy	1274 C-
SEO :	SEQ ID NO 1 LENGTH: 1829	qa	949 CD
£ 6	TYPE: PRT ORGANISM: rat	ογ	1315 PK
-60-SD	157-420-1	QQ	994 ES
Onez	2.08:	δλ	1375 RP
Best Lo	cal Similarity 18.7%; Pred. No. 1.9e-07; Edigua 365: Conservative 239: Mismatches 639: ThAble	qq	1019
â	EEEMEVAKKGI VEHGRNWAA TAK MVGTKSFA-OOKNIFVENVK BEHUTINNI TOOLKO 694	ΟY	1430 VE
. A	::::	QQ	1076 LS
à		Oy	1490 NT
. ද	: :: :   TLSKKEKKEKKEKEKEALROASDKEERPSOGDDSFUSTAAEVTSDAFF	qq	. 1108 TL
λč		QY	1537 GVI
ą	RROOKLEKRMOEERSSDGRPDSGGTLRIVADSLADVETILI.	qa	1166 GDI
<b>~</b>	-ETOVNDSISAETAEOMDVDOOEHSAEEGSVCNDD	ογ	1578 LD
, q	NPKDYCIARVMLPPGAQHSDERGAKEIILDDDECPLOI	qq	1226 YP
À		οy	1603 L-
. g	:	qq	1286 LR
Δ		οy	1641
ą	EVGTEKF	qq	1346 GP(
۸	PLDLPQLQHRAAVIPPMVSCTPCNIPIGTPVSGYALYQRHIKAMH	Οy	1693 YNS
•		qa	1400 AN

qq	434	DDNSIQLFGPGIQPHHCDLTNMDGVVTVTPRSMDAETYVDGQRIS 478
Oy	696	ESALLEEQRQRQEQIDLECRSSTSPCGTSKSPNREWEVLQPAPHQLIT 1016
qq	479	ETTMLQSGMRLQFGTSHVFKFVDPIQDHVLSKRSVDGGLMVKGPRHKPGAVQETTFELGG 538
Qy	1017	NLPEGVRLPTTRPTpp 1034
QQ	539	THE THE STALPASKSTITELDSDRVSSASSTAERGMYKPMIRLDQEQDYRRRESRIQDAAGPE 598
δŏ	1035	ISQGTPGT
qq	599	LMLPASIEFRESSEDSFLSAIINYINSTVHFKLSPTYVLYMACRYVLSSQHRPDISPTE 658
δy	1077	ETPKPSVGSISLGLPRQOESA1108
QQ	629	RTHKAIAVVNKMVSKMEGVIQEVDQVDQKQKNIAGALAFWMANASELLNFIKQDRDLSRI 718
οy	1109	EFSPRSQNSQPEGLLVRAQHEGVVRGTAGAIQ 1140
Q	719	TLDAQDVLAHLVQMAFKYLVHCLQSELNNYMPAFLDDPEENSLQRPKIDDVLHTLTGAM- 777
٥y	1141	GTPAL
qq	778	-SLLRRCRVNAALTIQLFSQLFHFINMWLFNRLVTDPDSGLCSHYWGAIIRQQLG 831
οy	1189	PIE
οg	832	HIEAWAEKQGLELAADCHLSRIVQATTLLIMDKYVPDDIPNINSTCFKLNSLQLQAL 888
Qy	1244	KRSYEPVSAPLEGLI 1273
QQ	889	LÄNYHCAPDEPFIPTDLIENVVAVAENTADELARSDGRDVQLEEDPDLQLPFLLPEDGYS 948
Óγ	1274	DLKERTVLSGSIMQGTPRATTESFEI
qa	949	CDVVRNIPNGLQEFLDPLCQRGFCRLVPHTRSPGTWTIYFE-GADY 993
Οy	1315	IRAFEGAITKGKPYDGITTIKEMGRSIHEIPRQDI
QQ	994	ESHIMRENTELTQPLKEDEVITVT 1018
QY	1375	RPIIEGSISQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSRCMPPLEIVPENIKV 1429
qq	1019	LKKQNGMGLSIVAAKGGAGDKLGIYVKSVVKGGAADVDGRLAAGDQLLSVDGRSLVG 1075
ōλ	1430	3KYEDVKAGETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPG
QQ	1076	
οy	1490	SDVTIPPNKSTNHERKSTLTPTQRESIPAKS
QQ	1108	TLINOPSPAMORISDRRGSGKPRPKSEGFELYNNSAQNGSPESPQMPWTEYSEPKKLP 1165
Qy	1537	GVDPVVSHSPFDPHHRGSTAGEVYWSHLPTQLDPAMPFHRA 1577
QQ	1166	GDDRLMKNRADHRSSPNVANQPPSPGGKSPYTSGTAAKITSVSTGNLCTEEQTPPPRPEA 1225
οy	1578	LDPAAAAYLSQXQ LSPTPGYPSQXQ 1602
QQ	1226	:::    PIPTQTYTREYFTFPASKSQDRMAPVQNQWPNYEEKPHMHTESDHASIAIQRVTRSQEE 1285
οy	1603	LYAMENTRQTILNDYITSQOMQVNLRPDVARGLSPREQ1640
Q	1286	
δλ	1641	YIPGTQITEPPR
qq	1346 (	GPGRWKTPAAVLPTPVAVSQPIRTDLPPPPPPPPAHYTSDFDGISMDLPLPPPP 1399
Οy	1693	#SPGHPTHLAAAASAERERERER!
qq	1400	ANOAAPOSAOVAAAERKKRERHORWYEKEKARIFERRER-KRERFERTAOMRT 1452

1736 LYLRPGSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQG 1777 	TNGTSVITPIDPTAQLRIMPLPAGGFSISQGLPASRYNTAA 1818 ::    ::    ::	DALAALVDAAASAPQMDVSKTKESKHEAARLEENLKSKSAAVSEQQQL 1866 	EOKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEACKDKGPPPKSRYEEELRTRGKTT 1926 	ITAANFIDVIITRQIASDKDARERGSQSSDSSSSLSSHRYETPSDAIEVISPA-SS 1981 	PAPPOEKLQTYQPEVVKANQAENDPTRQYEGPLHHYRPQOESPSPOQQLPPS 2033	SQAEGMGQVPRTHRLITLADHICQIITQDFARNOVSSQTPQQPPTSTFONSPSALVSTPV 2093	NLVDKSR 2129    :     NLTFRER 1799
5 LYLRPGSEQPGRPGSHGYVRSPSPS' 	TNGTSVITP ::    ::  KEELSSGDS-LSPDPWKRD	DALAALVDAAASAPQMDVSKTKESKHE		ITAANFIDVIITRQIA			2094 RIKTSNRYSPESQAQSVHHQRPGSRVSPENLVDKSR 2129 12   1   1   1   1   1   1   1   1   1
1736	1778 1507	1819	1867 1618	1927 1649	1982 1691	2034	2094
oy dg	Qy Dp	Oy Dp	Oy Dp	QQ OX	QY Dp	Qy Dp	Qy Db

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